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Polease 2 10 John F Callins, Biocomputing Posearch Unit Copyright (c) 1993, 1994, 1995, University of Ediaburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn MarPar time 54 64 Serverts 671.591 Million cell updates/sec Tae Fulk 24 29.18 02 1998,

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(1-318) from US08844215.seq 317 >US-08-844-215-21 Description: Perfect Score: ანაატიზიკ < Z

SSACCAAGSIBSAAA1CAAA 318 CCTGGTICCACCTITAGTIT

TABLE default Gap 6 Scoring table:

159651 seqs, 57698962 bases x 2 Searched:

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Minimum Match 0% Listing first 45 summaries Post-processing:

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Variance 4.872; scale 1.649 Mean 8.035; Statistics Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

	Pred. No.	2,106-160	3 100-160	9.348-157	4 346-157	1 390-152	3.410-151	3 410-151	4.15e·149	4.15e-149	4 150.149	1 026-147	1 236-145	6.10e-145	3.020-144	7.37e-143
	Description	per acisserqxe FdmeSq	Expression vector, pP	pc?AP?13 anti-tetanus	Anti-tetanus texeid 1	F105 rearranged varia	Anti-pseudomonas aeru	Anti-P aeruginosa st	Human DNA fragment vk	Human V kappa gene vk	DNA fragment vk65 8	F105Vk-F105Jk	# P P P P P P P P P P P P P P P P P P P	Gene for Ly region of	Ulcerative colitis as	Light chain of Amb al
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ALIGNMENTS

This sequence represents the prompt authority of the sequence represents the prompt page in a sequence represents the prompt page in a sequence represents the prompt of the sequences of the seq pcomb3: phagemid expression vector; bacteriophage; coat protein 3: Gene III; filamentous phage; minor phage coat protein; cplit; cp3: bacterial membrane; petipisan, E. coil, human, Pab, HIV, 49120: combinatorial Pab library; cassette; Fd/cp1 lazz promoter/operatori ribosome binding site, RBS, PeiB leader, spacer; tether sequence; MT4, pMT4-3, antibody, ss, cyclic. immunodeficiency virus - used for diagnosis and immuno:therapy of Barbas CF, Burton DR, Lerner RA; WPI; 95-170235/22. Synthetic human neutralising monoclonal antibodies to human Example 1; Page 185-188, 249pp, English. Q92546 standard; DNA; 4591 BP. 11-MAR-1996 (first entry) pComb3 expression vector (SCRI) SCRIPPS RES INST. 26-APR-1994; US-233619. 19-SEP-1994; US-308841. 10-001-1003; US-130400 HIV-induced disease 27-APR-1995. 19-0CT-1994: ml1907 W09511317-A1. Synthetic. RESULT

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sequences, a NotI restriction site, a ribosome binding site (RBS), a page B leader, a spacer region, a cloning region bordered by 5 XhOI and 3' SpeI restriction sites the tether sequence, the sequences encoding bacteriophage cp3 followed by a stop codon, a NheI restriction site between the two cassettes, and a second lac2 promoter/operator sequence, followed by an expression control RBS, a PelB leader, a spacer region, a cloning region bordered by 5' SacI and 3' XbaI restriction sites, followed by expression control stop sequences and a second NotI estriction site. The pocom3 expression vector iorns the basic construct of the MT4 Fab display phagemid expression vector; pMT4-3 (see also 092540), used in the invention for the production of synthetic human Fab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2: Page 193-197; 249pp; English.

This sequence represents the expression vector, pPho-TT which is a modified version of the phagemid expression vector, pComb3 given in 992546 ppho-TT provides for the expression of soluble Pabs which are secreted into the periplasmic space which is regulated from the alkaline phosphatase (phoA) promoter. This plasmid was used within the scope of the invention to express various mutagenised human Fab's which comprise heavy and light variable regions which bind to HIV gpl20. ppho-TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2674 geogageteacgeagtetecaggeaceetgtetttgtetecaggggaaagageeaceete 2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2734 teetgeagggeeagteacagtqttageagggeetaettageetggtaeeageagaaaeet 2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2794 ggccaggeteccaggetecteatetatggtacatecageagggeeaetggeateecagae 2853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2854 aggittoaqitggcagitgggitcigggacagacittoacitticaccoatoagcagaciggagcoi 2913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2914 gaagaittitgeagigtactacigteageagiatggggggetoaccgiggtieggceaaggg 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCCIGCAGGGCCAGTCAGAGTCTTAGCAGCAAATACTTAGCNTGGTACCAACAGAAACCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GGCCAGGCTCCCAGGCTCTTCATTATGATGCATCCAGCAGGGGCCACTGGCATCCCAGAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AGGITCAGIGGCAGIGGGICIGGGACAGAGITCACICICAGCAICAGCAGAAITIGGAGCCI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression vector, pPho-TT. Human red; variable chain, heavy, light, region, VH, VL, HIV, gpl20, Human; Fab; variable chain, heavy, light, region, VH, VL, HIV, gpl20, 3bl; 3b3; 3b4; 3b9; MI4; humanised; monoclonal antibody; MAb; immunoreaction; neutralisation; passive immunotherapy; tetanus toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCCGAGGTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCACCCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                       1118 T;
                                                                                                                                                                                                                                                                                                                                                                                                         o,
                                                                                                                                                                                                                                                                                                                                               Match 83.0%; Score 263; DB 16; Length 4691; Local Similarity 91 2%; Pred No. 4 10e-160; es 290; Conservative 0; Mismatches 28; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic human neutralising monoclonal antibodies to human
                                                                                                                                                                                                                                                                                                       1232 G;
                                                                                                                                                                                                                                                                                                       1171 C;
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                                                                                                                                                                                                                                                                             antibodies against gp120 of HIV. Sequence 4691 BP; 1170 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            092547 standard; DNA; 6166 BP.
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(SCRI ) SCRIPPS RES INST.
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WPI: 95-170235/22
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consists of a DNA molecule having two cassettes to express two soluble proteins a heavy chain and a light chain. The vector comprises operatively linked 5' to 3', a first cassette consisting of the phoad promoter/operator sequences, an ECORI restriction site, a ribosome binding site (RBS), an OmpA leader, a Sfil restriction site, a spacer region, a coloning region bordered by 5' saci and 3' XBal restriction second cassette consisting of an expression control RBS, a PelB leader, a human consensus amino terminus spacer region comprising the sequence EVULLE, a cloning region bordered by 5' XMOI and 3' Spel restriction sites followed by a Sfil site, expression control RBS, a PelB leader, a human consensus amino terminus spacer region control stop sequences and a Noti restriction site. The PPho-TT expression vector contains a light chain stuffer that is 1200 bp in length and a heavy chain stuffer that is 300 bp in length. The nucleocitide sequences of the heavy and light chain variable domains of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4604 gecgageteaegeagtetecaggeaeetgtetttgtetecagggggaaagageeeeete 4663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4784 aggiticagiggcagigggicigggacagaciticanicitrancatragcaganiggagnoi 4843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4844 gaagaittiigsagigtantaniginagnagiaiggiggninanngiggitngginnaaggg 4403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4564 teetgeagggeeagteacagtgttageagggeetaertageetggtaenagnagaaannt 4723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4724 ggocaggetoccaggetecteatetatggtacatecageagggeeactggeateceagae 4783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain gene CDR - useful for prodn. of Ig heavy and light chain combinatorial antibody libraries.

Example 1; Page 84: 125pp. English.

T1520 and T15203 are the heavy and light chain variable domains of a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a Pcomb3 based expression vector. The heavy and light chain variable domains are used in an example to demonstrate the prodn. of antibodies for an antibody library using mutagenic primers. Mutagenic primers of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCCTGCAGGGCGGGTGAGAGTCTTAGGAAAAAATAGTTAGGNTGGTAGTAAAAAGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC3AP313 anti-teranus toxoid Iq light chain variable domain cDNA. Mutagenesis; Ig; immunoglobulin; FR; framework region; variable: CDR; complementarity determining region; light; heavy chain: PCR; polymerase chain reaction; antibody library; diversity: affinity: immunospecificity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GEGGAGETCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1629 G; 1415 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.0%; Score 263; DB 16; Length 5166; 91.2%; Pred. No. 3.10e-160; vative 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                          1706 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burton DR, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                     tetanus toxin-specific Fab.
Sequence 6166 BP; 1416 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T15203 standard; cDNA; 646 BF.
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02-SEP-1994; US-300386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 290; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barbas CF, Burton
WPI; 96-171625/17
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oligo-nucleotides - used as PCR primers for producing increased diversity antibody libraries, for screening antigens claim 21: page 84-85: 120pp: English.

This sequence represents the light chain coding sequence derived from the surface display phagemid expression vector, pC3AP313. pC3AP313 contains the bacteriophage gene II and heavy and light chain variable domain sequences for encoding human hab antibodies against retains toxin This sequence was pref used in the method of the invention for the production of antibody libraries containing increased diversity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Anti-tetanus toxoid light chain cDNA from vector, pC3AP313.
Polymerase Chain reaction, primer; mutagenesis: PCR: amplify;
diversity; antibody; complementarity determining region; CDR:
framework: constant: light; heavy; phage; immunoglobulin; library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences given in 070480.86 are primers which were used for inducing mutagenesis in 1 mp.lementary determining region (508) of an immunoglobulin infinity and gene primers contain a 3' terminus capable of hybridising to a first framework region, a 5' terminus capable of hybridising to a second framework region and a nucleotide sequence between the 5' and 3' termini having the formula (NK)n, where n is 3-24. These primers may be used to produce antibody libraries with increased artibody directify by inducing matagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 tgcagggrcaqtcacagtgttagcagggcctacttagcctggtaccagcagaaacctggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 CAGGCTGCCAGGCTCTTCATTTATGATGCATCGAGGGCCACTGGCATGCCAGACAGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 tecagitgacaaigggietgggaacagaeticaeteteaeeaicageagaetggageetgaa 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 TGCAGGGGCAGTCAGAGTCTTAGCAGCAAATACTTAGCNTGGIACCAACAGAAGCTGGC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12) caddoteccaggotectcairiaigdaaaideaggaaqdaagaaggaecacidgcaicecagacagg 180
invention have sequences at their 3' and 5' ends both capable of binding different framework regions linked by a sequence 6 to 50 nucleotides long offerent immunoglobulins produced using the primers may be used to produce antibody libraries having diverse and
                                                                                                                                                               novel immunospecificities and affinities. By using mutagenic ONS an extremely large population of different randomised binding sites can be created and use of the universal light rhain increases the number of combinations which jield functional heterodimeric antibodies. Sequence 646 RP; 162 A; 187 C; 170 G; 127 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gageteaegeagtetecaggeaecetatettigtetecaggggaaagageaecetetee 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 258; DB 22; Length 646
Pred No 9 346-157;
0; Mismatches 29; Indels
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02-FEB-1993; 05-012556.
02-BEC-1993; 05-174674.
(SCRI ) SCRIPPS RES INST.
Barbas CF. Burton DR, Lerner RA;
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90 88;
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nes 286, Conservative
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        88888888888
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01-NOV-1993 (first entry)
F105 rearranged variable region light chain.
Monoclonal antibody: MAb: envelope: glycoprotein: gp120: HIV: AIDS:
CD4: receptor: hybridoma: polymerase chain reaction; PCR: heavy: light:
              are displayed on the surface of filamentous phage particles comprising the library. These primers pref. mutate the light chain CLR3.
Sequence: 646 RP; 162 A; 187 C; 179 S; 127 T;
                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                     : 83
                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                              5 4 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GATITIGGAGIGIATIACTGICA-STAGGAACA-CITCSCA-CITICS-CAGGAGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subjected to PIV amplification using primers corresp. to appropriate parts of the heavy or light chains and having restriction sites to perts of the heavy or light chains and having restriction sites to pertin cloning. The extension prods were isolated and separated. The recombinant human monoclonal and move (MAD) binds to a discontinuous opitope, in the HV 49226 eventuals, and neutralises a broad range of HIV isolates. The MAD may be used to treat immure deficiency, esp. at doses of 2.1-10 mg/kg.
                                                                                                                                                                         within the CDF regions of immnuoglobulins heavy or light chains that
                                                                                                                                      Gaps
                                                                                                                                                                                                              61 igcagggccagicacagigtiagcagggcciacitagrntggiarcagnagaaanciggr
                                                                                                                                                                                                                                                                                                                                121 caggeteceaggetecteatetatagtacatecageagggeeactggeateceagaeagg
                                                                                                                                                                                                                                                                                                                                                                     124 CAGGCTCCCAGGCTCTTCATTTATGATGCAGCAGGCCAGTGGCATGCCAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                           tecagigacagigagicigagacagacticacicicaccaicagcagacigaagmeidaa
                                                                                                                                                                                                                                                                                                                                                                                                                                      184 TICAGIGGCAGIGGGICIGGGACAGACITCACICICAGCAICAGCAGAIIGGAGCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 gattitigcagigiactacigicagcagiatggiggeicacegiggiteogecaagggee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Segments encoding monoclonal antibody - which binds to ap120 and neutralises HIV. for treating AIDS, and for diagnosing and monitoring HIV infection amonitoring HIV infection amonitoring HIV infection amonitoring HIV infection are selected to converted to converted to converted to this mRNA from the known hybridgma FIOS was converted to conver
                                                                                                                                    0; Mismatches 29; Indels
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                                                                                           Score 258; DB 12; I
Pred No 9.34c-157;
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Haseltine WA, Marasco WA, Posner MP, Sodro
WPI; 93-214174/26.
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Similarity 90 98; Prod
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Q49155 standard; cDNA; 387 BP.
                                                                                                                                    286; Conservative
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24-JUN-1993.
10-DEC-1992; UIC928.
10-DEC-1991; US-80465
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TP 7, 1004 14 197

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Query Match

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1011 BP;
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19-FEB-1988; 035395
                                                           Rest Local Similarity
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J01211498-A
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It also codes for a variable region recognising Fs.aeruginosa F4 and H1 types. The Ab can be used for immunologic control of infection caused by Ps.aeruginosa. The antibody is made effective against various classes or
                                   73 acgoagtetecaggcaecetgtetttgtetgcaggggaaagagccaeceteteetgcagg 132
                                                                                                                                                                                          190 GGCAGTGGGTCTGGGACAGACTTCACTCTCAGCATCAGCAGATTGGAGCCTGAAGATTT 249
                                                                                                                                                                                                                         313 gcagtgtattactgtcagcaatatgataactccgtttgtacttttggccaggggaccaag 372
                                                                                  gccagtcagagtgttagcaggcaggtacttagcctggtaccagcagaaacctggccaggct 192
                                                                                               193 occaggotecteatetatggtgeatecageagggeeactggeateceagaeaggtteagt 252
                                                                                                                                                     130 CCCAGGCTCTTCATTTATGATGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGT 189
                                                                                                                                                                              253 ggcagtgggtctgggacagacttcactctcaccatcagcagaqtggagcctgaagatttt 312
                                                                                                                                                                                                                                               250 GCAGTGTATTACTGTCAGCAGTATGG-AACACC--TCGCACCTTCGGCCAGGGGACCAAG 306
                                                10 ACGCAGTCTCCAGCCACCCTGTTTGTCTCTCAGGGAAAGAGCAGCCACTCTCTGTAGAGG 69
            3; Gaps
                                                                                                                                                                                                                                                                                                                                                                           Anti-pseudomonas aeruginosa human type antibody L-chain coding DNA contg. constant region of kappa and lambda types Pseudomonas aeruginosa F4: Pseudomonas aeruginosa H1;
Pred. No. 1.39e-152;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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N81537 standard; DNA; 1011 BP.
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 Best Local Similarity 92.6%;
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             Conservative
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                                                                                                                                                                                                                                                                                             307 GTGGAAATCAAA 318
                                                                                                                                                                                                                                                                       373 ctggagatcaaa 384
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/note="Claimed SQ"
                                                                                                                                                                                                                                                                                                                                                                                                                 immunotherapy; ss.
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/note="P81245"
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                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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/note="V"
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             Matches
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subclasses of resistant Ps aeruginosa by recombining corresp DNA 1-chain contg. versatile_coding_region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584 acgcagtetecaggeaecetgtetttgtetteaggggggaagageeaeceteteetgeagg 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 gonnagthagagtgittaghaanaattheettageniggtannaanagaaanetiggenagget 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 acgcagiciccaggcacccigicitigicicccaggggaaagaccacciciccigcagg 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 gecagteagagtgttageageaatteettageetggtaeeaacagaaacetggeeagget 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 CCCAGGCTCTTCATTTATGATGCATCCAGCAGGGCCAACTGGCATCCCAAGAGATTTAGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 ggcagtgggtctgggggcagacttcactctcaccatcagtagactggaacctgaagattct 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      824 gcagtgtattactgtcagcagtacgacgccctgatcacttccggcgagggaccaagttg 883
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Fred. No. 3.41e-151,
0; Mismatches 30; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 ACGCAGTCTCCAGGCACCCTGTTTGTCTCCAGGGAAAGAGCCACCTCTGTGTGTAGAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 ACCOMPANION CONTROL OF THE CONTROL OF ACCOMPANION OF ACCOMPANION OF THE CONTROL OF THE CONTRO
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-1990 (first entry)
Anti-P. aeruginosa strain F4 light chain V and J coding regions
Immunoglobulin.
                                                                                                                                                                                                                                                                         Length 1011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                           257 T;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 30;
                                                                                                                                                                                                                                                                   ), DB 2; L
3.41e-151;
                                                                                                                                           254 G;
                                                                                                                                                                                                                                                                   ch 78.9%; Score 250; 1 Similarity 90.3%; Prod No. 3 279; Conservative 0; Mismatu
                                                                                                                                           263 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N91359 standard; DNA; 1011 BP
                                                                                                                                           237 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.3%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1988; JP-035395.
(WAKU) Wakumaga Seiyaku KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325..372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          560..895
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824 gragigiaitacigicagoagiacgacocigaicacittcggoggaggacoaagtig 883
             70 GUCAGICASAGICIIASCAGCAAAIACIIAAGUNIGGIACCAAAAAAAAAGIIAGGGGASGAAAA
                                             704 pocadactestsatetatgestagsgsesaggssagsgseastggeateesagaeaggsteagt 763
                                                                           130 dojasaticiicaliialaadalocaacasaacasacacioscalocoasacasagaicasi 189
                                                                                                          764 yacaatagatotggggaagaottcactotoachaatagaatgaaartggaarntgaagattot 82%
                                                                                                                                                                                                   250 GCASTSTATTACTSTCASCASTATSGAACACCTCSCACCTTCSSCCASSGACCAASGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The V-Kappa specific offgonordecide 050327 was used to probe a human placental genomic DNA library cloned into lambdeEMBL3/SP6/T7. DNA fraqments containing V-mappa segments from positive phage clones were subclaned into plasmid vectors. Variable gene segments from the resulting clones were sequenced and functional clones were selected on the basis of open reading frames, intert donor and acceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were designated p65.3, p65.5, p65.8 and p65.15 (see Q44122.34425).
ransgenic non-human animals contq. immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                                                                          10-Nuv-1954 (first entry)

Human DNA fragment vk65.8 containing V-kappa gene segment.

Humanoglobulin: light chain variable region; minilocus;

isotype switching; unrearranged functional Vk gene segment;

human light chain transgene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trans gene · used to produce useful antibodies by isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //tag= e
/note= splicing and recombination signal sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiation codon, i.e. the start of the ORF; the precise start point of the ore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "splicing and recombination signal ?"
exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "ORF not terminated by a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 21; Fig 43; 195pp; English.
                                                                                                                                                                                                                                                                                                                              044224 standard; DNA; 900 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352..650
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Kay RM, Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165..351
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                                                                                                                                                                                                                                                                310 GAAATCAAA 318
                                                                                                                                                                                                                                    884 gacatcaaa 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAP-1992:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_siqnal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 - JUN - 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7-pPC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number= 1
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                                                                                                                                                                                                                                                                                                                                                044224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 GGGAGTGGGTGTGGGAGAGAGTTGAGTTGTGAGCATCAGGAGATTGGAGGTGTGAAGTTTT 249
                                                                                                                            375 angqaattotooaqasannootgtotttatstoonaaaqaaaaaaaacsoosessitottasaaa 434
                                                                                                                                                                                                                                                 435 godagidagagigitagoagoagoagotacitagoolygiaoosagoagaaaoolyggooaqqol 494
                                                                                                                                                                                       10 ACGCAGIGIGGAGGGAGGIGIGIIIIAIGIGGAGGGAAAAAAAGCACGTCICCIGCAGG
                                                                    Gaps (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig. 43: 296pp; English.

Human DNA fragments vk65.3, vk65.8 and vk65.15 (given in Human DNA fragments vk65.3, vk65.8 uk65.8 and vk55.15 (given in Human DNA fragments vk685.3, vk65.8 uk65.8 uk65.8 uk685.8 uk685
                                                                                                                                                                                                                                                                                                               70 GCCAGTCAGAGTGTTAGCAGCAAAIAGTTAGCNTGGTAGCAAGAGAAAAAGTGGGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                     130 CCCAGGCTCTTCATTTATGATGCATCCAGCAGGCCACTGGCATCCCAGACAGGTTCAGT
                                                                                                                                                                                                                                                                                                                                                                              495 choaggotootoatotaiggigoatopagggooatggooriggonatophaganaganitoagi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies – for binding a pre-determined human antiqen with increased affinity % \left( \frac{1}{2}\right) =0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.9%; Score 247; DB 12; Length 900; of 2%; Prod No. 4.15c-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic mouse, transgenic animal; antibody engineering; variable region; light chain; minilocus transgene; chimeric antibody; ss.
   المدوعية عمرا:
                                                                 Indels
Score 247: DR 7: 14
Pred. No. 4.15e-149;
                                                                 Mismatches 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 gcagtgtattactgtcagcagtatgg 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 GCAGIGTATIACTGICAGCAGTATGG 275
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Overy Match
Best Local Similarity 96.2%;
Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995 (first entry)
Human V-kappa gene vk65.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENP-) GENPHARM INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 350
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03-DEC-1993; US-161739.
10-DEC-1993; US-165699.
09-MAR-1994; US-209741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Splicing_signal
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2-JUL-1993: US-096762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APP-1994; U045AO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best (ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94-358263/44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09425585-A.
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/label= F105Vk
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/*tag= f
/label= CDR2
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/]abe]= cpR3
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mat_protein
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                                                                          435 gccagtcagagtgttagcagcagctacttagcctggtaccagcagaaacctggccaggct 494
                                                                                                  70 GCCAGTCAGAGTCTTAGCAGCAAATACTTAGCNTGGTACCAAAGAGAAACCTGGCCAGGCT 129
                                                                                                                                                                            555 ggcagtgggtctgggacagacttcactctcaccatcagcagactggagcctgaagatttt 614
                                                                                                                                                                                                    190 GGCASIGGGICIGGGACASACIICACICICAGCAICAGCAGAIIGGAGCCIGAAGAIITI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 acgcagiciccaggcacccigicitigicicaggggaaagagccaccciccigcagg 434
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                                                  10 ACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 ACGCAGTCT-CLANGCAUCCTGTCTTTGTCTCCAGGGAAAGAGCACCCTGTCTGCTGCAGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0. Mismatches 10. Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                            14-APR-1997 (first entry)
DNA fragment vk65.8, containing variable kappa chain gene.
Variable: kappa chain; gene segment; human; DNA fragment; vk65.8;
unrearranged; light chain; miniloous; transgene; transgenic; mouse;
production; heterologous; antibody; gamma; immunoglobulin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             day mouse embryo pronuclei, to generate an unrearranged light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    minilocus transque. The resulting transquence man be used for the production of heterologous (i e human) antibodies against preselected antiques, this comprises immunishing a mouse with a preselected antique and collecting antique binding heterologous human gamma immunoglobulins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the variable kappa chain gene segment containing human DNA fragment, vk65 8, which was co-injected along with the human DNA fragments vk65.3, vk65.5 and vk65.15 into half
                                                                                                                             495 occaggotoctcatotatggtgcatccagcagggccactggcatcccagacaggttcagt
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of heterologous human immunoglobulin(s) - by immunising
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 247; DB 27; I
Pred No. 4 15e-149;
 0; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 C;
                                                                                                                                                                                                                             615 gcagtgtattactgtcagcagtatgg 640
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                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic mice
Example 21; Fig 43; 94pp; English.
                                                                                                                                                                                                                                                                                                     T37182 standard; DNA; 900 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 A;
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 256; Conservative
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; US-810279.
; US-853408.
; US-904068.
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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17-DEC-1991;
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16-DEC-1992;
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                                                                                                                                                                                                           73. adgeagtetecaggeacettgt-etttgt.tt.vaggggaaaagag.var-etriteitetgeag
                                                                                                                130 COCASSOTOTTCATTATGATGCATCCAGCAGGCCACTGGCATGCCAGACAGGCTTCAGT 189
                                                                                                                                                                                  ggcagtgggtctgggacagacttcactctcaccatcagcagactggagcctgaagatttt 614
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The nucleoride sequence of F105 VK (Q42707 - sequence differs from other F105 VK sequences given elsewhere in the specification) was compared with germline gene HumvK325 (Q42706), showing 97.78 similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the VK III subgroup gene family.

Sequence 390 BP; 86 A; 115 C; 102 G; 87 T;
70 GCCASICAGAGIULTAGCAGCAAAIAUTIAGUNIGGIAUDAAGAGAAAAUTUTAGCA
                                                              cocaggotecteatetaggtgcatecageagggeeactggeateceagaeaggtteagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA segments enceding monoclonal antibody - which birds to 9p120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sodroski JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77,3%; Score 245; DR 7; L/
95,9%; Pred. No 1 02e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DAND) DANA FARRER CANCER INST INC
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL COPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marasco WA, Posner MR,
                                                                                                                                                                                                                                                                                                   615 gcagtgtattactgtcagcagtatgg 640
                                                                                                                                                                                                                                                                                                                                                            250 GCAGIGIATIACIGICAGCAGIAIGG 275
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Best Local Similarity 95 9%, pred
Matches 255; Conservative 0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q42707 standard; DNA; 390 BP Q42707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352..390
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10-DEC-1991; US-804652.
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WPI; 93-214174/26.
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vk325-Jk2.

Monoclonal antibody; MAb; envelope; qlycoprotein; qp120; HIV; AIDS;
CD4: receptor; hybridoma; polymorase chain reaction, FCR; heavy; light, chain; epitope; immune deficiency; ss.
193 occaggetecteatetatggtgeateeaggggeeactggeateeeagacteagt 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA segments encoding monoclonal antibody - which binds to gpl20 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
Discipling HIV infection
Discipling HIV infection
The nucleotide Sequence of F105 Vk (Q42707 - sequence differs from other F105 Vk sequences of F105 Vk (Q42707 - sequence differs from other F105 Vk sequences given elsewhere in the specification) was sompared with germline gene Humk325 (Q42705), showing 97 7% similarity. By uncleotide sequence analysis, F105 appears to be derived from a member of the Vk III subgroup gene family.

Sequence 390 BP, 88 A: 115 C, 99 G, 88 I;
                                                                                   130 CCCASSCICTICALITAISATSCALCCASCASCACISSCALCCASACAGGIICASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 76.3%; Score 242, DB 7; Leugth 390, Best Local Similarity 95.5%; Pred. No. 1.23e-145; Matches 253; Conservative 0; Mismatches 12, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sodroski 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DAND) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
Haseltine WA. Marason WA. Posner MP. Sodro
                                                                                                                                                                         313 gcagtgtattactytcagcagtatgg 338
                                                                                                                                                                                                   250 GCAGIGIATTACTGICAGCAGIAIGG 275
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                               r 12
042705 standard: DNA: 390 BP.
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10-DEC-1991; US-8046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- vk325
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/label= CDR1
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/label= Jk2
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                                                                                                                                                                                                                                                                           042706;
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0; Gaps

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253 ggcagtgggtctgggacagacttcactctcachofcagragagtggaagcctgabdatttt 312
                                                                                                                                                                    190 GGCAGTGGGGTGTGGGACAGACTTCACTCTCAGCATCAGCAGCATTGGAGCCTGAAGATTTT 249
                                                                                                130 cecassererrearriargargearceaseasseceacresearceeasacaserrease 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49. acgeagtetecaggeaechtgtetttgtetecaggagaaaaageaecethten acaag 108
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133 gecagteagagigitageageagetaettageeiggiaegaagaaaaeeiggeeagaa
                                70 GCCASTUAGACTITAGGAGGAAATAGITAGGNIGSTAGGAAGGAAAGGIGGGGAGGGT 129
                                                                     cocaggeterfeatetatggtgeatecageaggggeeetageateeeagaeeteetfeagt 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 GCCAGICCAGAGICIIASCASTAATIAGINIGGIATIAAAATIAGAAATIIGGITAGGCI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal human rheumatoid factor - obtd by prodn, and secretion of hybridoma obtd. from cell fusion of human bone marrow derived lymphocyte and P301 mouse myeloma cell bisclosure; Page 5; 7pp; Japanese.

The sequence shown encodes the variable region of the light chain of a human monoclonal antibody theumatoid factor YESG. The gene may be isolated from the bone marrow soln, of a rheumatoid arthritis patient and used to produce hybridomas, allowing prodn. of the rheumatoid arthritis factor at constant quality in large quantities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 76.0%; Score 241; DB 5; Length 324; Local Similarity 95 1%; Pred No 6 10e-145; nes 253; Conservative 0, Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                      18-MAR-1993 (first entry)
Gene for Lv region of human rheumatoid factor antibody.
Light chain; variable region, YES8C; arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 C;
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                      313 gcagtgtattactgtcagcaatatg 337
                                                                                                                                                                                                                                    250 GCAGIGIAITACIGICAGCAGIAIG 274
                                                                                                                                                                                                                                                                                      T 13
Q29766 standard; cDNA; 324 BP.
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(NISR ) NISSUI PHARM CO LID.
WPI; 92-368404/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                        25..288
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22-PEB-1991; 048704.
22-FEB-1991; JP-048704.
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"encodes CDR1"
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/note= "encodes CDR3"
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/note= "encodes CDR2"
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130 CCCAGGCTC11CAI111AIGA1GCAIGCAGGGGGGCTGGGATGGCAGAGAGAGGGTTCAGT 189
                                                                                                                                                                                                                                                                                                                                                                                      Ulcerative colitis-associáted pANCA Fab 5-4 light chain cDNA.
Ulcerative colitis; anti-neutrophil cytoplasmic antibody; ANCA;
PANCA; UCPANCA; antibody engineering; phage display; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //rocte= "complementarity determining region 3"
nisc PNA
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nisc_RNA
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//abel- WKSEGMENT
/note- "kappa light chain variable segment"
'-- bwa
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/label= CK
/note= "kappa light chain constant segment"
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/label- jk
/note- "kappa light chain joining segment"
---- RNA 328..645
                                                                                                                                                       289 gcagtgtattactgtcagcagtatgg 314
                                                                                                                                                                                250 GCAGTGTATTACTGTCAGCAGTATGG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                            T44091 standard; cDNA; 645 BP.
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/note= "framework_region 1"
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nisc_RNA 255 294
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nisc_RNA 148..168
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                                                                                                                                                                                                                                                                                                                                                             27-FEB-1997 (first entry)
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/label= CDR2
/note= "complementarity d
169..264
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06-JUN-1995; US-472688.
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/label* CDR1
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(CEDA-) CEDARS SINAI MEDICAL CENT

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181 aggiticaciggcagigggicigggacagactinacininannainanaganiggagnni 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood samples were collected from patients immunised with allergens including ragweed (Ambrosia elator) extracts. The dominant allergen in short ragweed is Amb a 1. Purified PBLs were immortalised and
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                            Antibody material associated with ulcerative colitis - comprising antineutrophil staining patter antibody, characterised by perinuclear neutrophil staining patter and the staining patter and staining pattern (panch and sociated with clearative colitis (UC) was recombinantly produced and characterised using a phage display technique. Libraries of VH-and VL-encoding DNA homologues having the immunoreactivity of UCPANCA antigen were created. Recombinant UCPANCA Fab clones 5-3
                                                                                                                                                                                                                                                                          and 5-4 were generated (see also W07613-16). These can be used in methods for screening for UCpANCA and for isolating UCpANCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contg. allergen specific IgA for treating mucosal tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Light chain of Amb al-specific 1gG4 antibody.
Allergen-specific immuoglobulin A; 1gA; AL 15-5.2; light chain: allergen Amb a 1; ragweed; Ambrosia elator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                    0

    and conjugates of allergen specific is with polymer, for
treating IgE mediated allergies and for isolation of specific

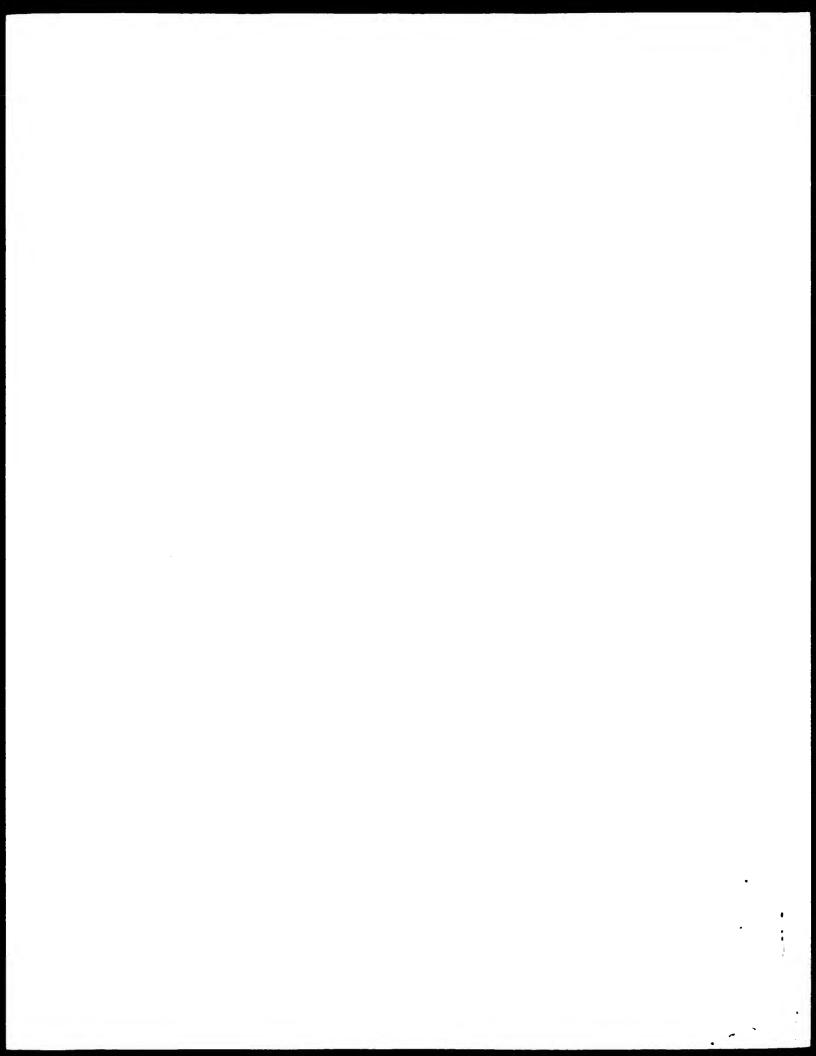
                                                                                                                                                                                                                                                                                                                                                            / Match
Local Similarity 93.5%; Pred. No. 3.02e-144;
les 257; Conservative 0; Mismatches 18; Indels 0
                                                                                                                                                                                                                                                                                                                               129 T;
                                                                                                                                                                                                                                                                                                                               171 G;
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                                                                                                                                                                                                                                                                                                                               189 C;
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              Eggena MP, Targan SR;
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                                                                                                                                                                                                                                                                                                                               156 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-1995 (first entry)
(REGC ) UNIV CALIFORNIA.
Braun J, Eggena MP, Ta
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20-DEC-1993; U12501
                                                                                                                                                                                                                                                                                                                                 645 BP;
                             WPI; 97-042866/04.
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                                                   P-PSDB; W07616
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W09414475-A.
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Match 75.1%: Score 238; DB 11; Length 325;
Local Similarity 90.4%: Pred. No. 7.37e-143;
les 292; Conservative 0; Mismatches 27; Indels 3; Gaps 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               then fused with mouse myloma cell line 553 and the resultant clones were screened using Amb a protein. A single cell sublone AL 16-5.2, secreting Amb al-specific 1gG4, kappa antibody was selected. Total RNA was prepd. from the AL 16-5.2 cells and first strand cDNA was pred. using oligo dI primers. When the first strand cDNA was the template, and the 5' and 3' kappa light chain primers (665540, ereplate, and the 5' and 3' kappa light chain primers (665540, noted). The DNA sequence of several subclones contg. this amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 gocagteagaetgitageageaactaettageetggiaecageacaaacetggeeagget 132
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                                                                                                                                                                                                                                                                                                                                                                                                                               DNA fragment was determined. The sequence and its deduced AA sequence are shown in Q65538 and R55286. Comparison of the deduced AA L6-5.2 L-chain sequence with human V region sequences indicates that the AL 16-5.2 L-chain is a member of the human VK III subgp. Sequence 325 RP; 79 A: 79 A: 79 G:
                                                                                                                                                                                                                                                                                                                         Query Match
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Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

15 STS 1 2:5752 3:5753 4:5754 6:5755 6:5756 7:575 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8:5759 8

Mean 9.779; Variance 1.804; scale 5.421 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.28e-216 3.71e-201
əsult No. Score Match Length DR ID Description Pred No	zw27f11.rl Spares ova 2.280-216 ng69c07.sl NCI_CGAP_L 3.710-201
QI	400 50 HS1244850 418 39 AA515239
Query Match Length DB ID	400 50 418 39
Query Match I	128 49.4 121 39.2
No. Score	11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00 11.00
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67-30N-1997 (Rel. 52, Created)
07-30N-1997 (Rel. 52, Last updated, Version 1)
07-30N-197 (Rel. 52, Last updated, Version 1)
57-30N-197 to garrs evary tumor Nahor Hemo eapines obna clone 770541
57 similar to garrofoff4 in Kappa CHAIN PRECURSOR V-III REGION
(HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson PK Washu-Merck EST Project Washington University School of Medicine 4444 Forest Parkway, Box 8501. St. Louis. Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estiwateon.wistl.edu This cione is available royally-free through LLNL; contact the IMAGE Consortium (infoliange.llnl.qcv) for
                                                                                                                                                                                                                                                                                                                    Hillier E., Allen M., Rowles F., Colboque T., Geisel G., Jost S., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wilson R., "Washure Y. Wilson R.; "Washureke ESI Project 1997":
                                                                                                                                                                                                                Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata; Eutheria; Primates: Catarrhini; Hominidae: Homo.
                      HS1244850 standard; RNA; EST; 400
AA456778;
                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished.
                                                                92177199
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RESULT
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ng69c07.s1 NCI_CGAP_Lip2 Homo sapiens cDNa clone 940044 similar to qb.M63438 IG KAPPA CHAIN PPECURSOR V-III REGION (HUMAN);
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Vertebrata; Mammalia; Eutheria, Primates, Catarrhini, Hominidae,
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further information. Trace considered overall poor quality Seq
primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                              Score 128; DB 60; Length 400; Pred No 2.28e-216;
                                                                                                                                                                                                                                                                                                /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                            /clone_lib="Soares ovary tumor NbHOT" /sex="Female"
                                                                                                                                                                                                                                                                                                                                 mRNA <1..>400
Sequence 400 BP; 90 A; 120 C; 106 G; 84 T; 0 other;
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                                                                                  /organism="Homo sapiens"
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Email: Robert_Strausberg@nih.gov
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                                  Location/Qualifiers
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Best Local Similarity 73 5%;
Matches 230, Conservative
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cDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                      /note="Vertor pAMP10; mRNA made from liposarroma. CDNA made by oligo-dr priming. Non-directionally cloned. Size-selected on agarose gal, average insert size 600 bp. Reference. Krizman et al. (1994) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 ggraattegtetgggaragaetteagteteannatngeraganiggagretgaagattet 333
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1-418
NCI-GGAP;
"National Cancer Institute, Cancer Genome Austony Project (CGAP).
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae.
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael Emmert-Buck, M.D., Ph.D.
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Pred No 3 710-201;
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                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                          Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 413.
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/tissuc_type="liposarcoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                            Location/Qualifiers
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AA515239;
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24-JUL-1997 (Rel. 52, Last upda
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Best Local Similarity 72.4%;
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     S THE FERTHER FRANKS STANDARD STANDS 
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                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pAMF10: mRNA made from liposarcoma, cDNA made by oligo-dT priming Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Pesearch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 acqcagtctccaqqrarcctq+rtttqtrtrnqqqqqaaagagcaccttttctcttgcagg 154
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                   Oppublished.

Contact Robert Strausberg, Ph D. Tel. (301) 49A-1550 Fmail.

Robert Strausbergfaith.gov Tissue Procurement: L. Jeffrey Medeiros.

M.D. Michael B. Emmert.Buck, M.D. Ph.D. cona Library Preparation:

Gavid B. Krizman, Ph D. cDNA Library Arrayed by Greg Lennon, Ph.D.

DNA Sequencing by: Washington University denome Sequencing Center-
flowe distribution. MI-GAP Glone distribution information can be
found through the 1.M.A.G. E. Consortium/LLNL at

www-bio.linh gov/brp/image/image html Insert Length: 1070 Std

Error: 9.00 Seq primer: -40ml3 fwd Er from Amersham High quality
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23-JUN-1997 (Rel. 52, Last updated, Version 1)
2035b05.rl Soares over tumor then Home sapiens chwa clone 719953
5' similar to gb:X06764 IG KAPPA CHAIN PRECURSOR V-III PECION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 cocaggotontratotanggigoatogaacagggocoactgga-toccagadaggtteagt
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Hillier L., Allen M., Bowles ( , Dubuque T , Geisel G , Jost S
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Vertebrata: Eutheria; Primates; Catarrhini; Hominidae: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 121; DB 71; Length 418;
Pred. No. 3.71e-201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH108"
<1..>418
                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
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/clone="940044"
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Matches 226; Conservative
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     'moor Gene Index";
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/note="forms" covery; Vector: pT713D (Pharmacia) with a modified polylinker; Site_1. Not 1, Site_2. Eco RI: 1st strand count was primed with a Not I. oligo(dT) primer [5] forthardandragageogeogeogeogeogeogram primer [5] double-stranded cDNAwas size selected. liquid to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo."
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DEFINITION ZU35b05 r1 Scares ovary tumor NbHOT Homo sapiens cDNA clone 74953
5' similar to gb:x06764 1G KAPPA CHAIN PRECUPSOR V-111 PESION
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Hillier, Allen, M. Rowles, I., Pubuque, T., Geisei G., Post, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, R., Schellenberg, K., Steptoe, M., Tan, F.,
Theislang, B., White, Y., Wylie, T., Waterston, R., and Wilson, F.,
Washo-NCI human EST Project
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                                                                                                                                                                          Contact: Wilson RK Washington University School of Medicine 4444
Forest Park Parkway, Box 8501, St. Louis, Mp. 53108 Tel: 314 286,
1800 Fax. 34, 286, 1810 Email estawatson wustleduthis clone is available royalty-free through LINE, contact the IMAGE Consortium (info@mage lln! gov) for further information. Seg primer: -28ml3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 GCTGCATCCAGITTGCAAASIGSSTTCCCAGSSTTCAGIGSCASTGSATCTSSACA
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Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
Martin J., Moore B., Schaltenberg K., Steptoe M., Tan F.,
Theising B., White Y., Wylle T., Materston P., Wilson R.,
"Washu-NoI human EST Project";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4414 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
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07-JUN-1997 (Rel. 52, Last updated, Version 1)
2x79h05-11 Soares ovary tumor NDHOT Homo sapiens CDNA Clone 810009
5' similar th gb-v00558_cds1 15 KAPPA CHAIN PPRCHPSOP V-I PRGION
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 242;
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/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 2.92e-175;
0; Mismatches 56;
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66 c 69 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.4%;
Best Local Similarity 75.0%;
Matches 171; Conservative
                                   Contact: Wilson RK
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COMMENT
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464224 324 bp mRNA RST 10-THN-1997
83c06.rl Soares ovary tumor NPHOT Home sapiens cDNA clone 810346
similar to gb:MI2740_cds1 IG KAPPA CHAIN PRECUPS.P V-TIT PEGION
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 324)
Hillier, L., Allen, M. Bowles, L., Unbuque, T., Geisel, G., Jost, S. Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 cagagtgaggtcgcatcaaaattcaatggcagtgcatctgggacatactgcactctctcc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 CAAAGIGGGGTCCCAICGAGGTICAGIGGCAGIGGAICIGGGACAGAITICACICIGACA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 GGTATCAGCAGAAGCAGGACAGGG-GGTAAGGTGGTGATGTATGGTGGATGAGTTG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ggtatcaggagaaaccagcgataaccacctaagtcgctgatctatgcggcatccagtttg 60
                      School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
Box 857444500. Wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE fonsortism (info@image llnl gov) for further information. Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Contact: Wilson PK Washil-Merck EST Project Washington University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duery Match
29.3%; Score 93; DB 78; Length 160;
Best Local Similarity 81.8%; Pred. No. 3.60e-141;
Aatches 126; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="ovarian tumor" /lab_host="DH10B (ampicillin resistant)"
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Sequence 160 BP; 45 A; 37 C; 39 G; 39 T; 0 other;
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                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                      Location/Qualifiers
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WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
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Fax: 314 286 1810
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/note--0rgan cvary. Voctor FTT3E (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Eco RI; 1st strand cDNA was primed with a Not I: -0igo(dI) primer [5' 15TIACCAATTGAAGTGGAGGGCGGGTITITITITITITITITITI 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
                            This clone is available royalty-free through LLNI. . contact the IMAGE Consortium (info@image llnl.gov) for further information Seq primer: -28ml3 rev2 ET from Amersham High quality -28ml3 rev2 ET from Amersham Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 acgeaqtetecageeacoetgtetqtgtateeeggggaaagageeacoeteteetgeagg 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 51; Indels 2; Gaps
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13-JUN-1997 (Rel. 52, Last updated, Version 1)
2x83c05.rl Soares ovary tumor NDHOT Homo sapiens CDNA clone 810346
5' similar to gb-M12740_cds1 IG KAPPA CHAIN PRECUPSOR V-III PEGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S. Kucaba T., Lacy M., Le N., Lennon G., Marra M. Martin T., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wylle T., Warerston P., Wilson P.; "WashU-Merck EST Project 1997";
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Vertebrata, Eutheria, Primates; Catarrhini; Hominidae; Homo.
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/sex-"Female"
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Email: est@watson.wustl.edu
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74.5%;
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Res 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 ACCCASTCTCCATCGTCCCTGTCTGCATTTGINGGAGACAGAGTCACCATCACTTGCGGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2: Gaps
LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information Seg primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 161.
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4-MAY-1997 (Rel. 52, Last updated, Version 2)
2V33c09.il Soares overy tumor NDHOT Home sapiens cena closs 755446
5' similar to gb.X72467 is KAPPA CHAIN PPECUPSOR V.II PPSICN
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School Tel: 314-286-1802 Fax: 314-286-1810 Email:
Extraction.wustl.edu This clone is available royalty-tree through LLNL; contact the IMAGE Consortium (intofimage.llnl.gov) for further information. Sea primer: '28m13 rev2 ET from Amersham. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier L., Allen M., Rowies I., Lubuque I., Geisel G., Jost S., Kucaba T., Lacy M., Lo N., Lennon G., Marra M., Martin J., Moore B. Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wylie T., Waterston P., Wilson P., "Washig-Merck EST Project 1997";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson PK WashU-Merck EST Project Washington University
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Vertebrata, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 92; DB 63; Length 224;
Pred. No. 3.60e-141;
0: Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 324 BF; 68 A; 102 C; 82 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="ovarian tumor"
                                                                                                                                                                         /organism="Homo sapiens"
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HS1212377 standard; RNA; EST; 240 BP.
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                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%;
ilarity 74.5%;
Conservative
                                                               quality sequence stop:
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Les 155; Conserv
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92078755
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25.2%;
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es 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/note="Organ: ovary: Vector: pT713D (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                            74 gggcctccgggggtccctgacaggttcagtggcagtggatcaggcacagattttacactga 133
                                                                                                                                                                                                                                                                                                                             218 CCATCACCASTCTSCAACCTGAAGATTTTGCAACTTACTATTGTAACAGGGTTACACAA 277
                                                                                                                                                                                                                                                                                           98 ATTGGTATCAGCASAAAGCAGGSACAGCCCCTAAGGTCCTGATCTATGCTGCAGTTTT 157
                                                                                                                                                                                                                                                                    14 attggtacctgcagaagccagggcagtctccacagctcctgatctatttgggttctaatc 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-1997 (Rel. 52, Created)
25-MAY-1997 (Rel. 52, Last updated, Version 1)
24-MAY-1997 (Rel. 52, Last updated, Version 1)
25-MAY-111.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 769869
25' similar to gb:x72467 IG KAFPA CHAIN FPECHESOF V.II FEGION (HUMAN)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108 Tel-314 285 1870 Fax: 314 285 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image llnl.gow) for further information. Seq primer: -28ml3 rev2 ET from Amersham. Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK Washu-Merck EST Project Washington University
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Moore B , Schellenberg K , Steptoe M., Tan F , Theising B ,
White Y , Wylle T., Waterston P , Wilson P ;
WashU-Merck EST Project 1997";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotas, mitochondrial eukaryotas, Matazoa, Chordata,
Vertebrata: Butheria: Primates: Catarrhini: Hominidas: Homo
                                                                                                                                                                                                                         Length 240;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                   /tissue_type*"ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                             /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                         193 accc--ggacgttcggccaagggaccaaggtggaaatcaaa 231
                                                                                                                                                                                                                                                                                                                                                                                                                               278 CCCCTCGGACGTTCGGCCAAGGGAAGGAAGGTGGAAGTCAAA 318
                                                                                                                                                                                          mPNA <1 >>240
Sequence 240 BF; 62 A; 54 C; 69 G; 55 T; 0 other;
                                                                                                                                                                                                                         Score 80; DB 55, Lc
Pred. No. 5.88e-114;
                                                                                                                                                                                                                                                Mismatches 60,
                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Standard; PNA; EST; 248 BP
                                                                                                                        M.Fatima Bonaldo."
/clone="755440"
                                                                                                                                                                                                                                                c)
                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                         Query Match 25.2%,
Best Local Similarity 71.5%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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AA430449;
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double-stranded CDNAwas size selected. ligated to For RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco PI sites of a modified pT773 vector (Pharmacia). Library constructed by Rento Soares and M.Fatina Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 charcachasterchaaderdaadartrischaachtachartsthaadagagtrahadaa 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 ATTGGTATGASGASAASGASGASAAGGCTAASATGTTATATGTTATATGTTAGAGTT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 gggcetecggggtecetgaeaggtteagtggeagtggateaggeaeaggttttaeaetda 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 attygtacctycagaagccagggcagtstecacagstectgatetatttgggttetaate 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: 3358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-1997 (Rel. 51, Created)
23-MAY-1997 (Pel. 52, Last updated, Version 2)
2456402.rl Sourcs ovary tumbr NDHOT Homo sapiens TENA Clone 741987
5' similar te gb:X72467 19 KAPPA CHAIN PRECURSOR V-11 PESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@waston.wustl.edu This clone is available royalty-free through LLNL; contact the IMASE Conscritt(info@image llnl qoy) for further information. Seq primer: 28m13 row2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson RK Washu-Merck EST Project Washington University
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidoe, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kucaba I., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Morre B., Schellenberg K., Steptoe M., Tan F., Theising B.,
White Y., Wylle T., Waterston R., Wilson R.;
"Washi-Merck EST Project 1997";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80, DB 57; Length 248;
Pred. No. 5.88e-114;
0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                       /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares ovary tumor NDHOT"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 accc--ggacgttcggccaagggaccaaggtggaaatcaaa 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 248 BP; 64 A; 54 C; 72 G; 58 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier L , Allen M., Rowles L , Duboque T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSAA54151 standard; RNA; EST; 442 BP.
AA405415;
92063652
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316 aaatcagcagagtqqaqqctgaggatqttgqggqtttatcactgcatqcaggctctacaat 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 attagtatotgcaqaagccaqqgcagtctccacagctcctqatctatttgggttctaatc 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 ATTGGTATCAGCAGAAGCAGGGGCCCTAAGGTGCTGATGTATGCTGCATCCAGTT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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MAY-1997 (Rel. 52, Last updated, Version 1)
ZWI-707 rl Sorres overtytumor UbHOT Home sapiens CDNA clone 769572
5' similar to ob:Z37335_cds1 IS KAPPA CHAIN V-I REGION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108 Tel. 314 286 1800 Fax. 314 286 1810 Email: estiwatson.wustl.edu This chone is available royalty-free through LLNL. : contact the IMAGE Consortium (info@image lln) gov) for further information. Seq primer: -28m13 rev2 ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                            Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                      72; Indels
                                                                                                                                                                                                                 /tissue_type="ovarian tumor" /lab_host="DH108 (ampicillin resistan+)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae: mitochondrial eukaryotes: Metazoa: Chordata:
                                                                                                                                                                                                                                                                              mPNA -1. 5442
Sequence 442 BP: 90 A; 120 C; 114 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 etecteacaettttggecaggggaecaagetggagateaaa 416
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                                                                                                                                                                                                                                                                                                                                                                      Score 77; DB 78; L
Fred No 9.37e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J 12
HS1226568 standard; FNA: EST: 95
AA426003:
                                                                                                                                                                                                                                                                                                                                                                      7 Match 24.3%;
Local Similarity 57.4%;
nes 149; Conservative
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AA485616 240 bp mPNA EST 24-JUN-1957 zx99h01 r1 Soares ovary tumor NbH01 Homo sapiens CNNA clone 811057 5' similar to gb:M12740_cds1 iG KAPPA CHAIN PRECUESCH V-111 HEGION (HUMAN):
AA485616 g2214835
                                                                                                                                                                      Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae, mitochondriai eukaryotes, Motazoa; Chordata;
Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@image llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Jases 1 to 240)
Hiller, I. Allen, M., Powles, I., Dubuque, T., Gelsel, G., Tost, Krizman, D., Kucaba, T., Ley, M., Ley, N., Ley, N., Leonon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Hylle, T., Waterston, P. and Wilson, R. Wash U-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MC £3108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 29, Length 240:
                                                                                                                                                                      5; Indels
                                                                                                                               Score 76; DB 57; Length 95;
Pred No. 1 0Re-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                   /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/clone_lib="Soares ovary timor NbHOT"
/sex="Female"
                                                                                           Sequence 95 BF, 30 A, 23 C, 21 G, 21 T; 0 other;
                                                                                                                                                                    0: Mismatches
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                                      Gaps
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27-JUN-1997 (Rel. 52, Last updated, Version 1)
2x90h01.r1 Soares ovary tumor NbHOT Homo sapiens CDNA clone 811057
5' similar to 9b:M12740_cds1 IG KAPPA CHAIN PPECUPSOR V-III REGION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Confact: Wilson kK Washington University School of Medicine 4444
Forest Park Parkway Box 8501, St. Louis, MO. 63108 Tel: 314 286
BOO Faz. 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@tmage.llni.gov) for further information. Seq primer: -28ml3
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 1.08e-105,
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Pred, No 1.08e-105;
0; Mismatches 35;
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Best Local Similarity 75.9%;
Matches 110; Conservative
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25-MAY-1997 (Rel. 52, Last updated, Version 1)
2W-2DA09.r1 Soares overy tumor NDHOT Home sapiens CDNA clone 770081
5' similar to gb:M12740_cds1 is KAPPA CHAIN PRECURSOR V-111 PESION
Contact: Wilson PK WashU-Merck EST Project Washington University School of Medicale 4444 Prorest Park Parkway, Box 8501, St. Losis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham. Key
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10b (ampicillin resistant)"
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Pred, No. 1.08e-105;
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Local Similarity 75.9%;
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1:BCT 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG3 7.HTG4 8.HUM1
9:HTM2 10:HTW9 11:INV1 12:TNV2 13:ORG 14 MAN 15 VFT
16:PLN 17:PRC1 18:PPC2 19:PC0 20:SYN 21:UNG 22:VER
Release 2.1D John F. Collins, Riccomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
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(1-318) from USC8844215.seq
317
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Pred. No. is the number of results predicted by chance to have a score greater than or right to the sorre of the result being prince).

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O. Box 594, Firth Court, Western
                                                                                                                                                                                              Hexham,J.M., Furmaniak,J., Pegg,C., Furton,D.P. and Smith,R.P. Cloning of a human autoimmune response: preparation and sequencing of a human anti-thyroglobulin autoantibody using a combinatorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"IgG1/K anti-thyroid peroxidase autoantibody Fab"
/product-"Ig kappa light chain variable region, subgroup
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Human hepatitis B surface antigen antibody variable domain MRNA,
partial cds.
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                                                                                                       Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept.
Mol. Riology and Riotechnology, P. O. Box S94, Firth Court, 1
Bank, Sheffield S10 2HH, UK
3 (bases 1 to 321)
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Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B., Colls,J.C., Pegg.C., Rees Smith, P. and Purton,D. P. Cloning and characterisation of TPO autoantibodies using combinatorial phage display libraries
Autoimmunity 17 (3), 157-179 (1994)
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/clone_lib="pComb3 phagemid library"
/clone="7F"
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Best Local Similarity 94.3%;
Matches 297; Conservative
                                           (bases 1 to 321)
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                                                                Hexham, J.
Direct Submission
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/product="hepatitis B surface antigen antibody"
/db_xref="PID:q183973"
/translation="AELTQSPGTLSLSPGERATLSCPASQSVSSSYLAWYQQKPGQAP
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Eukarebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 333)
Ditzel,H.J., Parren,P W.H.I., Binley,J.M., Sodroski,J., Moore,J.P.,
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antibody variable domain; hepatitis B surface antigen antibody
Homo sapiens (individual_isolate JM) (library: JM14) blood cDN
                                                                        Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata: Vertebrata; Eutheria; Primates; Calarthini, Hominidae; Homo. 1 (bases 1 to 324)
Zebedee,S.L. Barbas,C.F.III., Hom.Y.-L., Canthien.P., Graff P. Degraw,J., Pyati,J., Lapolla,P., Purton,D.P., Lerner P.A. and Thornton,G.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCCTGCAGGGCCAGTCAGAGTCTTAGCAGCAAATACTTAGCNTGGTACCAAGAAGCT 120
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92228746
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/tissue_lib="JM14"
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                                                                                                                                                                                                                                                                          /organism~"Homo sapiens"
/note-"prepared from bone-marrow of long-term asymptomatic HIV-1 seropositive individual"
/tissue_type-"bone-marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MAELTQSPGTLSLSPGEPATLSCPASQSVSSSYLAWYQQKPGQA
PRLLIYGASSRATGIPDRFSGSGSGTUPTLIISPLEPEDFAVYYGQQYGSSLIPGGGI
                                                                                                                                                                     Direct Submission
Submitted (20-DEG-1994) Immunology, The Scripps Research Institute,
10550 North Torrey Pines Road (IMM2), La Jolla, CA 92037, USA
                  Mapping the protein surface of human immunodeficiency virus type 1 gpl20 using human monoclonal antibodies from phage-display
                                                                          J. Wol. Biol. (1997) In press
2 (bases 1 to 333)
Ditzel,H I. Parren P W H I. Binley,J M., Sodroski,J , Moore,J P Parbas,C.F. and Burton,D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 330)
Chapman, C.J., Spellerberg, M. R., Hamblin, T. J. and Stevenson, F. K.
Pattern of usage of the VH4-21 gene by B. Lymphocytes in a patient
With FRV infection indicates ongoing mutation and class switching
Mol. Immunol. 32 (5), 347-353 (1995)
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/product-"anti-HIV-1 gp120 antibody p35 light chain
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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H.sapiens immunoglobulin kappa chain V-3 region (S17B VL).
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/db_xref="PID:g1785878"
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Farbas, C.F. and Burton, D.R.
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Best Local Similarity 93.4%,
Matches 297; Conservative
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    Human salivary gland B lymphocyte conv. to mENA. close Tayke 422.
Homo sapiens
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1 (bases 1 to 332)
Kipsv.T. 1 . Tombave.E., Chon.P.P. and Fox.P.1
Molecular characterization of a major autoantibody-associated
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                                                                                                                                                                                                                                                                                                                       /product="immunoglobulin, kappa chain, V-J region"
93 c 88 q 71 t
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 264; DB 93; Length 330;
Pred. No. 1.33e-211;
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                                                                                                                                                /organism="Homo sapiens"
/isolate="ERV infected individual"
/clone="S17B VL"
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                                                                                                                                                                                                                                          /cell_type="B-cell"
/cell_line="heterohybridoma"
/sex="Female"
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Rest Local Similarity 94 68:
Matches 295; Conservative
2 (bases 1 to 330)
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                                /db_xref-"PID:9185848"
/translation-"VPGSPGTLSLSPGEPATLSCPASGSVSSSYLAWYPQKPGGAPPL
LIYGTSSRATGIPNPPSGTGSGTNFTLTISPLEPEDPAVYYCQQYGSSPTFGGGTKVE
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The progenty of a single virgin B cell predominates the human recall
B-cell response to the capsular polysaccharide of Haemophilus
influencae type b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-pEC-1995) Torben Barrington, Tissue Typing Laboratory 7631, Pigshospitalet, National University Hospital, Tagensvej 20, DK-2200 Copenhagen N, DENMAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS HSSIMO05 345 bp DNA PRI 12-SEP-1996 DEFINITION H.sapiens mFNA for kappa immunoglobulin light chain (V-J-G region;
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immunoglobulin light chain; joining region; variable region.
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Vertebrata; Eutheria; Primates; Catarrhını; Hominidae; Homo.
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                                                                                                                                                            tength 332
/note="Ig kappa chain V-region (V-J1-C)"
                                                                                                                                                        Score 264; DB 99, C
Fred, No. 1.33e-211,
0; Mismatches 22,
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/cell_type="B lymphocyte"
/clone="SIM005"
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               /codon_start=3
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Best Local Similarity 92.8%,
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/gene="V-kappa-A27 and J-kappa-4"

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FETNITION Human clone Spa3-16VL immunoglobulin light-chain mRNA V-J region.

Partial cds.
ACCESSION 119910
AID 119910
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Institute for Research on Aging, University of California at San
Diego, La Tolla, CA 92093, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 ggcagtgggtntgggacagacttnantntnacatagnagactgaannttgaannttt 252
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/tissue_lib="pionb3-JTO" (Mi3 phagemid vector)"
/clone="SpA3-16VL"
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                   /product="immunoglobulin kappa light chain"
                                                                                                                                                                                                              Tength 345:
/note="variable region and joining region"
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Homo sapiens cDNA to mRNA.
Homo sapiens
                                                                /gene="V-kappa-A27 and J-kappa-4"
325..>345
/note="constant region"
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Best Local Similarity 92.8%; Fred. No. 1.33e-211;
Matches 285; Conservative 0; Mismatches 22;
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/cell_type="lymphocyte"
/dev_stage="adult"
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Silverman, G.J.
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Eukaryotae: mitochondrial eukaryotes; Metazwa. Chordata, Vertebrata: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 64)
Barbas, C.F.III., Kang, A.S., Lerner, R.A. and Benkovic, S.J.
Assembly of combinatorial antibody libraries on phage surfaces: The
/codon_start=1
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/broduct="immunoglobulin light-chain V-J region"
/d=xref="immunoglobulin light-chain V-J region"
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PRELIYGISSRATGIP:FFSSSSSGTUFTLIISRLEPEDFAVYYGOQYGSSPWFSGGT
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Proc Natl Acad Sci ii S.A 88, 7978-7982 (1991)
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Pred. No. 1.14e-210;
0, Mismatches 28;
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Human (clone 1.L) mRNA sequence.
L22157
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/dev_stage="adult"
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Direct Submission
Submitted (25-UV-1993) J. Hexham, Univ. of Sheffield, Dept. of
Mol Biology and Biotechnology, P. O. Box 594, Firth Court, Western
Bank, Sheffield S10 2UH, UK
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Hexham,J.M., Furmaniak,J., Pegg,C., Rurton,D.P. and Smith B.R.
Cloning of a human autoimmune response. preparation and sequencing
of a human anti-thyroglobulin autoantibody using a combinatorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoantibody; Ig J-segment; Ig kappa light chain: Ig subgroup III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae: mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata: Eutheria; Primates; Catarrhini; Hominidae: Homo.
1 (Dases 1 to 324)
Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B.,
Colls,J.C., Pega,C.A.S., Pees-Smith,B. and Burton.D.R.
Probing the human anti-thyroid peroxidase repertoire of a
Hashimoto's thyroiditis patient using combinatorial phage display.
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                                            181 AGGITCAGIGGCAGIGGGICIGGGACAGACIICACICIGAGGAICAGCAGAILGAGAGIT 240
                                                                                                                                                                                                                                               243 gaagattttgcagtgtactactgtcagcagtatggtggctcaccgtggttcggccaaggg 302
                                                                                                                                                                                                                                                                                           241 GAAGAITTIGCAGIGTATTACIGICAGCAGTAIGGAACACCITGGGACCITGGGCAGGGG 300
61 TGCTGCAGGGGCCAGTCAGAGTCTTAGCAGCAATACTTAAGCNTGGTACCAACAGAAAACCT 120
                                                                                                                                            183 aggttcagtggcagtgggtctgagacagacttcactctcaccatcagcagactcgagcct
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Autoimmunity 17 (3), 167-179 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION H.sapiens mRNA for Iq kappa light chain variable reuion (V-\mathcal{I}), subgroup III (clone C3).
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/clone_lib="lambda phage"
/clone="C3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/isolate="Hashimoto patient"
/note="rearranged"
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/translation="METPAQLLFLLLWLPDTTGEIVLTQSP3TLSLSP3EPA11.SCP
ASQSVSSSYLAWYQQKPGQAPPLLIYGASSRATGIPDPFSGSGSGTDFTLTISPLEPE
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/note="Ig kappa chain V-region (V-J1-C) mature peptide"
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                                                                                                                                                                                                                                                                                                                              Query Match 82.6%; Score 262; DB 99; Length 402;
Best Local Similarity 94.2%; Pred. No. 9.79e-210;
Matches 294; Conservative 0; Mismatches 15; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                       121 caggeteccaggetecteatetatggtgeatecageagggeeaetggeateccagaeagg 180
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                                                                                                                                                                                                                                                  64 IGCAGGGCCAGICAGAGICITAGCAGCAAATACITAGCNIGGIACCAACAAAACCIGGC 123
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Human Ig active kappa chain mRNA V-region (V-J1-C), clone NOV.
M27025
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Molecular characterization of a major autoantibody-associated
cross-reactive idlotype in Sjogren's syndrome
J. Immunol. 142, 4261-4268 (1989)
                                                                                                    1 gageteaegeagteteeaggeaecetgtetttgteteeaggggaaagageeaecetetee 60
                                                                                                                                                4 GAGCTCACGCAGTCTCCAGGCALCTTTTTTTTTTCTCCAGGGGAAAAAGAGCAGTCTTTTT 63
                                                  Gaps
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1 (bases 1 to 402)
Kipps,T J., Tomhave,E., Chen,P P and Fox,R I.
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Human salivary gland B lymphocyte cDNA to mRNA, clone NOV
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  Length 324;
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Score 262; DB 91; I
Pred No 9 79e-210;
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Local Similarity 93 48;
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                                                    297, Conservative
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Kipps.T.J., Tomhave.E., Chen,P.P. and Carson,D.A.
Autoantibody-Associated k Light Chain Variable Reviou Gene
Expressed in Chronic Lymphocytic Leukemia with Little or No Somatic
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Asgsvsssylawyogkpggappliliygasspatgipdepsgrssgidetliisrlepe
Dpavyycqqygtspptpgggtkvetkptvaap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (08-FEB-1988) Kipps T.J., Scripps Clinic and Research
Foudation, 10656 North Torrey Pines Road, La Jolla, California
                                                                                                             erraggistricteatetatggtycatoragoayggisariggisatoragasaggtteagt 252
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                                                                                                                                                                                     253 ggcagtgggtctgggacagacttcactctcaccatcagcagactggagcctgaagattt 312
                                                                                                                                                                                                         Ig kappa light chain: Ig light chain imminoglobulin: variable
                                     133 gecagicagagigitageageagetaetiageeiggiaeceageagiaaceiggeeiggei 192
                                                                        70 GCCAGICAGAGICITAGCAGCAAATACITAGCNIGGIACCAACAAGAAACCIGGCCAAGAT 129
Eukaryoiae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
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Human mRNA for 1g kappa L-chain variable region (HumkeHAH).
200763 YOO648
                                                                                                                                                Tenath 402:
                                                                                                                                  /note="mat. peptide; variable region"
133..168
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see M15038 for corresponding genomic sequence.
Location/Qualifiers
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Pred No 9 796-210;
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/product="rearranged Igm light chain V region"
Alexxet="PID::g16787803"
//translation="EIVITGSPGIISISPGERAIISCPASGSVSSSYIAWY.uk PGUA
PPLLIYGASSRATGIPURESGSGSIDE:ILIISPLEPEDFAVYGAVGSSPPTFYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-001-1996) Aguilera I., Hospital V. Virgen del Pocio,
Immunology, Manuel Siurot s/n, Seville, Seville, Spain, 41013
                                                                                                                                                                                                                                                                                                                                                                                                                                 313 gcaqtgtattactgtcagcagtatgqtagctcaccttggacgttcggccaagggaccaag 372 HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH 372 SCASIGTATIAGIGTCAGCASTATGSAA---CACCTCGGACTTGGGCGAGGAGCAAA 364
                                                                                                                                                                                                                                                                         193 cccaggetecteatetatggtgeatecageaggeeaetggeateceagaeteagt 252
                                                                                                                                                                                                                                                                                                                                                       253 ggcagtgggtctgggacagacttcactctcacoatcagcagactggacctnaaqatttt 312 [[]][[][[]][[]][[]][[]][]
                                                                                                                    73 angmagintonaggnamnoigintiigintenaggggaaagagnoannoisinoidonagg 132
                                                                                                                                                                                                                                                                                                                130 GCCAGGCTCTTCATTTATGATGATGATGATGAGGGGGGGATGGGATAGGAAAAGAGAGTTAGA
                                                                                                                                                                                                                                                                                                                                                                                              190 GGCAGTGGGTGTGGGACAGACTTCACTCTCAGCAICAGCAGAITGGAGCCTGAAGATTTT 249
                                                                                                                                                                                                133 gecagicagagigitageageagetacitageeiggiaeeageagaaaeetgqeeaggei 192
                                                                                                                                      13 acgoagtetecaggeaccetgtetttgtetecaggggaaagagemaneetetertgeagg 72
                                                                               3: Gaps
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Best Local Similarity 93.9%; Pred. No. 7.19e-208;
Matches 293; Conservative 0, Mismatches 16; Indels 3; Gaps
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Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates: Catarrhini: Hominidae: Homo.
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                                                                                                                                                                                                                    Length 45m;
                                        Score 251, 28 91, Length 40 Pred. No. 8.39e-209; O. Mismatches 15; Indels
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/organism="Homo sapiens"
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/clone="IRM-101c"
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                                        Guery Match
Best Local Similarity 93.9%;
Matches 293; Conservative
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Aguilera, I.
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Kipps.T.2 Tombave.E., Chen.P.P. and Carson.D.A.

Autoantibody.Sasociated k Light Chain Variable Region Gene

Expressed in Chronic Lymphocytic Leukemia with Little or No Somatic
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/translation="METPAQXLFLLLMLPDTTGEIVLTQSPGTLSLSPGERATLSGR
ASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDFFSGSGSGTDFTLIISRLEPX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-FEB-1988) Kipps T J., Scripps Clinic and Research Foudation, 10666 North Torrey Pines Road, La Jolla, California
                                                                                                                253 ggmagigggtmigggacagacitmanteimencateagaciggageoigaagaittt 312
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    0: Mismatches 15; Indels 3; Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
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133.169
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/ceil_line="CLL B lymphocytes"
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120 c
Matches "294; Conservative
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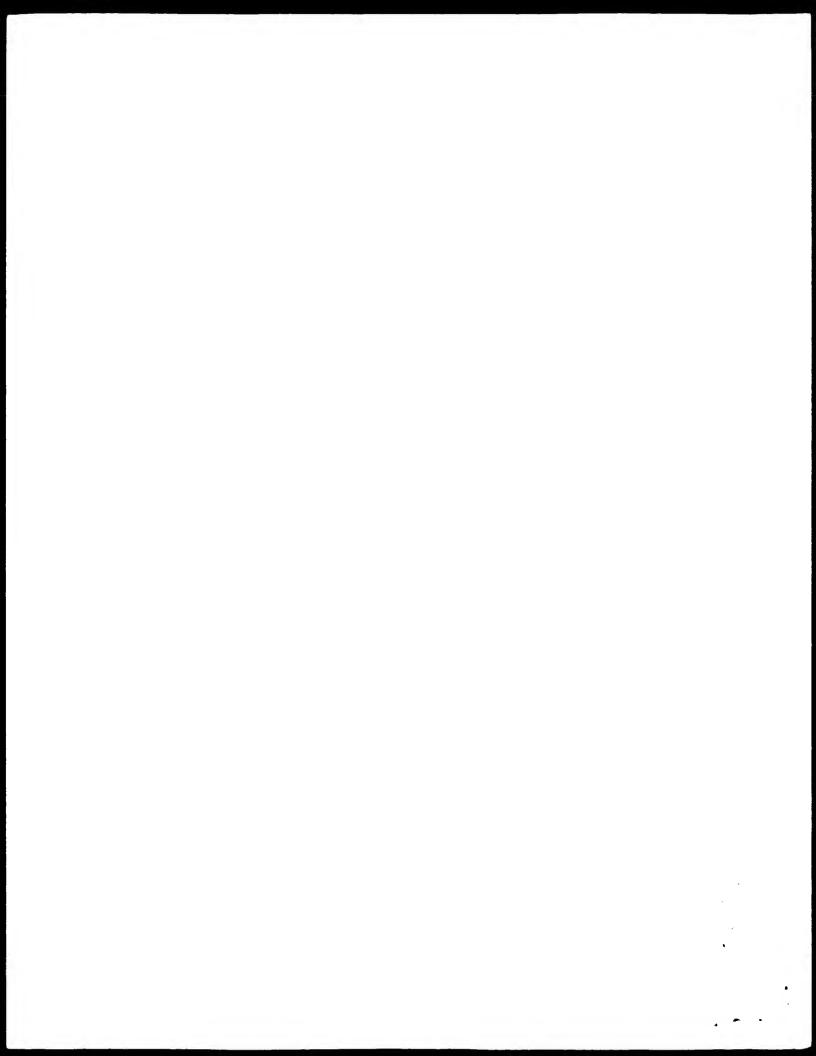
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ETKRIVAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"immunoglobulin superfamily, IgM; immunoglobulin kappa chain; variable region; joining region; rheumatoid factor; autoantibody; hybridomas; secreted immunoglobulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Control of autoantibody affinity by selection against amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-JUN-1994) Thompson K. M., I G.R I, Immunolgoy, Fr. Qvams Gt.1, Oslo, Norway, 0172
Q to Ses I to 329)
Borretzen, W. Panden, I., Zdarsky, E., Porre, O., Natvig, J. R. and
                                                                                                                                                                                                                                                           253 gcagtgtattactgtcagcagtatggtagctcacctccgacgttcggccaagggaccaag 312
70 GCCAGTCAGAGTCTTAGCAGCAAAIACTIAGCNTGGTACCAACAGAAAGCTGGGCAGGGT 129
                                                                                       133 cccaggeteeteatettatggtgeatecageagggeeaetggeateecagacaggtteagt 192
                                                                                                                                                                          193 ggcagtgggtctggggacagacttcactctcaccatcagcagactggagcctgaagatttt 252
                                                                                                                                                                                                                                                                                                    250 GCAGTGTATTACTGTCAGCAGTATGGAA---CACCTCGCACCTTCGGCCAGGGGACCAAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin mu chain variable
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Vertebrata, Eutheria, Primates, Catarrhin: Hominidae, Homo
                                                                                                                                                                                                 /product="IgM, variable region, rheumatoid factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin mu chain variable region; rheumatoid factor.
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Proc Natl Acad Sci U.S.A. 91 (26), 12917-12921 (1994) 
95108069
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Pred No. 7 196:208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.sapiens (RFMR16K) mRNA for immun region, rheumatoid factor (329bp).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Hybridoma"
/cell_line="RF-MR16"
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Thompson, K.M.
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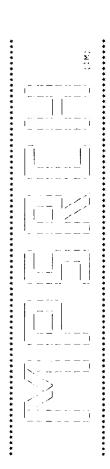
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae. Homo.
1 (bases 1 to 447)
Collet, T.A., Roben, P., O'Kennedy, R., Barbas, C. F. III., Rurton, D.R.,
and Lerner, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation of the corresponding V_region. Presently translation gualifiers on V_region features are illegal."
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                                 4 acgoagtococaggoaccotgtotttgtotocoaggggaaagagooaccototoctgoagg 63
3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A binary plasmid system for shuffling combinatorial antibody
                                                   190 GGCAGTGGGTCTGGGACAGACTTCACTCTCAGCACCAGCAGTTGGAGGCTGAAGATTT
                                                                                                                                                                         cccaggetecteatetaggtgcatecageagggeeactggeateceagaeaggtteagt
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L03162
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93066172
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16; Indels
 Mismatches
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/tissue_lib="BMHIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/cell_type="T-cell"
/dev_stage="adult"
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/codon_start=1
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ORIGIN

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Score 260; DB 99; Length 447;
Pred. No. 7.19e*208,
C; Mismatches 19; Indels 3; Gaps 1;
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                            301 accaaggtggaaatcaaa 318
Query Match
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Pelease 2.1D John F Collins, Riccomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc

n a database search, using Smith-Waterman algorithm

Tue Feb 24 09:05:21 1998: MasPar time 118:99 Seconds 753.699 Million cell updates/sec

not generated. Tabular output >US:08:844-215:20 (1-318) from US08844215.seq 317 1 GOGGASCTGACCASTCFGG. Description: Perfect Score: N.A. Sequence:

Comp.

OSAGGAASTSSAAGICAAA *18 GOTGSTTOGAGGTTGAGTTI

Scoring table:

TABLE default Gap f

397346 seqs. 141010104 bases x 2 Searched:

Dbase 0: Query 0

Nmatch STD:

Minimum Match 0% Listing first 45 summaries Post-processing:

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Database:

98:EST294 EST-D

Mean 9 746; Variance 1 743; scale 5 593 119:EST315 Statistics:

09-EST295 100-EST296 101-EST297 102-EST298 103-EST299 104-EST300 105-EST301 106-EST302 107-EST309 108-EST304 109-EST30 110-EST301 116-EST312 117-EST313 118-EST314 114-EST310 115-EST311 116-EST312 117-EST313 118-EST314

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7.48e-146 7.48e-146 70e-298 33e 284 74e-241 ve80a03.rl Soares mou 1.15e-130 EST97387 Thymus 11 Ho 2.77e-126 EST9731216 Hybrus trony 4 74-122 EW20fill:rl Soares Gro 9.12e-114 1.000-00 1.000-00 1.000-00 1.000-00 00.000 00.000 00-060. 0.000-00 O. Oge-Oa FSTERNM Spiner I Hom 1. Walfill I Soares ova 3 EST101165 Injunes 111 EST101065 Pancreas 111 EST37625 Pancreas tum EST37625 Pancreas tum EST37625 Pancreas tum EST37621 Pancreas tum EST3332 Ence marrow EST3332 Ence marrow EST5931 Ence and row ESTIGOTEL PERCESS to ESTIMATE Testis tomor ESTIMATED PERCESS to ESTATORO PERCESS tom ESTATORO PERCESS TOM EST14179 Testis tumor EST14181 Testis tumor EST100471 Parcreas tu EST100400 Pancreas tu EST51505 Gall bladder EST100058 Pancreas tu EST70983 T-cell lymph EST37844 7010h I Homm EST20620 Spleen I Hom EST39457 Esophagus tu EST30547 Colon I Homo BSI71040 T-noll lymph PST100087 Dandroas tu ESIL3847 Testus tumor PST89837 Small intest EST13404 Testis tumor EST13648 Testis tumor Testis tumor SUMMARIES AA455218 AA295622 AA361678 AA327497 AA318624 AA456778 AA366902 AA300582 AA367405 AA3211456 AA379044 AA360654 AA360281 AA423447 AA383914 AA299576 AA366827 AA327542 AA295311 AA295093 AA294843 AA295941 AA366485 AA430449 339 2398 4288 525 367 367 367 Length Query Match Score Result らからとていらる くみらかそとてしいらん とうかとさていちのくりらかんていちょくりょくととととととととととととこごごごごごごごごごにしてしてしてしてもない

1 (bases 1 to 413)

Madams, M. D. Kerlavage, A.P., Fletschmann, P.D., Fyldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Godane, J.D.,
White, C.J., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, G.,
White, C.J., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, G.,
Filoyfon, R.A., Cline, T.P., Cotton, M.D., Earle-Hophes, J., Filo, L.D.,
Filozofadd, L.M., Filohyh W.M., Frichman T., Godan, G.M.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., ESTITE 18 APR-1997
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Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Morono-Palanques, P. F., McDonald, L.A., Nuyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Fengi, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Ho, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

L. Nature 377 (5547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse.
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EcoRI: Site_2: XhoI"
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Pred. No. 0.00e+00;
0; Mismatches 36; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Pockville, MP 20850 USA
Tel: 3018699055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Testis tumor"
/sex="male"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 74.8%;
Local Similarity 88.3%;
les 278; Conservative
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18-APP-1997

EST14181 Testis tumor Homo sapiens CDNA 5' end similar to immunoqlobulin kappa light chain, V region AA301261

DEFINITION ACCESSION

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A dagas M.D. Kerlavage, A.P. Fleischmann, P.D., Fuldner, P.A., Bradis, M.D., Lee, N.H., Kirkness, E.F., Weinstork, K.G., Gorayne, T.D., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstork, K.G., Gorayne, T.D., Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J. Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Eritchman, J.L., Geoghagen, N.S., Glodek, A., Ghehn, C.L., Hanna, M.C., Heddhlow, E., Hinkler, P.S.J., Kelley, J.G., Hanna, M.C., Heddhlow, E., Hinkler, P.S.J., Moreno-Palanques, P.F., McDenald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, G.A., Ryder, J.E., Sundak, D. P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Pinkler, D., Pengy, D.F., Perrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melsener, P.S., Olsen, H., Payen, C.M., Rand, M., Finkler, C., Hungjun, J., Li, H., Melsener, P.S., Olsen, H., Praser, C.M., and Venfer, J.C., Haselfine, M.A., Fischer, J., Praser, C.M., and Venfer, J.C., Haselfine, M.A., Fischer, J., Fraser, C.M., and Venfer, J.C., M., Haselfine, M.A., Fischer, J.C., Fraser, J.C., M., Fraser, J.C., M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                   Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata;
Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: testis; Vector: pBluescript SK-: Site_1:
RooRI; Site_2: XhoI"

        67 agatgacccagtctccatcctccctgtctgcatctgtaggagagaggcanoatnant
        126

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0; Mismatches 19; Indels 1;
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9712 Medical Center Drive, Rockville. MD 20850 USA
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<1..>352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_ESTs: THC167177
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Best Local Similarity 92.6%;
Matches 251; Conservative
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Adams, M. D. Kerlavage, A. P., Fleischmann, P. D., Fuldner, P. A.,
Bult, C.J., Lee, N. H., Kirkness, E.F., Wentercok, K. G., Gocayne, J. D.,
White, O., Sutton, G. Blake, J. A., Brandon, P. C., Man-Mai, C.,
Clayton, R. A., Cline, T. R., Cotton, M. D., Earle-Hughes, J. Fine, L. D.,
Flizgerald, L.M., Fitzhugh, W. M., Fritchnan, J. L., Geoglagen, N. S.,
Glodek, A., Gnehm, C. L., Hanna M. C., Hachlow, F., Hinkle, P. S., Jr.
Kelley, J. M., Kelley, J. C., Liu, L. -I., Marmaros, S. M., Merrick, J. M.,
Morroo Palanques, R. P., McDenald, L. A., Nayyen, D. T., Pelligrino, S. M.,
Philips, C. A., Byder, S. E., Schott, I. Sabjek, D. M., Shirley, P.,
Small, K. V., Spriggs, T. A., Utterback, T. P., Weidman, J. F. Li, Y.
Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. P. Li, Y.
Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, F. J.
Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, F. J.
Bennarik, D. P., Garene, J. M., Gruber, T., Havison, P., Kim, A.,
Kozak, D. L., Kursch, C., Hungjun, J. Li, H., Meissner, P. S., Glsen, H.
Raymond, L., Well, Y. Fannon, M. P., Pallion, P. J., Fannon, M. P., Fannon, M. A., Fields, C.,
Fraser, C. M., and Venter, J. C., France, L., Mellion, P. J., Fannon, M. P., Fannon, C., Fraser, C. M., and Venter, T. C., France, L., Mellion, P. J., Fannon, M. P., Fallion, P. J., Fallish, C., France, L., Mellion, P. J., Fallish, C., France, L., Mellish, C., France, L., Mellish, C., France, L., France, L., Mellish, C., France, L., France, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone availability, additional sequence and expression information related to this ESI, please check the TIGR Human Gene Index (http://www.ligr.org/tdb/hgi/hgi html) Seq primer: MI3 Reverse.
                                                                                                                                                                                                   LOCUS AA318377 335 bp mRNA EST 19-APR-1997
DFFINITION EST2665 SEJeen I Home Saptens CONA 5' end Similar to similar to immunoglobulin Kappa light chain, V region, anti-thyroglobulin (GR-X79286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhin; Hominidae;
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ECORI; Site_2: XhoI"
/clone_lib="Spleen I"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 aaccaggtaaagcccctaaactcctgatctatgntacatccactttgcaaagtggggtcc 120
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    reaccateacitgnnqqqqqaaqteaqaqeattaqcaqetatttacattqqtatcaqcaca 60

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Nature 377 (5547 Suppl), 3-174 (1995)
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9712 Medical Conter Drive, Pockville, Mp 20850 USA
Tel: 3018999056
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Pred No 0.00e+00;
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307 tttqcaaattactactgtcaacaqnqttaca 337
                                    244 TITGCAACTTACTATTGICAACAGAGTTACA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
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Best Local Similarity 90-5%;
Matches 241; Conservative
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A (Dases I to 342)

La (Dases I to 342)

Rult C. V. Lee.N.H. Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C., Sutton, G., Rilke, F.F., Weinstock, K.G., Gocayne, J.D., White, C., Sutton, G., Rilke, T. B., Man-Wal, C., Clayton, P. A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Pritchman, J. I., Geoghagen, N.S., Gloddwa, A. Gnehm, C.L., Hanna, M.C., Hedblom, E. Hinkley, R.J., Kelley, T.W., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D. I., Hinkley, R.J., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D. I., Felliorino, S.M., Phillips, C.A., Kyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bednarik, D.P., Cach, J. C., Ferdeck, T.R., Weidan, J.F., Li, Y., Bednarik, D.P., Cach, J., Capeda, M.A., Colemon, T.A., Collins, F.J., Dimke, D.F., Ferrie, A., Fischer, C., Hadson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, T., Li, H., Meissner, R.S., Clsen, H., Flanch, M., Based, Li, Weil, Y.F., Wing, J., Xy, C., Yaseltine, W.A., Fiolds, C., Fraser, C.M. and Venter, J.C., Puben, S.M., Pased, upon R3 million, P.J., Fannon, M. P., Rosen, C.A., Haseltine, W.A., Fiolds, C., Intital assessment of human gene diversity and expression patterns based upon R3 million p. J. S., Glose, L. M., S., Close, J. M., Sauder, C.D., M., Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: esuphagus; Vortor: pBlunsoript SK-; Sito_i: BcoRi, Site_2: XhoI"
/clone_lib="Esophagus tumor"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hqi/hqi.html) Seq primer: MI3 Resease.
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Vertebrata, Mammalia, Futheria, Primates, Catarrhini, Hominidae.
113 AACCAGGACAGCCCTAAGGTCCTGATGTAGCTGCATCCAGTTGCAAACGGGGGCC 172
                                                                                                                                                                                                                                                                                                 121 catcaaggitcagiggcaciggatetgggacagaitteacieteaceateaggaquietge 180
                                                                                                                                                                                                                173 CATCGAGGIICAGIGGCAGIGGAICIGGGACAGAIIICACIGIGACGAICACAAGAGTGIGC 232
                                                                                                                                                                                                                                                                                                                                                                                   233 AACCTGAAGATTTTGGAACTTACTATTGTGAAGAGTTACACAAGGGGGTGAGAAGTTGG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA335086 345 bp mRNA EST 21-APR-1997 EST39457 Esophagus tumor Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain. V region.
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9712 Medical Center Drive, Pockville, MD 20850 USA
Tel: 3018699056
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Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 gccaagggnccaaggtggcaatcaaa 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 GOCAAGGGACCAAGGIGAAAGICAAA 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 345)
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9712 Medical Center Drive, Porkville, MD 20850 HSA
/organism="Homo sapiens"
                                                                                                                                                                     ch 67.8%;
l Similarity 90.8%;
247; Conservative
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                                                                                                            RASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hdi)
Seq primer: M13 Reverse.
                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae;
                                                                          78 acceagiciccatecteectgietgeatetgiaggagagaeagagteaecateaettgeegg 137
                                                                                                                                                                                                                                                                  130 AAGGICCIGAICTAIGCIGCAICCAGIIIIGCAAAGIGGGGICCCAICGAGGIICAGIGGC 189
                                                                                                                                                                                                                                                                                                                                            190 AGIGGATCTGGGACAGATTTGACTCTCACCATCACTAGTGGCAACCTGAAGATTTTGCA 249
                                                                                                                                                     138 gcaagtcagaccattagcacccatttaaattggtatcaacaaaaaacctgggaaagcccct 197
                                                                                                                                                                                       198 aageteetgatetatggtgeateeagtttgeaaaetggggteeeateaaggtteagtgge 257
                                                                                                                                                                                                                                                                                                        258 ggtggctctggggacagatttcactctcaccatcagcagtctgcaacctgacggttttgca 317
                                  0, Mismatches 25, Indels 0, Gaps
                                                                                                              10 ACCCAGICICCAICGICCCIGICIGCAITIGINGGAGACAGAGICACCAICACTIGGGGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION EST71640 T-cell lymphoma Homo sapiens cDNA 5' end similar immunoglobulin kappa light chain, V region.
  Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              based upon 83 million nucleotides of cDNA sequence Nature 377 (5547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Score 217; DB 39;
Fred. No. 0.00e+00,
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                                                                                                                                                                                                                                                                                                                                                                                     318 acttattactgtcaacagagttatac 343
                                                                                                                                                                                                                                                                                                                                                                                                                       250 ACTIACTATIGICAACAGAGITACAC 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 bp
Query Match 68.5%;
Best Local Similarity 90.6%,
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                                      241, Conservative
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92014052
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MEDLINE
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                                      Matches
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Adams, M. D., Kerlavage, A.R., Fleischwann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinston, K.G., Mann Wal, C.J.,
White, O., Sutton, G., Blake, B.F., Weinston, R.C., Mann Wal, C.J.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Flizgerald, L.M., Flizhugh, W.M., Fritchman, J. Geoghagen, D.S.,
Glodek, A., Gnehm, C.L., Hanna, M.G., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-T., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.E., McConald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.T., Sandek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Rednarik, D.P., Gao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Weily F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Praser, C.M., and Vener, J.C., Rosen, C.A., Haseltine, W.A., Fields, C.,
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EST100987 Pancreas tumor I Homo sapiens CDNA 5' end similar to
similar to immunoglobulin kappa light chain, V region (GR-101279).
AA295786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae, mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini: Hominidae:
/ncte-"Vector. pBluescript SK·, Sitc_1. EcoRI, Sitc_2. XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 agtggcagtggalctgggacagattttcactctcancatcagcggtctgcaacctgaaga 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 ASTGGCASTSGATCTSGGCACASATTT-CACTCTCACCATCACCAST-TG-AACCTGAACA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 gccgggcaagtnagagaattaacaactatttaaattggtatcaacagaaaaccagggaaag 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 ccectaagetectgatetacggtgeatecagtetgeaaagtgggggteecateaaggtte 252
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 23; Indels 2: Gaps
                                                                                                                                                                                                                                                                                                                       Length 357;
                                                                                                                                                                                                                                                                                                                       Score 215; DB 53;
Pred. No () 000+00);
                                                                    /clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
<1...>357
                                                                                                                                                                                                             87 t
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The Institute for Genomic Research •
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The fases 1 to 334)

Adams M. Kerlavare, A. P., Fleischmann, P. D., Fuldner, P. A.,

Bull, C. J. Lee, N. H., Kirkess, E. F., Weinstock, K. G., Gocayne, J. D.,

White, O., Sutton, G. Blake, J. A., Brandon, P. C., Man-Wai, C.,

Clayron, R. A. (line, T. P., Corton, M. D. Barle-Hughes, J. Fine, L. D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J. L., Geoghagen, N. S.,

Clodek, A., Gnehm, I., Hanna M. C., Hardhom, F., Hinkio, P. F.,

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Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,

Raymond, L., Munsch, C., Wing, T., Xu, C., Yu, G.L., Puben, S. M.,

Bullnon, P. J., Fannon, M. P., Pesen, C. A., Haseltine, W. A., Fields, C.,

Fraser, C. M., and Venter, J. C.
                                                                                            For clone availability, additional sequence and expression information related to this EST, please check the TiGR Human Gene Index (http://www.tigr.org/tdb/hqi/hqi html) Seq primer: MI3 Reverse.
                                                                                                                                                                                                                                                                                                                                  /note="Organ: pancreas; Vector: pBluescript SK-: Site_1:
BCORI Site_2: MboI
/clone_lib=Pancreas tumor I"
/dev_stage="adult"
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Vertebrata; Mammalia: Eutheria: Primates; Catarrhini: Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS AA327254 334 bp mRNA EST 20.AFR.1997 DEFINITION EST30547 Colon I Home sapiens GFNA 5' end similar to similar to immunoglobulin kappa light chain, V region (GB:L01279).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 giageagigdatetaggacagaaticagieteaneateageagietagaanetgaaggit 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GCCGGGCAAGICAGAGIAITAGGAGGAAGTTIAATTGGTATGAGGAGAAAGGAGGAGGAGAG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 agaigacccagictccalcetcctgcaictgcaictgiggggggggggggggdcaccaicaett 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.5%; Score 214; DB 25;
88 9%; Pred No 0 00e+00;
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                                                                                                                                                                                                                                                                      1..382
/ordanism="Homo sapiens"
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                                                                                                                                                                                                                                      Location/Qualifiers
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                                                        Email: arkerlavitigr.org
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102 c
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Tel: 3018599055
                               Fax. 3018699423
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1 (bases 1 to 303)
Adams, M.D. Kerlavage, A.P. Fleischmann, P.D., Fuldner, R.A.,
Adams, M.D. Kerlavage, A.P. Fleischmann, P.D., Fuldner, R.A.,
Bult, C.J. Lee, N.H. Kirkness, E.F. Weinstock, L.G. Gocayne, J.D.,
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Kelley, J.M., Kelley, J., Liu, L.I., Marmarcs, W., Morrin, P.M.
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Generates (http://www.tigr.org/tdb/hgi/hgi.html)
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Homisidue;
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/hord="Organ: colon: Vector: pBluescript SK:: Site_i:
/hord="Trans...xhol"
/clone_lib="Colon I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 agatgaegecagetnecatectecetgtetgeatetgtaggagaeagagttaceateaeet 134
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Immunoglobulin Kappa light chain, V region.
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9712 Medical Conter Drive, Perkville, MD 20450 USA
Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
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                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
Phillips,C.A., Pydor,S.E., Scott,J.L., Saudek,D.M., Shirley,P., Small,K.V., Spriggs,T.A., utterback,T.F., Weidman,J.F., Li,Y., Bednalik,D.P., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hi, T.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Ölsen,H., Paymond,I., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Puben,S.M., Dillion,P.J., Fannon, R. & Posen,C.A., Haseltine,W.A., FieldS,C., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Adams,M D., Kerlavage,A R , Fleischmann,R D., Fuldner.R.A ,
Bult,C.J., Lee,N H , Kirkness,E.F , Weinstock,K G , Gocayne.J D.,
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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2 Medical Center Drive, Rockville, MD 20859 USA
3018699056
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White.O., Sutton.G., Rlake.T.A., Brandon,R.C., Man-Wai.C., Clayton.R.A., Cline.T.P., Cotton.M.D., Earle-Hughes J., Fine.L.D., Fitzgeradd.L.M., Fitzhoyhw.M., Fritchenal.T. Geogragen.N.S., Glodek,A., Gnehm,C.L., Hanna.M.C., Hedblom.E., Hinkle.P.S.Jr., Kelley.T.M., Kelley.J.C., Liu,L.-T., Marmaros S.M., Merrick.T.M., Moreno-Palangnes.R.F., McDonald.L.A., Nguyen.D.T., Pedilgrino.S.M., Phillips.C. A. Ryder.S.E., Scott.J.L., Sandok.n.M. Shirley.R., Smill.K.V., Spriggs.T.A., Hiterback.T.P., Weidman.J.F., Liyy. Bednarik.D.P., Cao.L., Cepeda.M.A., Coleman.T.A., Collins.E.J., Dimke.D., Feng.D.-F., Ferrie.A., Fischer.C., Hastings.G.A., Kozak.D.L., Kunsch,C., Hudjun.J., Li.H., Meissner.P.S., Olsen.H., Faynon,L., Weily.P., Wing,J., Xu,C., Yu,G.L., Puben.S.M., Dillion.P.J., Fannon,M.P., Posen,C.A., Haseltine.W.A., Fields.C., Ersser.C.M. and Venter.J.C.
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AA300732
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BcoRI: Site_2: XhoI"
/clone_lib="Testis tumor"
/sex="male"
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9712 Medical Center Drive, Prokville, Mp 20850 USA
Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other_ESTs: THC167177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 C
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                                                                        Initial assessment of human gene diversity and expression patterns
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Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: testis; Vector: pRluescript SK-; Site_1:
FroRI: Site_2: XhoI"
/clone_lib="Testis tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
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9712 Medical Center Drive, Rectville, Mp 20850 USA
Tel: 3018699056
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Contact: Kerlavage, AR
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                                                         (bases 1 to 333)
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                                                                                 AUTHORS
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Homo.

S. Adams, M.D. Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A..

S. Adams, M.D. Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A..

Bult, C.J. Lee, N. H. Kirkness, E.F., Weinstork, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, P.A., Cline, T.P., Corton, M.D., Frite-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritehman, T., Gecahaden, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.J.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marrares, S.M., Merrick, J.M.,

Moreno-Palanques, P.E., Moronald, L.A., Nguyen, D.T., Pelligtino, S.M.,

Phillips, C.A., Byder, S.E., Scott, J.I., Sandow, D.M., Shirloy, R.,

Small, K.V., Spriggs, T.A., Utterback, J.T.M., Weldman, J.F., Liry,

Bednarik, D.P., Gao, L., Celeman, T.A., Collins, E.J.,

Rednarik, D.P., Gao, L., Celeman, T.A., Collins, E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (5547 Suppl), 3-174 (1995)
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Site_1: EcoRi, Site_2: Xho!"
/clone_lib="Small intestine i!"
/dev_stage="adult"
                                                                                                                                                                                                                      Eukaryotae: mitochondrial eukaryotes; Metazoa: Chordata:
Vertekrata: Mammalia: Eutheria; Primates: Catarrhini: Hominibe:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 agatgacccagiciccaicciccigicigcaicigiagaagacaaqatcaacaicarii 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 geogggeaagteagageattaaacaactatgtaaattggtateaceeaaaaecaqouaaae 191
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9712 Modinal Contor Erivo, Pockvillo, MD 20850 USA
immunoglobulin kappa light chain. V region.
AA377295
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Bost Local Similarity 89.1%:
Matches 205; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M. D. Kerlavage, A. R., Fleischmann, P. D. Fuldner, P. A., M. Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., Bullt, C.J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., Bulte, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Wai, C. Clayton, R. A., Cilne, T. R., Cotton, M. D., Eatle-Hughes, J., Fine, L. D., Fitzgradd, L. M. Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblow, E., Hinkle, P. S. Jr., Kelley, J. G., M., Merrire, J. M., Moreno-Palanques, P. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Pyden, J. L., Saudek, D. M., Shirley, P., Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y., Bednarik, D. P., Grene, J., Ferrie, A., Fischer, C., Hastings, G. A., Kozak, D. L., Kunsch, C., Hungjun, J. Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wai, Y. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K., Raymond, L., Weil, Y. F., Wing, J., Xu, C., Yu, G. L., Flack, C., Mallino, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Frais, C., Mallino, P., J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Li, H., Meissner, C. M., and Venter, J., C., Marter, J., Rosen, C. A., Haseltine, W. A., Fields, C., Li, H., Meissner, C. M., and Venter, J., C., Marter, J., M., Standar, J., M., Standar, J., Li, H., Weissner, D., Eraser, C. M., and Venter, J., France, J., Kosen, C., Marter, J., Rosen, C., Marter, J., Rosen, C., Marter, J., Kosen, C., Marter, J., Kosen, C., Marter, J., Rosen, C., Marter, J., Marter, J., Marter, J., Marter, J., Marter, J
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                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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EcoRI, Site_2. XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 agatgacccaginiccaiceicectginigeaicigiagagagagagagicaccaicaett 133
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                    EST1404 Testis tumor Homo sapiens CDNA 5' end similar to immunosopolobulin kappa light chain, V region.
AA300491
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Nature 377 (6547 Suppl), 3-174 (1995)
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9712 Medical Genter Drive, Rockville, MD 20850 USA
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Contact: Kerlavage, AR
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Best Local Similarity 92.8%;
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Adams,M D , Kerlava
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                                                                                                                                                                                                                                                                                                                       ORGANISM
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AUTHORS
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COMMENT
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                                                                                                                                                         ACCESSION
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                                                                                                                                                                                                                                    KEYWORDS
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Adams M P. Kerlavage, A P. Fleischmann, P. D. Fuldner, B.A.,
Adams M D. Kerlavage, A P. Fleischmann, P. D. Fuldner, B.A.,
Bult, C.J., ILee, N H. Kirkness, E.F. Weinstock, K.G. Gorayne, T.D.,
White, O. Sutton, G. Ralke, J. A., Brandon, P.C., Man-Wal, C.,
Clayron, P. A., Cline, T. P., Cotton, M. D., Farle-Hughes, J. Fine, L.D.,
Flitzgerald, L M. Flizhugh, W.M. Fritchman, J.L., Geoghagen, N. S.,
Glodek, A., Ghebm, C.L., Hanna, M.C., Heddlom, E. Hinkle, P.S.J.,
Kelley, J.M., Kelley, J.C., Liu, L.J., Marmaros, S.M., Merrick, J.M.,
Moreon-Palanques, P.F., McDonald, L.A., Nauyen, D. T., Pelligrin, S.M.,
Phillips, C.A., Papeley, I.A., Utterback, I.K., Weidman, J.E., Li, Y.,
Bednarik, D., Ford, E., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Praser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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/note:"Organ. pancreas, Vector. pBluescript SK . Sitc_1:
EcoRI; Site_2: XhoI"
/clone_lib="Pancreas tumor I"
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                   EST100751 Pancreas tumor I Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region.
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                       125 CCCCTAAGGTCCTGATCTAIGCTGCATCCAGITIGCAAAGTGGGGTCTCATTGAGGTCA 184
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Contact: Kerlavage, AR
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Verfebrata: Mammalia: Eutheria: Primatos; Catarrhini; Hominidae;
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                                       AA301347 297 kp mPNA EST 18-APP-1907 ESTL4275 Testis tumor Homo sapiens CDNA 5' end similar to immunoglobulin kappa light chain. V region.
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9712 Medical Center Drive, Rockville, Mp 20850 USA
Tel: 3018699056
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Contact: Kerlavage, AR
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ECORI; Site_2: XhoI"
/clone_lib="Pancreas tumor I"
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Vertebrata; Mammalia: Eutheria: Primates; Catarrhin; HominiJae;
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EST101050 Pancreas tumor I Homo sapiens cDNA 5' end similar to
immunoglobulin kappa light chain, V region.
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Tel: 3018699056
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ALIGNMENTS

RESULT 1 ID US-300-386A-62 STANDAPP: DNA: MC: 280 BP.						GE	APPLICANT: Barbas, Carlos	APPLICANT: Burton,	APPLICANT: Lerner, R	TITLE OF INVENTION:	TITLE OF INVENTION:	CHAINS	CC NUMBER OF SEQUENCES: 70						COUNTE	ZIP:				OPERATING SYSTEM	STEIWARE	CUPPENT APPLICATION DATA.				SS PRICE APPLICATION DATA:			qq	APPLICATION N	FILING DATE:	PRIOR APPLICATI			CC PRIOR APPLICATION DATA:	
NXXXXX 01-JAN-1900 Sequence £2, Application Sequence £2, Application Patent No. 566/988 GENERAL INFORMATION: APPLICANT: Barbas, C APPLICANT: Lerner, R TITLE OF INVENTION: TO COPPLE PROPERTY APPLICATION: TITLE OF THE OF THE OFFICE OFFICE OF THE OFFICE OF THE OFFICE OFFICE OFFICE OFFICE OF THE OFFICE OF	Sequence 52, Application Sequence 52, Application Sequence 52, Application Patent No. 5667988 GENERAL INFORMATION: APPLICANT: BARDAS, C APPLICANTON: TITLE OF INVENTION: TITLE OF INVENTION OF SECULATION APPLICATION DATA PRILICATION OF SECULATION APPLICATION OF SECULATION APPLICATION OF SECULATION APPLICATION NUMBER: FILING DATE: 27-3A FRICK APPLICATION NUMBER: FILING DATE: 27-3A	Sequence 62, Application Patent No. 5667989 GENERAL INFORMATION: APPLICANT: Barbas, C APPLICANT: Barbas, C APPLICANT: Burbas, C APPLICANT: Berent P TILLE OF INVENTION: TILLE OF APPLICATION: TILLING DATE:	Sequence 62, Application Patent No. 566798 GENERAL INFORMATION: APPLICANT: Barbas, C APPLICANT: Barbas, C APPLICANT: Lerner. 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CA COUNTRY: USA 2 IP: 92037 CONTINE PROBABLE FORM: MEDIUM TYPE: Floppy disk COMPABLIAL OFFERTING FORM: NO. SYSTEM POT CONSTITUTION DATA. POT CONTINE FOR SETWARE. FOR POT CONTES. CAN APPLICATION DATA. APPLICATION: 435 FILING DATE: CP-SEP: 1994 FILING DATE: 28-DEC 1993 FILING DATE: 28-DEC 1993 FILING DATE: 27-3AN-1992 FILING DATE: 27-3AN-1992 FILING DATE: 30-SEP-1992 FILING DATE: 30-SEP-1992 FILING DATE: 30-SEP-1992 PRICK APPLICATION DATA. 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APPLICATION NUMBER: US 07/24.674 FILING DATE: 27-3AN-1992 PRICE APPLICATION DATA: APPLICATION NUMBER: US 07/954.148 FILING DATE: 30-SEP-1992 PRICE APPLICATION NUMBER: US 07/954.148 FILING DATE: 30-SEP-1992 PRICE APPLICATION NUMBER: US 08/012.566 FILING DATE: AC-FER-1093	COMPUTER: IBM PC COMPATIBLE OURDINEST ISSUE PRODUCTORY SUFFWARE. FALCELID PEDCASE PLIL, VOISION BE APPLICATION NUMBER US/0%/x(0,386A) FILTYD DATE: 0.7 SFP 1.994 FILTYD DATE: 0.7 SFP 1.994 FILTYD DATE: 28 DEC 1.293 PRICE APPLICATION DATA: APPLICATION NUMBER: 0.5 0.74,674 FILTYD DATE: 28 DEC 1.293 PRICE APPLICATION DATA: APPLICATION NUMBER: 0.7 /265,623 FILTYS DATE: 27 JAN 1.992 FILTYS DATE: 27 JAN 1.992 FILTYS DATE: 37 JAN 1.992 FILTYS DATE: 37 JAN 1.992 FILTYS DATE: 37 SEP 1.992 PRICE APPLICATION DATA: APPLICATION NUMBER: 0.5 0.9 /212,566 FILTYS DATE: 0.7 FER 1.993	OPERATING SYSTEM POLOGS/MS-DOS SOFTWARE. SUFFWARE. SEFWARE. APPLICATION DATA. APPLICATION NUMBER 105/06/300.386A FILLYS DATE. PRICE APPLICATION DATA. APPLICATION NUMBER 105/06/300.386A FILLYS DATE. APPLICATION DATA. APPLICATION NUMBER: US 08/174,674 FILLYS DATE. 28-DEC1093 FPIOR APPLICATION DATA. APPLICATION NUMBER: US 07/826.623 FPIOR APPLICATION DATA. APPLICATION NUMBER: US 07/844.148 FILLYS DATE: 30-SEP-1992 PRICE APPLICATION DATA. APPLICATION NUMBER: US 07/844.148 FILLYS DATE: 30-SEP-1992 PRICE APPLICATION DATE: US 08/012,566 FILLYS DATE: US 05-FER-1093	SEFTWARE Parentin belease #111 Version at Current Arbitration Data. Application Data. Application Number 1924 CLASSIPATION OF \$194 CLASSIPATION OF \$194 CLASSIPATION OF \$194 APPLICATION NUMBER 198 APPLICATION NUMBER 198 FILLYS DATE: 28-DEC1193 FILLYS DATE: 27-DAN-1992 FILLYS DATE: 27-DAN-1992 FILLYS DATE: 27-DAN-1992 FILLYS DATE: 30-SEP-1992 PRICE APPLICATION DATA: APPLICATION NUMBER 118 FILLYS DATE: 30-SEP-1992 PRICE APPLICATION DATA: APPLICATION NUMBER: 188 FILLYS DATE: 30-SEP-1992 PRICE APPLICATION NUMBER: 188 FILLYS DATE: 30-SEP-1993 FILLYS DATE: 00-FER-1993		4 4 4	g. g. g. g.	CLASSIFICATION: 435 PRICE APPLICATION DATA: APPLICATION NUMBER: US 08/174, FILING DATE: 28.DEC-1293 APPLICATION NUMBER: US 07/826, FILING DATE: 27.5AN-1392 FILING DATE: 27.5AN-1392 FILING DATE: 30.SEP-1992 PRICK APPLICATION NUMBER: US 08/012, FILING DATE: 30.SEP-1993 APPLICATION NUMBER: US 08/012, FILING DATE: O2.FER-1993	PPICE APPLICATION DATA: PRICE AND STATE 28 20,174, FILING DATE 28 202 1293 PPICE APPLICATION DATA: APPLICATION NUMBER: US 07/826, FILING DATE: PPICK APPLICATION DATA: APPLICATION NUMBER: US 07/954, FILING DATE: 30.5EP-1992 PRICE APPLICATION DATA: APPLICATION NUMBER: US 08/012, FILING DATE: 02.FER-1993	APPLICATION NUMBER: US 08/174, FILINS DATE: 28-DEC-1993 APPLICATION DATA: APPLICATION NUMBER: US 07/826, EPION APPLICATION NUMBER: US 07/954, APPLICATION NUMBER: US 07/954, ELINS DATE: 30.SEP-1992 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/012, FILING DATE: O2-FER-1993	FILING DATE: 28.DEC-1993 PPICH APPLICATION DATA: AUTLICATION NUMBER: US 07/826, FILING DATE: 27.5AN-1992 FYION APPLICATION DATA: APPLICATION NUMBER: US 07/954, FILING DATE: 30.SEP-1992 PRICH DATE: 30.SEP-1992 PRICH DATE: 02.FER-1993 FILING DATE: 02.FER-1993	PPICP APPLICATION DATA: AFPLICATION NUMBER: US 07/826, FILING DATE: 27.5AN-1392 PPIOR APPLICATION DATA: APPLICATION NUMBER: US 07/954, FILING DATE: 30.SEP-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/012, FILING DATE: 02.FER-1993	APPLICATION NUMBER: US 01/826, FILINS DATE: 27-3AN-1992 PPOR APPLICATION DATA: APPLICATION NUMBER: US 07/954, FILING DATE: 30.SEP-1992 PRICH APPLICATION DATA: APPLICATION NUMBER: US 08/012, FILING DATE: 02-FER-1993	FILING DATE: 27.3AN-1992 FPION APPLICATION DATA: APPLICATION NUMBEP: 15 07/954, FILING DATE: 30.SEP-1992 PRIOR APPLICATION DATA: APPLICATION NUMBEP: US 08/012, FILING DATE: 02.FER-1993	FPIOR APPLICATION DATA: APPLICATION NUMBER: IS 07/954, FILINS DATE: 30.SEP-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/012, FILINS DATE: 02.FER-1993	APPLICATION NUMBER: US 07/954, FILING DATE: 30 SEP-1992 PRIOR APPLICATION DATE: 05 08/012, FILING DATE: 02-FER-1993	ad.	a. a.		

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Result No.

Sequence 62 Application and application application application application and application applicatio

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APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIRODY LIBRARIES
TITLE OF INVENTION: USING UNIVERSAL OR PANDOMIZED IMMUNOSLOBULIN LIGHT
                                                                                                                                                                                                                                                            Indels 1; Gars 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 CAGTGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCACCAGTCTGCAACTGGCAACTGAAGA 242
                                                                                                                                                                                                                                                                                                                                                                                                   121 GCCCCTAAGCTCCTGATCTATGCTGCAGGTFTGCAAAGTGGGGTCCCATCAAGGTT 180
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                                                                                                                                                                                                                                                                                                                                              61 IGCCGGGCAAGTCAGGGCATTAGCAGCTAITTAAATTGGTATGAGGAGGAACAGGGAAA 120
                                                                                                                                                                                                                                                                                                                                                           124 GCCCCTAAGGTCCTGATCTATGCTGCATCCAG-TTTGCAAAGTGGGGTCCCATCGAGGTT 182
                                                                                                                                                                                                                                                                                                    1 GAGCTCACCCAGICICCATCCTCTGTGTGTGTATGTGAGGAGACAGAGTCACCATCACT 60
                                                                                                                                                                                                                            Score 239; DB 7; Length 280;
Pred. No. 3.54e·166,
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER - IRM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE - Patentin Release #1.0, Version #1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS -
ADDRESSEE - The Scripps Pesearch Institute
STREET - 10666 North Torrey Pines Road, TPCR
                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
Sequence 280 BP; 70 A; 78 C; 65 G; 67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TITIGGAACTIACTACTGTCAACAGAGTTACAGTACCCC 279
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PCT-US95-11235-62 STANDARD; DNA; UNC; 280 BP.
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTATION NUMBER: 34,163
REFERENCE/POCKET NUMBER: 15RI 409.1
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-2937
INFORMATION FOR SEQ. ID NO: 62: SEQUENCE CHARACTERIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/11235
FILING DATE: 01-SEP-1995
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Sequence 62, Application PC/TUS9511235
GENERAL INFOPMATION
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                              : 280 base pairs
nucleic acid
EDNESS: double
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Local Similarity 93.5%,
les 261; Conservative
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                                                                                                                                                                           linear
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APPLICANT: Ostberg, Lars G.
IITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPAIITIS R SUPFACE ANTIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TGCCGGGCAAGTCAGCGCATTAGCAGCTATTTAAATTGGTATCAGCAGGAACCAGGGGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CAGTGGCAGTGGATCTGGGACACAGATTTCACTCTCACCATCAGCAGTCTGCAACACGAAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGCTCACCCAGTCTCCALCCTCCCTGTGTGTGTGTGTGGGAGAGAGAGTCACCATCACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GAGCTCACCCAGICTCCATCGICCCTGTCTGCATTTGINGGAGACAGAGTCACCATCACT 63
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                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.4%; Score 239; DB 13; Length 280; Sest Local Similarity 93.5%; Pred. No. 3.54e-166; Atches 261; Conservative 0; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORPESPONDENCE ADDRESS.
ADPRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genemic)
Sequence 280 BP: 70 A; 78 C; 65 G; 67 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TITIGGAACTTACTACTGTCAACAGAGTTACAGTACCCC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 TITIGGAACTTACTATIGTGAACAGAGTTACACAAGGGC 281
                                                                                                                                                                                            TSRI 409.1 (PC)
                                                                               US 07/954,148
APPLICATION NUMBER: US 08/174,674
                                                                                                                          US 08/012,566
                                        US 07/825,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08259372A, Sequence 13, Application US/08259372A Patent No. 5565354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-259-372A-13 STANDARD, DNA; UNC.
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEG ID NO: 62:
                                                                                                                                                                               34,163
                                                FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                    FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 NAME: Fitting, Thomas REGISTRATION NUMBER: 34, PEFERENCE/DOCKET NUMBER.
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH 280 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER PEADABLE FORM:
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COUNTRY: USA
--- 94111-3834
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Sequence 13, Application US/08468671.
Sequence 13, Application US/08468671
Patent No. 5648077
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TELEPRONE: (415) 326 2400
TELEPRAY: (415) 476-63400
INPORMATION FOR SEQ 15 NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Smith, William M. PEGISTRATION NUMBER: 30.223
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ATTOPNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER US 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 98
FILING DATE: 14 JUN-1994
APPLICATION NUMBER: US 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 384 base pairs
nucleic acid
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                           368 AGGTGGACTTCAAA 381
                                                                                                                       305 AGGIGGAAGICAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NAMIT-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 AGAIGACCCASICICCAICIICCGIGICIGCAICIGIGGGAGACAGAGICACCGICACII 127
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                                                                                   SOFTWARF: Patentin Pelease #1.0, Version #1.30
CURRENI AFFLICATION DAIA:
FILICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 384 BP; 83 A; 108 C; 100 G; 93 T; 0 other;
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Pred. No. 3.16e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/192.754
PRIOR APPLICATION DATA:
PROCE APPLICATION DATA:
APPLICATION NUMBER: US 06/925.196
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904.517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05 SEP-1986
ALTGREY/AGENT INFURMATION:
NAME: Smith, William M.
PEGISTRATION NUMBER: 30.222
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/676.035 FILING DATE: 27-MAR-1991 PRIOR APPLICATION DATA APPLICATION NUMBER: US 07/538,796 FLING DATE: 15-JUN-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPFRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/JOCKET NIMMER 1182
TELECOMMUNICATION INFORMATION
TELECOM (415) 226-2400
TELECOM (415) 576-0300
INFORMATION FOR SEQ. 10 NO. 13 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 384 base pairs
TYPE: nucleic acid
STPANNEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: 2M1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.3%;
Matches 271: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE CDNA
HYPOTHETTT
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                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
OPIGINAL SOUPCE:
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APPLICANT OSTRETG, LAIS G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SUPFACE ANTIGE
245 IIGGAACIIACIAIIGIGAACAGAGIIACACAACOOCIGGGAGGIIGGGCGAA3GGACA 🕫4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111-3834
COMPUTER PEDABLE FORM:
MEGIN TYPE. FLEEPY disk
COMPUTER: ISM PG Compatible
COMPUTER: ISM PG Compatible
COMPUTER: PATCHIN PG COMPATIBLE
COMPUTER: PATCHIN PELGGE #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORPESPONDENCE ADOPESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                         .r 4
US-08-468-671-13 STANDARD; DNA; UNC; 384 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MRR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-70N-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMRER: US 07/871,426
21-APR-1992
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
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68 AGAIGACCCAGICTCCAICTICCGIGITCIGCAICIGIGGGAGACAGAGICACCGICACTT 127
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                                                                                                                                                                                                                                                                                                                                                                                                              308 TIGCAACCTACTATIGICAACAGGCTGACAGICTCCCTITIACTITICGGCGGAGGGACCA 367
                                                                                                                                                                                                                                    128 GTCGGGCGAGTCAGGGTATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGAAAG 187
                                                                                                                                                                                                                                                                 65 GCCGGGCAAGTCAGAGTATTAACAGGAACTTAAATTGGTATCAGAAAAACGAGGGGGGA 124
                                                                                                                                                                                                                                                                                             188 CCCCTAAACTCCTGATGCTATGCTGCATTTGCAAAGTGGGGTCCCATCAAGGTTCA 247
                                                                                                                                                                                                                                                                                                           248 TCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCACCAGCCTGCAGGCTGAAGATT 307
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION. Transgenic No. 5661016-Human Animals for ITILE OF INVENTION. Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                  Score 229, DB 7; Length 384; Pred, No. 3.16e-159;
                                                                                                                                              0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Pelgase #1 0, Version #1 25 CURRENT APPLICATION DATA:
                                                                       LOCATION: 1.384
Sequence 384 BP; 83 A; 108 C; 100 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-053-131-184 STANDARD; DNA; UNC; 847 BP.
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APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
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APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 184, Application US/08053131.
Sequence 184, Application US/08053131
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   Homo sapiens
Hybridoma
                                                                                                                  Query Match 72.2%,
Best Local Similarity 86.3%;
Matches 271; Conservative
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MEDIUM TYPE: Floppy
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STATE: Californi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 AGGTGGAAGTCAAA 318
ORGANISM: Homo sa
CELL TYPE: Hybrid
CELL LINE: ZMI-2
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GENERAL INFORMATION:
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                                                            CDS
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                                                          NAME/KEY:
LOCATION:
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01-JAN-1900
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424 AGATGACCCAGTCCTCCACTCACTGCATCTGTAGSAGACAGAGTCACCATCACTT 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>604 GCGGCAGTGGATGTGGGAGAGAGTTTGACTGTGACCATGAGCAGCCTGCAGGCTGAAGATT 663</u>
                                                                                                                                                                                                                                                                                                                                                                                   5 AGCTCACCCAGTCTCCATCGTCCCTGTCTGCATTIGTNGGAGACAGAGTCACTT 64
                                                                                                                                                                                                                                                                                                                            0; Mismatches 28; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                65.6%; Score 208; DB 7; Length 847; 89 4%; Pred No. 1 44e-141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend and Townsend Phourie and Crew
                                                                                                                                                                                                                                                       LOCATION: $0in(226 279, 405, 700)
Sequence 847 BP: 200 A: 231 C: 203 G: 213 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1 0, Version #1 25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HOMAN ANTIBODLES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-217-919-1 STANDAPD; DNA, UNC. 387 BP
                                                                    REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPRA: 415-326-2402
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 07/853,408 FILING DATE: 18 MAR-1992 ATTORNEY/AGENT INFORMATION: NAME: Smith, william M. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/217,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08217918. Sequence 1, Application US/08217918 Patent No. 5506132
                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     664 TIGCAACITAITACIGCCAACAG 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alburasen. STPEET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                      : 847 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                              Rest Local Similarity 89 4%:
Matches 235; Conservative
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                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                   STRANDEDNESS:
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01-JAN-1900
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APPLICANT: Better, Marc D.
  Illinois
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            COUNTRY:
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                                                                                                                                                                                                      NAME:
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Preparation and Use for Pibosome-Inactivating Prot
                                                                                                                                                                                                                                                                                                                                                                                                        74 AGATGACCCAGICIOCIFICACOMIGICATOTOTATATATATAGGAGAGAGAGAGAGTAGAGATGAGTIT 1.33
                                                                                                                                                                                                                                                                                                                                                                           314 IIGCAACTIATIACIGICAACAGIAIAAGAGIIAIAICGCIGGAGGIIGGGCCAAGGGACGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 GCCGGGCCAGTCAGACTATTACTACTIGCTTGCCTGGTATCAGCAGACACACGGAAAG 193
                                                                                                                                                                                                                                                                                                                                  194 COPTIAAACIGAISAIGIAIAAAGGATGIAIIIIASAAAARSSSGIOCCAICAAGGIIGA 253
                                                                                                                                                                                                                                                                                                 5 AGCICACCCASICICCATCAICCCIGICIDISATITAINSSASACAGACICACCAICACTI 64
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                   Score 207: DR 6: Length 387;
Pred. No. 8.93e-141;
                                                                                                                                                                                                                                                       Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall o'Toole, Gerstein, Murray s
ADDRESSEE: Ricknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two First National Plaza, 29 South Clark
STREET: Street
CIIY: Chicago
                                                                                                                                                                                                             Sequence 387 8P; 97 A; 107 C; 94 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US92-09487-74 STANDARD; DNA; UNC; 321 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1900
Sequence 74. Application PC/TUS9209487.
Sequence 74. Application PC/TUS9209487
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
                               NAME: Smith, Willaim M
REGISTATION UNMREP: 30,223
TELECOMMUNICATION INFORMATION
TELEFACE: (415) 325-2400
TELEFACE: (415) 325-2402
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lene, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials CC
TITLE OF INVENTION: Preparation
                                                                                                                                                                                                                                                          .
.
                     ATTORNEY/AGENT INFORMATION:
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
                                                                                                      LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             Local Similarity 82.8%;
nes 250: Conservative
                                                                                                                                                                                                                                   182 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10
                                                                                                                                                  CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 AGGIGGAAAICAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 AGGTGGAAGTCAAA 318
                                                                                                                                    MOLECULE TYPE: CDNA HYPOTHETTONA
                                                                                                                                                                                                   387
           CLASSIFICATION:
                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 1..3
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65 GCCGGGCAAGTCAGAGTATTAGGAAGITAAAITGGTA1CAGGAAAACCAGGACAG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 GIGGCASIGGAICIGGGACAGAITALACICICACCARCAGINGCRISCAATATGAAGAIT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 ITGGAATTIATIAILGICAACAGIATGATGAGTCICHGTGGAAGGITGGGTGGAGGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 IIGCAACTIACIAIIGIGAAGAGAGITACACAACCCTIGGGAGGIIGGGCCAAGGGAACA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 GCCGGCCAGICAGGACAIIAAIAGGIAIIIAAGCIGGIIGCAGCAGAAAGGAGAAG 127
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Best Local Similarity 80.9%: Pred. No. 2.78e-131:
Matches 254: Conservative 0: Mismatches 60: Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AGAIGACICAGICICCAICIICCCIGICIGCAICIGIAGGAGACAGAGICACIAICACII 67
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                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPEMADE: Pater'in Felease #1 0, Version #1 25
CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCLECULE TYPE: DNA
Sequence 321 BF; 89 A; 73 C; 77 G; 82 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-425-336-72 STANDARD; DNA; UNC; 321 BP.
                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,557
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Sequence 72, Application US/09425236
Patent No. 5621083
GENEPAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-885
INFOPMATION FOR SEQ ID NO: 74:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Noland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
STRANDEDNESS: Singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 AGCITGAAAICAAA 321
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USA
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68 GCCGGGCGAGTCAGGACATTAATAGCTATTTAAGCTGGTTCCAGCAGAAACCAGGGAAAG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 GTGGCAGTGGATCTGGGACAGATTATACTCTCACCATCAGCAGCCTGCAATATGAAGATT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 TYGGAATTTATTATTGTCAACAGTATGAGTCTCCGTGGACGTTGGGTGGAGGCACA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 TIGCAACITACIATIGICAACAAAGITACACAAACCCTCGGAACGITACGGCAAAAGAAAAA 304
Carroll, Stephen F.
Studnika, Gary M.
VEWITON: Immunotoxins Comprising Ribsome-Inactivating VENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AGCTCACCCAGTCTCCATCGTCCTGTCTGCATTTGTNGGAGACAGAGTCACCTTACTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                    :: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 195; DB 7; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.78e-131;
0; Mismatches 60; Indels
                                                                                                                                                                              COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DoS/MS-DOS
SOFTWARE: Fatenin Pc-case #1 0, Vorsion #1 25
SOFTWARE: PATENIN DATA:
APPLICATION UMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 321 BP; 89 A; 73 C, 77 G, 82 T; 0 other,
                                                                                                                                                                                                                                                      APPLICALLON.

FILING DATE: 18-APN-1220
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
TITM DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         p-36,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312/474-5300
                                                        NUMBER OF SEQUENCES: 140
COPPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Thomas C. PEGISTPATION NUMBER: P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312/474-0448
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Best Local Similarity 80.9%;
Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-JUN-3
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                     COMPUTER READABLE FORM-
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 AGGTGGAAGTCAAA 318
                            TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                              Illinois
                                                                                                                                                      ZIP: 60506-6402
                                                                                                              CITY: Chicago
                                                                                                                                           USA
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                                                                                    ADDRESSEE:
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                                                                                                                                          COUNTRY.
                APPLICANT:
  APPLICANT:
                                                                                                                           STATE:
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Materials Comprising and Methods of Preparation and Use for Pibosome-Inactivating Prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 GCCGGGCGAGTCAGGACATTAATAATAGCTATTAARTTGGTTGCTTGCAGGAAACCAGGAAAG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 195; PB 5: Long+h 321;
Pred. No. 2.786-131;
O: Mismatches An: Indels O: Gaps
                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza. 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENTIN PS-LOSAMS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
Sequence 321 BF, 89 A, 73 G, 77 G; R2 T: 0 other:
            ВP
          US-07-988-430-74 STANDAFD; DNA; UNC: 321
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSITION 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                              Sequence 74, Application US/07988430.
Sequence 74, Application US/07988430
Patent No. 5416202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5416292and, Greta E
ON NUMBER: 35302
                                                                                              APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 321 base pairs
NUCLEIC ACID
                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COUNTR: USA
ZIP: 60603
COMPUTEP PEADARIE FORM:
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                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                    01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME
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RESULT
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188 GIGGGASTGSAIGIGSSACAGAIIATAGIGIGAGGAIGAGGAGGIGGAAIAIGAAGAII 247
                                                                                                                                            APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TILLE OF INVENTION: Immunofoxins Comprising Ribsome-Inactivating
TILLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F. Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: 111...
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOSAMS-DOS
SOFTWAPE: Parentin Palease #1 0, Version #1 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FTILNG DATE: 18 AAPP-1995
TTILNG DATE: 18 AAPP-1995
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MOLECULE TYPE: DNA
Sequence 723 BP; 178 A; 162 C; 207 G; 176 T; 0 other;
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US+08-425-336-90 STANDARD: DNA; UNC; 723 BP.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTOPNEY/ANTENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 90, Application US/08425336 Sequence 90, Application US/08425336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEG ID NO: 90:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meyers, Thomas C
REGISTRATION NUMBER: P
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STREET: bacc
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          308 AGCTIGAAAICAAA 321
                                                                                                                                                                                                                                                                 305 AGGIGGAAGICAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5621083
GENERAL INFORMATION:
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Score 191; DB 7; Length 723; Pred. No. 4.01e-128;

Match Local Similarity 80.3%;

Query Match Best Local

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407 AGAIGACTCAGCICCATCITCCCTGTCTGCATCIGTAGGAGAGAGAGICACIAICACIT 466
                                                                                          587 GIGGGAGIGGAIGIGGAGAGAGAIIAIAIAIGIGAGGGAGAGGAAGGIIAGAAIAIAAAAAII 646
                                                                            GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunictualing Comprising Pilesone-Tinating IIILE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ANDRESS:
ALDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                        0; Gaps
                                                                                                                                                527 CICCIAAGACCCIGAICIAICSISCAAACAGAIIISSAAICISSSSICWAAAAGAGIIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC_compatible
GEENATING SYSTEM: PC-C.3/MS-LUS
SGEIWARE: Patentin Pclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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US-08-425-336-89 STANDARD; DNA; UNC; 723 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/425,336
FILICAG DATE: 18-APP-1995
CLASSIFICATION: 530
PPICH APPLICATION DATA:
APPLICATION NUMBER: 09/064.591
FILING DATE: 12-XAY-1993
APPLICATION NUMBER: US/07/901.707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 89, Application US/08425336, Sequence 89, Application US/08425336 Patent No. 5621083
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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PEGISTRATION NUMBER: P-
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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252; Conservative
                                                                                                                                                                                                                                                                                         707 AGCITGAGAIGAAA 720
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STATE: Illi
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TELEX: 25-3856
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    Preparation and Use for Pibosome-Inactivating Prot
                                                                                                                                                                                                                                                                                                                                                                                                         128 CTCCTAAGACCCTGATCTATCGTGCAAACAGATTGGAATCTGGGGTCCCATCAAGGTTCA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 GIGGCAGIGGALCIGGGACAGAITATACICICACCAICAGCAGCITGCAATAIGAAGAIT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCACCAGTCTGCAACCTGAAGATT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 TTGGAATTTATTATTGTCAACAGTATGATGAGTCTCCGTGGACGTTCGGTGGAGGCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 TIGCAACTTACTATTGTCAACAGAGTTACACAACCCTCGGACGTTCGGCCAAGGGACCA 304
                                                                                                                                                                                                                                                                                                                                                                                      68 GCCGGGCGAGTCAGGACATTAATAGCTATTTAAGCTGGTTCCAGCAGAAACCAGGAAAAG 127
                                                                                                                                                                                                                                                                                              8 AGAIGACTCAGICICCATCITCCCTGTCTGCATCTGTAGGAGACAGAGTCACTATCACTT 67
                                                                                                                                                                                                                                                                                                                      5 AGCICACCGAGTCTGCATCGTGCGTGTCTGGATTTGTNGGAGAGAGAGAGTGACTT 64
                                                                                                                                                                                                                                                    Saps
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                                                                                                                                                                                                       Ouery Match 60.3%; Score 191; DB 7; Length 723; Best Local Similarity 80.3%; Pred. No. 4.01e-128;
                                                                                                                                                                                                                                                    Indels
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                                                                                                                                    MOLECULE TYPE: DNA
Sequence 723 BF, 178 A, 162 C, 207 G, 176 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PG-DGS/MS-DGS
SOFTWARE: Patentin Pelease #1.0, Version #1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .T 12
PCT-US92-09487-93 STANDARD: DNA; UNC: 723 BP
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence 93, Application PC/TUS9209487, equence 93, Application PC/TUS9209487 GENEPAL INPOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berthard, Susan L.
Better, Marc D.
Carroll, Stephen F.
Lane, Julie A.
Lei, Shau-Ping
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INFOPMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS.
LENGTH: 723 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                      252, Conservative
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Country usa
                                                                                                                    linear
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                                                                                                                    TOPOLOGY:
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APPLICANT:
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Materials Comprising and Methods of
Preparation and Gse for Fibusome Inactivation Prot
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Pred No 4 Ole-128;
0; Mismatches £2; Indels 0:
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                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MCLECULE TYPE: DNA Sequence 723 BP: 178 A: 162 C: 207 G: 176 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JT 13
PCT-US92-09487-92 STANDARD, DNA, UNC, 723 BF.
APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                             US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92, Application Pc/TUS9209487.
Sequence 92, Application Pc/TUS9209487
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Better, Marc D.
Carroll, Stephen F
                                                                                                                              NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/POCKET NUMBER: 311
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 93:
                                                                               FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lane, Julie A
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: MATERI
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LENGTH 723 base pairs
                                                                                                                                                                                                                                                                                                                       LENGTH 723 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS single
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                                        PRICE APPLICATION DATA:
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                                                               APPLICATION NUMBER:
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APPLICANT:
APPLICANT:
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COPPESPONDENCE ADDRESS:
ANGRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                 STREET: Two First National Plaza, 20 South Clark
STREET: Street
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Sequence 723 BF: 178 A: 162 G: 207 G: 175 T: 0 other;
                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Polease #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                   FILING DATE: USACION TO CLASSIFICATION 435
PRIOR APPLICATION 435
PRIOR APPLICATION ATM.
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTOKNEY/AGENT INFORMATION
NAME: NO. 515.0223nd, Greta E.
REGISTRATION NUMBER: 33302
PEFERENCE/DOCKET NUMBER: 31133
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/988,430 FILING DATE: 19921209
                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-POS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
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NUCLEIC ACID
DEDNESS: single
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INFORMATION FOR SEQ ID NO-
SEQUENCE CHAPACTEPISTICS:
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                                                                                               NUMBER OF SEQUENCES:
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TOPOLOGY: lir
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Fred. No. 4.01e-128; 
C: Mismatches £2: Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCLECULE IYPE: DNA
Sequence 723 BP; 178 A: 162 G; 207 G; 176 T; 0 other:
                                                  MEDIUM IYPE: Floppy disk
COMBUIDE: EHW PC Comparish
ODENTING SYSTEM: PC-nos/Ms-poS
SOFTWARE: Patentin Felease #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION DATA
FILLING DATE: 19921104
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                                                                                                                                                                                          FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-MOV-1991
ATTORNEY/AGENT INFORMATION
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Sequence 92, Application US/07988430
Patent No. 5416202.
GENERAL: INFORMATION:
APPLICANT: Bernhard, Susan L.
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
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TELEX: 25-3856
INFORMATION FOP SEC ID NO: 92-SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                          (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 723 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                 NAME: Noland, Greta E. PEGISTRATION NUMBER: 3
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Matches 252; Conservation
                                                                                                                                    FILING DATE: 19921104
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                      COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
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Illinois
           USA
                         50603
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           COUNTRY:
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Land, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Mothods of
TITLE OF INVENTION: Proparation and Use for Pibosome-Inactivating Prof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 GCCGGCGAGTCAGGACATTAATAGCTATTTAAGCTGGTTCCAGCAGAAACCA3GGAAGG 127
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APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION. Freparation and Use for Ribosome Inactivating Frot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 CCCSGCCGAGTCAGGATTAATAGCTATTTAACCTGSTTCSAGCAGAACSAGSGAAAG 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 723;
                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                  STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA Sequence 723 RP, 178 A, 162 C, 207 G, 176 T, 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
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Pred. No. 4.01e-128;
0; Mismatches 62:
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US-07-988-430-93 STANDARD; DNA; UNC; 723 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-00N-1992
PPIOP APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        Sequence 93, Application US/07988430. Sequence 93, Application US/07988430 Patent No. 5415202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 31133 TELECOMMUNICATION INFORMATION:
                                                                                                                                                      Bernhard, Susan L.
Better, Marc D.
Carroll, Stephen F.
Lane, Julie A.
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(312) 984-9740
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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|larity 80.3%;
|Conservative
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                       305 AGGTGGAAGTCAAA 318
308 AGCITGAGAIGAAA 321
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nes 252; Conser
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APPLICANT:
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Search completed: Tue Feb 24 14:42:57 1998 Job time : 58 secs.

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Searched:	ე X მმმი გაქგები რანი ამ 2008 წეგები რანი გიგებები
Post-propostag.	Minimum Match Oa Listing first 45 summarios
Database:	ESTI 2:EST2 3:EST3 4:EST4 5:EST5 7:EST7 8*EST9 7:EST1 11:EST11 12:EST12 14:EST13 14:EST14 15:EST14 15:EST14 15:EST15 15:EST15 14:EST15 14:EST16 15:EST17 15:ES
	4.EST174 175.EST175 176.EST175 177.EST177 178.EST177

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179:EST179 180:EST180 181:EST181 182:EST182 183:EST184 184:EST184 185:EST185 186:EST186 187:EST187 188:EST198 189:EST189 190:EST190 191:EST191 192:EST192 193:EST193 194:EST194 195:EST195 196:EST196
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Statistics: Mean 9.787; Variance 1.766; scale 5.543

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	pred.	ore sapien 0.00e+∪	sapie €.00e.0	sapie 0.00e+0	Tropic Store	0.900 € 900id	apien 3.020-25	sapie 1.25e-12	Sapic Billeria	Piers 5.070-22	Sal in 1 Chev. 23	Sarie 7 930 21	sapic 2.1(e.20	Sapie 2.49c 19	piens 2.50e-18	Sapie 6.45e-17	piers 6.45e 17	piens 1.01e-17	Sapie 2.44e-17	Sar:e '.77e-17	Sapie 1.49e-15	Sapie 2.18e-14	Sapie 4.580-14	Sarie 5.086 12	Sapie 5.08e-12	sapic 5.09e-12	piens 5.080-12	Sapie 5.08e-12	sapic 6.970 12	Saple 1.280 12	sapic 1,726-12	TILASTIT ATMES	Safin 4 020-1	Sapie 0.016 11	Sapie 1.346-10	Sabia 1.66e-10	69.07.77 07468	Sapt. 2.374-9	p.063 6 05368	Sorio 3 can	ダールサダ サール・エルピケ	8 - to t - 1388	BE:0 4.840.8	8-99°,5 92558	فعلان د ورد 8
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	06-SEP-1995	DEFINITION - ESTIDOSS Home sapiens obnA 5° end similar to immuneglothlin kappa					
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	mRNA	S pro . S VNGS	light chain, V region (GB:L01279) (HT:3043).				human primer-MIS Reverse library Human Fancreas.
	393 bp	sualdes ou	V region (MIB Renera
	T27593	ESTICOEE? HOW	light chain,	127593	g609591	ESI.	human primer-
KESUL1 L	LOCUS	NOILINIAGO		ACCESSION	NID	KEYWORDS	SCURCE

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For clone availability, additional sequence and expression information related to this ESI, please contact the TIGR Database
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Pred. No. 0.00e+00;
0; Mismatches 30;
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ilarity 90.2%;
Conservative
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ORGANISM
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human clone=141957 library=Soares placenta Nb2HP vector=pT7T3D (Pharmacia) with a modified polylinker host=bH10B (ampicillin resistant) primer=M13PP1 Psite1=Mot I Psite2=Eco PI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5* AACTGGAAGAATTTTTTTTTTTT 3*) double-stranded
                                                                                                                                                                                                                                                                                                             cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not in and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization. Library constructed by Bento Scares and M Patima Ponaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deuterostomia, Chordata, Vertebrata, Gnathostomana, Ostelohthyes,
Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                   yidzhilirl Homo sapiens cowa clone 141957 5' similar to
gb.x00465_cdsl IG KAPPA CHAIN PPECHRSOP V-I REGION (HUMAN);
R67559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Archonta; Primates: Catarrhini; Hominidae: Homo.

1 (bases 1 to 516)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kuraba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rehlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.9%; Score 209; DB 33;
84.9%; Pred. No. 0 00e+00;
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/clone="141957"
137 c 120 q 134
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  mPNA
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516 bp
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Fax: 314 286 1810
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                                                                                                                                                                                  human clone-133862 library-Soarcs placenta Nb2HP vector-pT713D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-M13RPl Rsitcl-Not I Rsitc2-Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Nct I oligo(3T) primer (5" AACTGGAASAATIGGGSGGGAGSAATITTTTTTTTTT 3"), double-stranded
                                                                                                                                                                                                                                                                                                                                    CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
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                              yhstech it Home saptems chara cloce 133862 C'similar to jbilliot
IG KAPPA CHAIN V-1 REGION (HRMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stops. 282
Source: IMAGE Consortium, LLNL
This clone is available regalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
[coation/Qualifiers
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[ bases 1 to 503)

Hilier,L. Clark,N., Dubuque,I, Elliston,K. Hawkins,M., Holman,M., Rucaba,T., Le,M. Lennon,G., Marra,M. Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 503,
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/clone="133862"
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WashU-Merck EST Project
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Fax: 314 285 1810
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Admis M. N. Kerlavage, A. P. Fleischmann, P. P., Fyldber, P. A., Bult, C. J., Lee, N. Kirkness, E. F., Weinstock, K. G., Grayne, L.D., White, C. Sitten, R. Blake, J. A., Branishork, K. G., Ghuu, M.-W., Clayton, P. M., Ciline, P. T., Cotton, M.D., Earle-Hudhes, J., Fine, L., Britzgerald, L.M., Fitzhugh, K.M., Fritchman, J.L., Goodbagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S., Kelley, J.M., Milmek, K. M., Kelley, J.G., If in, J. I., Marmarca, S. M., Merrick, J. M., Morror-Palagries, P. Mchopald, L.A., Nouyeu, D.T., Pellegrino, S. M., Phillips, C. A., Pydor, S. E., Scott, J.L., Nouyeu, D.T., Sauddek, D.M., Shirley, B. Granl, R.V., Spriger, T.A., Tricrback, T.R., Weldman, T.E., Li, Y., Bedantik, P. P., Grou, L., Cepeda, M.A., Coleman, T.A., Collins, E. J., Dimke, D., Feng, P., Ferrie, A., Gruber, J. Hudson, P. Kim, A., Weizek, D. L., Kunsch, C., Ji, H., Li, H., Weisser, P.S., Olsen H., Raymond, L., Weise, P. F., Weiger, C. A., Weise, C. A., Weise, L., Weise, L., Weise, L., Weise, C. A., Weise, L., Weise, C. A., Weise, C
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Initial Assessment of Human Gene Diversity and Expression Fatterns
Based Upon 52 Million Basepairs of cDNA Sequence
LOCUS T29112 395 bp mRNA EST 34 SET 1995 PEFINITION EST69384 Home saplens of NA 57 end similar to incorported trappa light chair V region (TE K 2006) (HF13819).
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Deuterostomia. Chordata. Vartebrata, Gnathostomata; Osteichthyes;
Sarcopterygii: Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria, Archonta. Primates, Catarrhini; Hominidar, Homo.
1 (bases 1 to 395)
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Pred No 0 00+00;
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Other_ESTs: EST69383
Contact: Venter, JC
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Other_ESTS: THC24356
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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
                                                                                                                                                                                                                             T27721 288 bp mRNA EST 06-SEP-1995 EST13641 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V region, rearranged (HT:3785).
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The Institute for Genomic Research
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Rult.C.J. Lee.N. Kirkness.E.F. Weinstock, K. G. Gorgyne. J. D. Bult.C.J. Lee.N. Kirkness.E.F. Weinstock, K. G. Gorgyne. J. D. Glayton, R. A. Cline, R. T. Cotton, M.D., Earle-Hughes, J., Fine, L. D. FitzGerald, L. M., FitzHugh, W.M., Fritchman, J. L., Geoghagen, N. S. M., Glode, A. Gnehm. C. L., Hanna, M.C., Hedblom. E. Hinkle Jr. P. S. Kelley, J. M., Moreno-Palanques, P. F., Moreno-B. J. Moreno-B. Cott. J. C. Luu, L. I. Marmaros, S. M. Merikk, J. M., Moreno-Palanques, P. F., Moreno-B. L. A. Nguyen, D. T., Pellegrino, S. M., Phillips. G. A. Ryder, S. E., Scott, J. L. Saudek, D. M., Shirley, R. Sedarik, D. P. Cao, L., Cepeda, M.A., Collaman, T. F., Li, Y., Rednarik, D. P. Geott, Cepeda, M.A., Collaman, T. A., Collins, E. J., Dinke, D., Feng, P. Ferrie, A., Fischer, J., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Ji, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M., Dillon, P. J., Fannon, M. R., Rosen, C. A., Haselline, M.A., Fields, C., Fraser, C. M. and Verper, I. C. Thender, C. M. A., Fields, C., Fraser, C. M. and Verper, I. C. Thender, C. Thender, C. M. A., Fields, C., Fraser, C. M. and Verper, I. C. Thender, C. Thender, C. M. A., Fields, C., Fraser, C. M. and Verper, I. M. A., Fields, C., Fraser, C. M. and Verper, I. M. A., Fields, C., Fraser, C. M. and Verper, I. M. A., Fields, C., Fraser, C. M. and Verper, I. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, I. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, I. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, I. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, M. A. Fields, C., Fraser, C. M. and Verper, M. A. Fields, C., Fraser, C. M. and Fraser, C. M. and A. 
                                                                                                                                                                                                                                                              LOCUS 127581 288 bp mRNA EST 06-SEP-1995 DEFINITION EST100107 Homo sapiens CDNA 5 end similar to immunoglobulin Rappa
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For clone availability, additional sequence and expression
information related to this ESI, please contact the TIGR Database
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Deuterostomia, Chordata; Vertebrata; Gnathostomata: Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda: Amnicta; Mammalia: Theria;
Eutheria; Archonta: Primates; Catarrhini, Huminidae; Humo
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932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
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                                                                        yolded ri Home sapiens cond clene 118592 5' similar to gb.L33034
IG KAPPA CHAIN V-1 REGION (HUMAN):
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                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 434)
Hillier, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Pifkin, L., Pohlfing, T., Tan, F. Trevaskis, E.
Waterston, R., Williamson, A., Wohldmann, P. and Wilson, P.
Washu-Merck EST project
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4444 Forest tarkway, Box 8501, St. Louis, MO 63108
121: 314 285 1800
Fax: 314 285 1810
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3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
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Eukaryotae; Metazoa; Eumetazoa; Bilateria: Coelomata:
Deuterostomia; Chordata: Vertebrata; Gnathostomata: Ostelchthyes;
Sarcopterygli: Choanata, Tetrapoda: Amniota, Mammalia; Theria:
Bitheria, Arthoria, Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 463)
Hallier, Clark, N. Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Pifkin, L., Pohlfing, T., Soares, M., Tan, P.,
Direvaskis, E., Waterston, P., Williamson, A., Wohldmann, P., and
                        S171.01 1. ub:M63438
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Mr 53108
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                     yjszdős il Homo saplums olká olono 19024/ ( s. ig Kappa Chain PRECUPSOR V-III PEGION (HUMAN):
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/clone="155249"
| 125 c | 115 q | 114
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Source: IMAGE Consortium, LLNL
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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Best Local Similarity 75.5%;
Matches 189; Conservative
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Based Upon 52 Million Basepairs of CDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
              T29556 279 bp mRNA EST 06-SEP-1995
EST89211 Homo sapions cDNA 5' end similar to immunoglobulin gamma
heavy chain V region (GB:L03140) (HT:3044).
                                                                                                                                                                        Eukaryotae; Metisou; Eumetaroa; Bilateria; Coelomata; Steichthyes: Bouterostomia; Chordata; Vertebrata; Gathostomata; Cherichthyes: Sarcopterygii, Chouata, Tetrapoda, Amniota; Mammalia, Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                   human primer=M13 Peverse library~Human Small intestine
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Adams,M.D., Kerlavage,A.P., Fleischmann,P.D.,
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Pred No 6 07e-221;
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DEFINITION yj83c03.rl Homo sapiens cDNA clone 155332 5' similar to qb:L09085 IG KAPPA CHAIN V-I REGION (HUMAN);.
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Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria:
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                                                                                                                           human clone=152581 library=Scares breast 2NbHBs+ vector=pT7T3D
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Saroopterygii; Choanata: Tetrapoda; Amniota; Mammalia; Theria;
Eutheria: Archonta: Primates; Catarrhini; Hominidae; Homo.
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Washington University School of Medicine
4444 Forest Park Parkway, Rox 8F01, St. Louis, Mo 63108
Tel: 314 286 1800
Fax: 314 286 1810
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JOURNAL
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ACCESSION
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                                                                     KEYWORDS
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Eucaryotae, Metazoa, Chordata, Vertebrata: Gnathostomata, Mammalia:
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Source: IMAGE Consortium, LLNL
This clone is available royally-free through LLNL: contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human clone=161218 libraty=Soares breast 3NbHBst religi-pf713N
(Pharmacia) with a modified polylinker host-DH10B (ampicillic
resistant) primer=M13RF1 Rsitel=Not I Rsite2-Eco RI Adult human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 geceggecaagteagaceattagegaetatttaaattggtateageagaaaeceagngaaa 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GCCGGGCAAGICAGAGIAIIAGGAGGAAGIIAAAIIGGIAICAGCAGAAAUUAGGGACA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 GCCCCTAAGGTCCTGATCTATGCTG-CATCCAGTTTG-CAAAGTGGGG-TCCCATCGAGG 180
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                                                                                                                                                                                                                                                                                                                                                     Eutheria: Frimates. Catarrhin: Hominidae. Homo.

(bases 1 to 451)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kuzaba,T., Le,M.. Lennon G.. Marra,M.,
Parsons,J., Rifkin,L., Pohlfing,T., Soares,M.. Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 64108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.2%; Score 121; DB 23: Length 451: Best Local Similarity 86.3%; Fred. No. 2.150-205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Washu-Merck ESI Project
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco PI sites of a modified pT7T3 vector (Pharmacia) Library went through one room of normalization to a Cot - 20. Library constructed by Rento Scares
                                                                                                                                                                                                                                                                              Deuterostomia; Chordata: Verreprafa; Gnathostomata; Gsteichthyes; Sarcopterygii; Chonnata: Terrapoda, Amricta: Mammalia, Theria. Eutheria: Archorda: Primates: Catarrhini; Hominidae; Homo. 1 (bases: 1 to 243)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hilman, M., Huchay, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohling, T., Soares, M., Tan, F., Tar, F., Welliamson, A., Wohldmann, P., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T29916 383 bp mRNA EST 06-SEP-1995 EST99871 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region (GB:M27025) (HT:3778).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata,
Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes,
Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams.M.D. Kerlaváge,A.P. Fleischmann.R.D., Fuldner.R.A.,
Bult.C.J. Lee,N. Kirkness.E.F. Weinstock, K.G., Gorayne,T.D.,
White,O., Sutton,G., Blake,J.A., Brandon.P.C., Chiu,M.-W.
Clayton.R.A., Cline.P.T., Cotton.M.D., Barle-Hughes,J., Fine,I.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 agatgacccagtctccatcctncctgtctgcttctgtgggggacgggggaccatcactt 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GCCGGCCAAGTCAGAGTATTAGCAGGAACTTAAATTGGTATCAGCAGAAACCAGGGACAG 124
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lst strand chNa was primed with a Not I - oligo(dI) primer [5/
ISTIACCAAICIGAAGIGGGAGGGGCGCGTTITITITITITITITIT 3/3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AGCICACCAGICICCAICGICCCIGICIGCAIIIGINGGAGACAGAGICACCAICACII 64
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1 (bases 1 to 383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                       Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 243;
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Pred. No. 2.49e-194;
0; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 cccctaagctcctgatctctggtgcatccactttgcaaa 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-Merck EST Project
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                                                                                                                                                                                    and M.Fatima Bonaldo.
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Local Similarity 85.5%;
Les 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
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                                                                                                                                                                                                                            Homo sapiens
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Fitzgerald, L. M., FitzHugh, W. M., Fritchman, J. L., Geoghagen, N. S. M., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, Jr. P. S., Kelley, J. M., Kilmek, K. M., Kelley, J. C., Liu, L.-I., Marmaros, S. M., Merrick, J. M., Moreon-balanques, P. F., Mohonald, I. A., Nguyen, D. T., Pellegrino, S. M., Phillips, C. A., Pyder, S. E., Scott, J. L., Saudek, D. M., Shirley, P., Small, K. V., Spriggs, T. A., "Hyterbark, I. P., Weidman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., Dimke, D., Feng, P., Ferrie, A., Gruber, J. Hudson, P., Kim, A., Kozak, D. I., Kunsch, C., Ii, H., Li, H., Weisster, E. S., Olsen, H. Haw, W. Hu, J. S., Greene, J. M., Weisster, E. S., Olsen, H. Hawmond, L., Weil, Y. F., Wing, J. Xu, C., Vu, G. -L., Ruben, S. M., Dillon, P. J., Fannon, M. R., Rosen, C., Haseltine, W. A., Fields, C., Fraser, C. M. and Venter, J. C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon, S. Million, Basepairs of FDNA Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION y147d10 rl Homo sapiens cona clone 151395 57 similar to dr-112106
IG KAPPA CHAIN V-I REGION (HUMAN);.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 atggtacatroatoagggnoactggoatocoagacagttoagtggoagtggggtotggga 245
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Fred. No. 2.60e-183;
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Best Local Similarity 73.2%;
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of normalization to a Cot = 20. Library constructed by Bento Soares and M.Falima Bonaldo.
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Hillier L. Clark, N. Dubuque T. Elliston K. Hawkins, M. Holfman, M. Hultman, M. Kuraha, T. Te, M. Lennon, G. Marra, M. Parsons, J. Riktin, L. Rohlfing, T. Scares, M., Tan, F. Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stops: 133
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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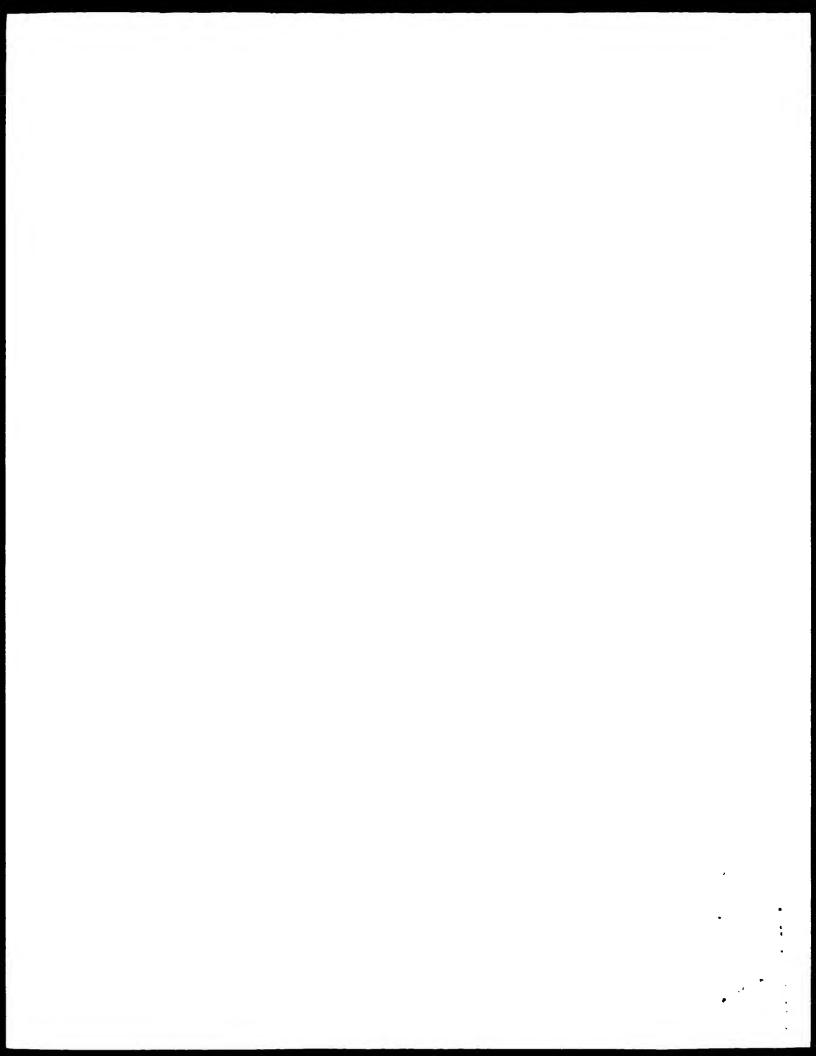
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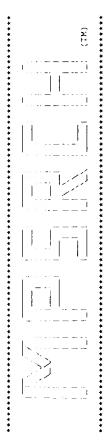
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Pred. No. 6.46e-179;
0; Mismatches 31: Indels 1: Gaps
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Washington University School of Medicine
4444 Forest Park Parkway Rox 8501 St Iquis, MC 63109
444 Forest Barkway Rox 8501 St Iquis, MC 63109
Fex: 314 286 1810
Email: est@watson.wustl.edu
                                                     Homo Sapiens
Bukaryotasa Metaroa Pumetaroa Bilateria Coelomata.
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Best Local Similarity 81.9%;
Matches 145; Conservative
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                                                        ORGANISM
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COMMENT
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Search completed: Tue Feb 24 09:04:59 1998

216 secs.

Job time :





Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, V.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Tue Feb 24 (9.50.59 1998) MasPar time 54 62 Seconds 671.816 Million only updates/sec Run on

fabular output not generated.

(1-318) from USOR844215.seq 317 TOTOTA ACCOUNTABLO ACCOUNT >US-08-844-215-20 Description: Perfect Score: N.A. Sequence

CGCCTCGAGTGGGTCAGAGG

GIACTAAGICIAAFCIGIAAA 319

CCTGGITCCACCTTCAGTTT

TARLE default Gap 6 Scoring table:

159651 seqs, 57698962 bases x 2 Searched:

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Nmatch STD

Minimum Match 0% Listing first 45 summaries Post-processing:

Database.

n-geneseq30 l:part1 2.part2 3.part3 4.part4 5:part5 6:part6 7:part7 8:part8 9:part8 10:part10 11:part11 12:part12 13:part13 14:part8 20:part15 15:part15 17.part18 19:part19 20:part26 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 36:part20 31:part31 32:part32 33:part33

Mean 7.378; Variance 4.645; scale 1.718 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Nesult.	Score	Ouery Match	Query Match Length	и. С.	Ē	Description	Fred, No.
	279	0.00	395		T75423	Human anti-tumour ant	9.55e-179
C	276	r:	- T	(1)	160117	Coding sequence for 1	1 440 176
3	260	0.28	341	œ	160119	sednence	5.826-165
4	247	ر د. د.	, o C	7	089324	Statat VK-1 gene	1 520-155
ഗ	10.00	77.9	7.00	ထ	161240	Human anti-RSV monocl	1.526.155
5	246	3.7.	285	7.4	089217	KIC12 VK dermline gen	9.026.155
~	급	76.0		(1) (1)	161236	Human anti-RSV monocl	3.32e-151
α	240	7.00		(1) (1)	15091	ARTI-TOP EDTO-2 SCEW	750-15
F	239	75.4		C	C4 C4 C4	Universal human immun	9.278-150
10	533	. i.		5	T60385		4.90-149
11	238	75.1	341	28	T60123	Coding sequence for 1	4.90e-149
15	C.	14.1	238	C1	160101	Coding seguence for 1	7 226-147
	12.7	5.3		C.	126621	Immunoqlobulin rB6B7	5.59e-144
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ALIGNMENTS

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Anticancer human monoclonal antibody variable region sequences - and
                                           Human anti-tumour antigen antibody light chain variable region cDNA. Human, tumour antigen, cancer, monoclonal, antibody, light chain; variable region; medicine; pharmacology; blochemistry; ds.
                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human anti-tumour antigen monoclonal antibody (MAb) light chain variable region, useful in medicine, pharmacology and blochemistry. The isotype of a MAb socreted by the human/human hybridoma HT was determined to be much and kape. Human MAb was Furfiled, and the antigen reconsisted human MAb CLM*-19M identified by western blotting.

Sequence 306 BF, 1016, 1016, 97 G, 97 E.
                                                                                                              Location/Qualifiers
T75423 standard; cDNA; 396 BP.
                              12-SEP-1997 (first entry)
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(HAGIZ) HAGIWAPA Y.
WPI: 97-276726/25.
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15-APR-1997.
03-00T-1995; 278266.
03-00T-1995; JP-27826
                                                                                                                                                                                                                                                                                                                   related DNA and RNA
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                                                                                               Home sapiens.
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mat_peptide
                                                                                                                           sig_peptide
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Query March Best Local Similarity 94.3%, Fred. No. 9.55e-179. Matches 296; Conservative 0, Mismatches 18, Indels v. Gaps 2

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of the invention preferably contains the sequence represented by W13912 in the complementarity determining region-1 (CBR1) or the heavy chain variable region. The antibody of the invention also contains the sequence represented by W13913 in the CDR-3 of the light chain variable region. The antibody is capable of binding to adr type hepatitis B (HB) virus antigen. A human anti HH virus monoclonal antibody preparation which is highly safe and is effective to adr type HB virus can be provided, using the monoclonal antibody. It can also be used as a vaccine against HB infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-1997 (first entry)
Coding sequence for light chain #1.
Antibody, heavy chain; light chain; variable region; human; monoclonal; complementarity determining region, human; adr type hepatitis B virus, HB virus; CDR; virus antigen; anti-HB antibody; vaccine; ss.
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                                         65 GCCGGGCAAGICAGAGIATTAGCAGGAAGITAAATIGGIATCAGCAGAAACCAGGACAG 124
                                                                                     194 cocctaagetectgatetatgetgeatecagtttgeaaagtggggteecateaaggttea 253
                                                                                                                               125 CCCCTAAGGTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATGGAGGTTCA 184
                                                                                                                                                                           254 giggeagiggaictgggacagaitteacteteaceateageagietgeaaceigaagait 313
                                                                                                                                                                                                  314 ttgcaacttactactgtcaacagagttacagtacccctcagacgttcggccaagggacca 373
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87 1%; Score 276; DP 28; Length 341;
Best Local Similarity 93.7%; Pred No. 1.44e-176;
Matches 295; Conservative of Co.
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T60117 standard; cDNA; 341 BP.
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11-JUL-1995; JP-174752.
(ASAH ) ASAHI KASEI KOGYO KK
WPI; 97-140911/13.
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J09020798-A.
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Cidim 8; Page 13, 20pp, Japanese.

T60116-T60123 represent the coding sequences for the heavy and light chains of the human monoclonal antibody of the invention. The antibody of the invention preferably contains the sequence represented by W13912 in the complementarity determining region-1 (CDP-1) of the heavy chain variable region. The antibody of the invention also contains the sequence represented by W13913 in the CDR-3 of the light chain variable region. The antibody wis capable of brinding to adr type hepatitis B (HB) virus antigen. A human anti-HB virus monoclonal antibody preparation provided, using the monoclonal antibody. It can be provided, using the monoclonal antibody. It can also be used as a vaccine against HB infection.
                                                                                                                                                                                                                                                                              Coding sequence for light chain #2. Antibode region: human: monoclonal: Antibody; heavy chain; light chain; variable region: human; adr type hepatitis B virus: complementarity determining region; human; adr type hepatitis B virus: HB virus; CDR; virus antigen; anti-HB antibody; vaccine; ss.
                                           244 TTTGCAACTTACTATTGTCAACAAGTTACACAACCTCGGGAAGGTTGGGGAAGGGAAGGGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 geocotaagotootgatotatgetgetgeatecagitigeaaagigggieeealeaagdite 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 agiggcagiggatcigggacagatticacicicaccatcagcagicigcaaccigaads 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgccqqqcaaqtcaqaqcattaqcaqctatttaaattqqtatcaqcaqaaaccaqqqaaa 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Puery Match 82.9%; Score 260; 19 28; Length 341; dest Local Similarity 91.1%; Pred. No. 5.82e-165; datches 287; Conservative 0; Mismatches 28; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GABGTCACCCASTCTCTCTATCTCTCTGTCTGCATTTGTNGGAGAGAGAGAGAGTCACCATCACT 63
tttgcaacttactactgtcaacagagttacagtacccctcgaacgttcggccaagggacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human anti-Hepatitis B antibody - used in a adr type HB virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 C;
                                                                                                                                                                                                                   T60119 standard; cDNA; 341 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLT 4
Q89324 standard; DNA; 285 BP.
Q89324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASAH ) ASAHI KASET KOGYO KK
WPI; 97-140911/13.
                                                                                                                                                                                                                                                         15-MAY-1997 (first entry)
                                                                                                                            304 AAGGTGGAAGTCAAA 318
                                                                                      304 aaggtggaaatcaaa 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AAGGTGGAAGTCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-1995; 174752.
11-JUL-1995; JP-174752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 BP;
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 cccntaaqottottqatotatgotgotgoatooagtttgoaaagtgggggtoocatoaaggttoa 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 giggeagiggalcigggacagaittcactcicaccaicagcagicigcaaccigaagait 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qooqqqqqaaqtcaqqqqttqqqqaqctattaaattqqtatcqaqqaqaaqqqaaaq 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 agaigacccagiciccaicciccigicity at agains agaigacagacaga agaileaccaicactí 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AGCTCACCCAGTCTCGTCGTGTGTGTGTGTTTGINGGAGAGAGAGTCACTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 247; DB 14; Length 285;
Pred. No. 1.52e-155;
0: Mismatches 16; Indels 0: Saps
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Human anti-RSV monoclonal antibody RF-1 light chain DNA.
Monoclonal antibody: MAb: PF-1: RF-2: rospiratory syncytial virus:
HSV: (usion protein: P-protein: vaccine: immunotherapy: therapy:
Epstein Rarr virus: immortalisation: recombinant antibody: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue and clones encoding autoimmune associated immunoglobulin fragments were obtained. 14/15 clones of L chain (kappa) regions showed homology to the putative VK germline gene KLO12 (given in UB9317) and also to the S4434 VK-1 gene used in a myasthenna gravis striational muscle autoantibody of thymic B-cell origin; the DNA (099318-2) and corresp amino and (P72059-64) sequences of 6 clones (OFFK 3, 16, 11, 9, 19 and 17) are provided. Sequence 285 RP: 75 A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ophthalmopathy-associated monoclonal antibody - produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by molecular cloning of immunoglobulin genes by PCP Disclosure: Page 59: 94pp: English.
L- and H-chain DNA was amplified by PCP from Graves' orbital
                                                      $43434 VK-1 gene.
The state of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newman RA, Pan L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 tigcaacttactactgicaacagagitacagtaccect 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 IIGCAACIIACIAIIGICAACAGAGIIACAAGAGGI 292
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                                                                                                                                                                                                                                                                                                              22-SPP-1993 US-124469
(NICH-) NICHOLS INST DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chamat SS, Heard CJ,
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Best Local Similarity 94.2%;
Matches 252; Corservative
                       26-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Papoport B;
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07-JUN-1995, US-488376.
(IDEC-) IDEC PHARM COPP.
Brams P, Chamat SS, He
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                                                                                                                                                                                                                                                                                   22-9FP-1994; M10756
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Wpr: 95-139383/19
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                                                                                                                                                                                       Homo sapiens.
W09508336-A.
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mat_peptide
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                                                                                                                                                                                                                                                        30-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Graves'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 codditAagaiddigaidialgaigaacaacaagiligcaaastgagailcoalogaggiloa 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AGCTCACCCAGTCTCCATCGTCCCTGTCTGCATTTGTNGGAGACAGACAGACACACCATCACTT 64
                                                                                                                                                                                                                                                            A DNA sequence (161240) codes for a polypeptide (W1638) comprising a leader Sequence (161240) codes for a polypeptide (W1638) comprising a leader Sequence. RF1 light chain variable region (see also W1634), and human kappa constant region. PF1 is a human monoclonal antibody (hMAb) specific for the fusion protein of respiratory syncytial virus (PSV). The DNA sequence, in vertor w1628pt. can be used to produce the light chain constructs (see also 1614-42, T61279) and light chain constructs (see also 1614-42, T61279) are similarly used. The transfected host cells provide a constant, or prevention of RSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 34; Indels (; Gaps
                                                                                                      Human monoclonal antibody specific for respiratory syncytial virus fusion protein - used for the prevention and treatment of RSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graves' ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR bisclosure, Page 56, 94pp. English Brown Brow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 STOSCASISSATCISSSACASAITICACICICACCATCACCASICISCAACCISAASATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FF GEGGGGAAGICAGAGIATIAGGAGGAAGITAAAIFGGIAGAGGAGAAAGGAGGAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247; DB 28; Length 705; No. 1 520-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 ن:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.9%; Score Rest Local Similarity 89.2%; Prod Matches 280; Conservative 0; A
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22-SEP-1994: U10756.
22-SEP-1993: US-124469.
(NICH-) NICHOLS INST DIAGNOSTICS.
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089317 standard; DNA; 285 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-1995 (first entry)
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WPI; 95-139383/18.
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WPI; 97-099892/09.
                                                      P-PSDB; W11638
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P-PSDB; R72058
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324 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
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                                                                                                                                                                                                       73 gcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaagcccct 132
                                                                                                                                                                                                                                                      70 GCAAGTCAGASTATTAGCAGGAACTTAAATTGGTATCAGCAGAAACCAGGGAGAGCCGGT 129
                                                                                                                                                                                                                                                                                                      133 aagetteetgatetatgetgeateeagtttgeaaagtggggteeeateaaggtteagtgge 192
                                                                                                                                                                                                                                                                                                                                                      130 AAGGICCTGAICTAIGCTGCAICCAGITTGCAAAGTGGGGICCCAICGAGGITGAGTGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                              68 cccgggcaggtcagaggattgctagttatttaaattggtatcagcacaaaccagggaaag 127
                                                                                                                                                    10 ACCCAGTCTCCATCGTCCCTGTCTGCATTTGTNGGAGACAGAGTCACCATCACTTGCCGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AGCT. ACCPAGICICCATGGGGGGGGGGTGTGGTNGGAGGAGACAGAGTCACTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 agatgacccagtctccatcctrrrigtrighatrigingragagagagagagatrarit 67
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Nucleic acids (T61236-39) respectively code for the RF-1 VL domain, PR-2 VH domain, FR-2 VL domain and RF-1 VH domain (W11634-37) of human monoclonal antibodies (hMAbs) RF-1 and RF-2, which show high affinity for respiratory syncytial virus (RSV) fusion protein. The hMAbs were obto. by; antigen priming of naive human splenocytes in vitro; transferral of the primed splenocytes to a SCID mouse; boosting with antigen; isolating human antibody-producing B-cells from the SCID mice; and immortalisation of the B-cells using Epstein Barr virus. DNA encoding the RF-1 and RF-2 heavy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 241; DB 28; Length 321;
Pred. No. 3.32e-151;
0, Mismatches 37; Indels C. Saps
                                                       Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human anti-RSV monoclonal antibody RF-1 VL domain DNA.
Monoclonal antibody: MAb; RF-1; RF-2; respiratory syncytial virus;
RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;
Epstein Barr virus; immortalisation, recombinant antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epstein Barr virus. DNA encoding the RF-1 and RF-2 heavy and light variable domains can be incorporated into vectors (e.g. NEOSPLA) and used to transfect eukaryotic (e.g. CHO) cells (see also T61240-42, T61279) to provide a constant, stable supply of anti-RSV F-protein hMAbs for use in the treatment or prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human monoclonal antibody specific for respiratory syncytial virus
                                                                                                       13 acceagicticeaticities of the same of
                                                                                                                                                                                                                                                                                                                                                                                                        agtggatctgggacagatttcactctcaccatcagcagtctgcaacctgaagattttgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  usion protein - used for the prevention and treatment of RSV
                                                     c.
     Length 285,
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 I.
  Scorp 246, DB 14, T
Pred. No. 8.02e-155;
0, Mismatches 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heard CJ, Newman PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 acttactactgtcaacagagttacagtacccct 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 ACTTACTATTGTCAACAGAGTTACACAACGCCT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T61236 standard; DNA; 321 BF.
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Best Local Similarity 88.2%;
Matches 277, Conservative
, Match
Local Similarity 94.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-1997 (first entry)
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995; US-488376.
(IDEC-) IDEC PHAPM COPP
Brams P, Chamat SS, He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1996.
06-JUN-1996; U10070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 RP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                     259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walsh EE;
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                     Matches
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128 chichtaagchichtgatatatatgctggaticeaatttigcachgtggggtchnigticaagstich
                                                                                                                                                                Agent contg, antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myocardial infarction, post-ingloplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis), or (ii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune and inflammatory disease

Example 1: Fig 2b(i): 184pp: English.

Example 1: Fig 2b(i): 184pp: English.

Wisson Asquence comprises the gene encoding the VL domain
(Wisson) of human sorv antibody 2A.Hil (also known as 6H1), which
is specific for transforming growth factor (TGF) beta-2. It was
isolated from a light chain shuffle repertoire of a peripheral
blood lymphocyte library. The antigen-binding domains of human
antibodies (see Wisson 40) to TGF beta-1 and/or beta-2 can be used
to counter the adverse effects of TGF beta, such as (i) promotion
of fibrosis (in dermal, coular or keloid scarring, lung fibrosis,
arterial injury, proliferative retinopathy, retinal detachment,
adult respiratory distress syndrome, liver cirrhosis, post
                                                                                                                                                                                                                                                                                          188 gtggcggtggatctgggacagatttcactctcaccatcaacagtctgcaacctgaagatt
                                                                                                                                                                                                                                                                                                                                                                      185 GIGGCAGIGGAICIGGGACAGAIIIICACICIGACCAICACCAICACGACIGCAACCIAAAGAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 tigcaactiactaticicaacaggetiacagtaceeeiggactieggactii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-TGE beta-2 scFv antipy)
Anti-TGE beta-2 scFv antibody 6-H1 VL gene.
Transforming growth factor beta-2; TGF-beta-2; human;
antibody engineering; scFv; phage display; lung fibrosis;
arterial injury; proliferative retinopathy; retinal detachment;
adult respiratory distress syndrome; liver cirrhosis;
post myocardial infarction; post-angioplasty restenosis;
scleroderma; vascular didease; cataract; glaucoma; scarring;
glomerulonephritis; osteoporosis; immune disease; inflammation;
rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection, therapy, chain shuffling, ss. Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jackson RH, Johnson KS, Pope AR;
n JE, Vaughan TJ, Williams AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 G;
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T60371 standard; DNA; 324 BP.
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7, Thompson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 AGGTGGAAGTCAAA 318
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19-JAN-1996; GB-001081.
06-0CT-1995; GR-020486.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iniversal human immunoglobulin light chain, 6F.
Mutagenesis, 1g, immunoglobulin, FP. framework region; variable, CDP; complementarity determining region; light; heavy chain; PCR; polymerase chain reaction; antibody library; diversity; affinity;
                                                                                                                                                                                                                                                                          73 godagtdagggdattagdaattatttaggddtatoagddaaaaaddagggaaagddddt 132
                                                                                                                                                                                                                                                                                                                                       70 GGAAGTGAGAGTATTAGGAAGAAAGIIAAAIIGGIATGAGAAAAAAGGAGAAAAGGGGGGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AAGSTOCTGATGTATGCTGCATCCAGTITGCAAAGTGGGGTCCCATCGAGGTGAGTGGC 189
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                                                                                                                                     13 acteagletecatecteseigteigealetgiaggagagagagegeseseitgeegg 72
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                                                                                                                                                                                                         10. ACCCAGICICCATGGICCGIGIGIGIGANIIISINSGAGAGGAGGAGICACGACTTGCGGG 69
                                                                Indels 0: Saps
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Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ر
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                                                                    Mismatches 35;
Score 240; DB 33; I
Pred No 1.75e-150;
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(SCRI ) SCRIPPS RES INST
Barbas CF. Burton DR, Lerner RA;
WPI: 96-171625/47.
                                   Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T15227 standard; DNA; 280 BP.
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Query Match
Best Local Similarity 98 78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-0CT-1995 (first entry)
                                                                       274; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-1995; U11235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 GAAGTCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 gatatcaaa 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 BP-
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                                                                       Matches
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181 cagigeagiggaicigggacagaitteacicteacraicagcagicigcaaccigaagu 240
                                          64 TGGGGGGGAAGTGAGAGTAITAGCAGGAAGTTAAATIGGIATATGAGTAAAAAGAGAGGAGA 123
                                                                                                                                                                                                61 tgeogggeaagicagegeattageaqeiatitaaaiiqgiateaaqqqqaa 120
                                                                                    lli geocetaagoteetgatetatgetgeatecaggtttgeaagitggggteecatggeact 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of IGF, e.g. for control of fiblosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune and inflammatory disease
Example 1; Fig la(iii); 184pp. English.

This DNA sequence comprises the gene encoding the VL domain
(W1539) of human scFv antibody 3169, which is specific for
transforming growth factor (IGF) beta 1. Antienn-binding domains
of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can
be used to counter the adverse effects of TGF beta, such as (i)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               post mycoardial infarction, post-angioplasty rectenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) esteperosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathoge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection). Nucleic acids encoding human antibody VH and VI can be used for prodn of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low ISSo for neutralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promotion of fibrosis (in dermal, ocular or keloid scarring, lunfibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis,
                                                                                                            Anti-TGF beta-1 scFv antibody 31G9 VL gene.

Anti-TGF beta-1 scFv antibody 31G9 VL gene.

Transforming growth factor beta-1; TGF-beta-1; human;

antibody engineering; scFv. phage display; lung fibrosis;

arterial injury; proliferative retinopathy; retinal detachment;

adult respiratory distress syndrome; liver cirrhosis;

post myocardial infarction; post-anoioplasty restenosis;

scleroderma; vascular didease; cataract; glaucoma; scarring;

glomerulomephritis; osteoporosis; immune disease; inflammation;

rheumatoid arthritis; macrophage deficiency disease;

macrophage pathogen infection; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams AJ;
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0; Mismatches 35;
                                                                                                                                                                                                                                                                  241 ttttgcaacttactactgtcaacagagttacagtugccc 279
                                                                                                                                                                                                                                                                                                            243 ITTIGGAAGTIAGTAITGIGAAGAGAIIAGAGAAGGCC 281
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83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tempest PR, Thompson JE, Vaughan TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jackson RH,
                                                                                                                                                                                                                                                                                                                                                                                                 T60385 standard; DNA; 324 BP.
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Best Local Similarity 88.3%;
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 A.
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GB2305921-A.
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07-0CT-1996;
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21-JAN-1997.
11-JUL-1995; 174752.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention preferably contains the sequence represented by Wilsolz in the complementarity determining region-1 (CDR-1) of the heavy chain variable region. The antibody of the invention also contains the region. The antibody wilsold in the CDR-3 of the light chain variable region. The antibody is capable of binding to adr type hepatitis B (HB) virus antigen. A human anti-HB virus monoclonal antibody preparation which is highly safe and is effective to adr type HB virus can be provided, using the monoclonal antibody. It can also be used as a vaccine against HB infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 17; 20pp, Japanese.
160116-T60123 represent the coding sequences for the heavy and light
chains of the human monoclonal antibody of the invention. The antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coding sequence for light chain #4.

Antibody, heavy chain, light chain, variable region; human, monoclonal, complementarity determining region, human, adr type hepatitis B virus, HB virus, CDR, virus antigen, anti-HB antibody; vaccine; ss. Homo sapiens.
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                                                            gocagicagggiattagtagciggitiggcotggiatcagcagaaaccagggagagccoci 132
                                                                                                                                                                                         133 aaaqtettgatetaataqqeatetaetttaqaaaqtqqqqteeeateaaqgtteagege 192
                                                                                                                                                                                                                                                  130 AAGGICCIGATCIATGCIGCATCCAGITTGCAAAGIGGGGTCCCATCGAGGTTCAGIGGC 189
                                                                                                                                                                                                                                                                                                                  193 agiggatotigggacagatiticactotoaccatoagcagtotiggaaccigaagatitigca 252
                                                                                                                                                                                                                                                                                                                                                                                  190 AGTGGATCTGGGACAGATTTCACTCTCACCATCACCAGTCTGCAACCTGAAGATTTTGCA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 acttactactgtcaacagagttacagtaccccgtggacgttcggccaagggaccaagctg 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 tgccqggcaagtcagannatnggnaannatttaaattggtatnggcanaagnnagggaaa 123
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                                                                                                                         70 GCAAGTCAGAGTATTAGCAGGAACTTAAATTGGTATCAGCAGAAACGAGGGACAGGGGT 129
10 ACCCARTOTOCATORICOCTS/CONSCATINGIASASACAGAGACTCACCATCACTTGCCGG 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human anti-Hepatitis B antibody - used in a adr type HB virus
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T60123 standard; cDNA; 341 BP
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(ASAH ) ASAHI KASEI KOGYO KK.
WPI; 97-140911/13.
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Best Local Similarity 87.6%;
Matches 276, Conservation
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Tibili 19; Fage 14; 20pp; Japanese.

Tibili Trough are represent the coding sequences for the heavy and light chains of the human monoclonal antihody of the invention. The antibody of the invention preferably contains the sequence represented by Wilseld in the complementarity determining region. The triping region. The antibody of the invention also contains the sequence represented by Wilseld in the CDP-3 of the light chain variable region. The antibody of scapable of binding to addrugue hepatitis B (HB) virus antipen. A human anti-HB virus monoclonal antibody preparation which is highly safe and is effective to adrugue HB virus can be provided, using the monoclonal antibody. It can also be used as a sequence against HB infection. 89 C, 79 G, 82 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; heavy chain; light chain; variable region; human; monoclonal; complementarity determining region; human; adr type hepatitis B virus; HB virus; CDR; virus antigen; anti-HR antibody; varcine: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 ASTGGCASTGSATCTGGSACASALTTCACTCACCACCASTCTGACTGAACTCTAAAGAT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 TITGCAACTTACTATTGTCAAGASASITACACAAGGGCCTGGGACGTTGGGCCAAGGACC 303
184. AGTGGGAG GGGATGTGGGANAGATTTGAGTGTGAGGATGAGGAGTGTGAGGTGAAAGTTGAAGAT 243
                                                                               244 ottgoaacttactactgicaacagagitacgataocccitegeacticgeacticgecacticgecoaggec<math>acc
                                                                                                                       64 tgccgggcaagtcagaacattgacagatatttaaattggtatcagcagaaaccanggaaa 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 tttgcaacttactactgtcagcagagttacagtgccc-tc--actttcggcggagvgacc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 TGCCGGGCAAGTCAGAGTATTAGCAGGAACTTAAATTGGTATCAGCAGAAACCAGGGGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GAGCTCACCCASTCTCCATCSTCCTGTCTCTATTTGTWGGAGACACAGGTCACTATCTGT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 gaggtgacccagtctccttcctccctgtctgcatctgtaggagacagagtcaccatcacct 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human anti-Hepatitis B antibody - used in a adr type HB virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coding sequence for light chain #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T60121 standard; cDNA; 338 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-1995; JP-174752.
(ASAH ) ASAHI KASEI KOGYO KK
WPI; 97-140911/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282; Conservative
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                                                                                                                                                                                                           Antibody containing immunoalobulin heavy chain mutation - with thyroid function stimulating activity
Claim 4: Page 12: 18pp Japanese.
T19912 Impresent the immunoalobulin heavy and light chain variable regions isolated from peripheral blowd lymphoryte strains These sequences were isolated from the B687 and 101-2 strains of peripheral blood lymphocytes of a Basedow's disease patient. These sequences are replaced, deleted or inserted into an antibody, to create the antibodies of the invention. The antibodies of the invention antibody and act by combining with thyrotropin receptor. The antibody can be used in a method to detect autoantibodies which have thyroid function stimulating activity.
Sequence 365 RP: 90 A: 101 C: 85 G; 90 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                09-001-1997 (first entry)
Immunoqlobulin rB6B7 light chain variable region coding sequence.
Immunoqlobulin: variable region; heavy chain: thyrotropin receptor;
thyroid stimulating activity, light chain. Pasedow's disease, antiboly,
peripheral blood lymphocyte; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 agatgacccagiciccaiccticcigiteigcaictigiaggagacagagicaccaicacti 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 geograpasattsagaapattagtaactatttaattaattagtatcaccagaaaccagagaag 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 GCCGGGAAGICAGAGTATTAGGAGGAGTTAAAITGGIAIGAGGAGAAACCAGGGACAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 giggcagigiaicigggacagailtcactotoaccaicagcagictgcaaccigaagail 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Granes' ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graves opithalmopathy associated immunoglobulin protein; orbital antiqen; monoclonal antibody: light chain; t chain; variable region; autoimmunity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                        DR 32; 100gth 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 20; indels
                                                                                                                                                                                                                                                                                                                                                                                                                     5.59e-144;
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 231:
                                                                                                                                                                                                                                                                                                                                                                                                        Match 72.9%; Source 231; Local Similarity 92.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEF-1994: C10755,
22-SEF-1993: US-121469.
MICH-) NICHOLE INST DIAGNOSTICS.
MCHACHLAN SM. Rapoport B:
WPI: 95-139383/18.
           T79921 standard; DNA; 366 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                089323 standard; DNA; 285 RP
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                                                                                                                                                                                                                                                                                                                                                                                                                                   250; Conservative
                                                                                                                                            22-NOV-1995; 328235;
22-NCV-1995- 3P-320235
(EIKE ) EIKEN KAGAKU KK.
WPI; 97-344899/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF7K.17 VK-1 L chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R72064.
                                                                                                                                                                                                    P-PSDB; W24538
                                                                                                        Homo sapiens.
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                                                                                                                     J09140386-A
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Monoclonal antibody ZMI-2 VI region coding sequence.

Monoclonal antibody ZMI-2 VI region coding sequence.

Monoclonal antibody ZMI-2 VI region coding sequence.

Meavy chain; light chain, variable region; human, monoclonal antibody;

immunisation, hepatitis B virus, HBV, vaccine, mouse, fusion, xenogencic;

peripheral blood lymphocyte; surface antigen; cell culture; ion exchange chromatography; size separation; primer; PCR; polymerase chain reaction;

amplification; hybridoma; infection; immunosuppression; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of hepatitis B · with human mencelonal antibody
Example B, Column 21.24, 15pp, English
This is the nucleotide sequence encoding the light chain variable (VI)
region from the human mencelonal antibody (MAD) 2M1-2. The MAD was
generated by immunishing humans with a hepatitis B virus (HHV) vaccine,
isolating peripheral blood lymphocytes (PBL) and fusing them with a
mouse/human xenogencic cell line Shard for and fusing them pell.; 2M1-1, 2M1-2, M33-4 and L03-3. The cell lines were included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 AGIGGAICIGGSACASAIIICACITEACTEFACANTGACAACAACTAGCAACATIIIGGA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 SCARTICASAGIATIASCASSAACIIAAAIIGSIAICASCAGAAACCAGGGACAG 22001 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 gcaagtcagaggattagcacctatttaaattgqtatcagcagaaaccaugdaaaagcuoct i32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 aagritootgatotatgitgtatooagitiggaago 1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25, Page 58, 94pp, English.

L- and H-chain DNA was amplified by PCP from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 14/15 clease of Lohain (Apppa) regions showed homology to the putative VK germline gene KL012 (given in PG9312). The DNA (26318-13) and colrect mino ucid (RT0359-64) sequences of 6 clones (OPPR.3, 16, 11, 9, 19 and 17) are provided. Sequence 285 BP: 75 A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 AAGGICCIGAICIAIGCIGCAICGASITIGCAAASTGGGGTDCCAICGAGGIICAGIGGC
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                                                                                                                                                                                                                                                                                                                     Query Motch 72 2%; Score 229; DR 14; Lergth 285; Best Local Similarity 91.9%; Fred. No. 1.56e-142;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Or Mismatches
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185844 standard; cDNA; 384 BP.
                                                                                                                                                                                                                                                                                                                                                                                                250: Conservative
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US-904517.
US-925196.
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06-JUN-1995; US-468671.
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27-MAR-1991; US-676036.
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21-APR-1992;
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31-OCT-1986;
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US5648077-A.
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for production of an anti-hepatitis B virus surface antigen antibody by ELISA. The MADS are then purified from large scale cell culture by protein A chromatography, size separation on Sephacryl 3300 gel and ion exchange chromatography on O.Sepharose. The heavy and light chains of the MADS were isolated and their amino acid sequences determined. Primers were generated and used to amplify cDNA synchesised from RNA purified from each hybridoma cell line. The sequences of the heavy and light chains (nucleic acid and amino acid) from MADS PEI-1, ZMI-2, and MO3-4 are shown in T85838-45 and M24984-91. The MADS can be used to treat HBV infections in immunosupressed patients or patients with chronic active hepatitis, especially liver transplant patients.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 CCCCTAAGGTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCGAGGTTCA 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 tigcaacciactatigicaacaggeigacagieteceetitiactiicggeggaggacea 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 TTGCAACTTACTATTGTCAACAGAGTTACACAACCCCTCGGACGTTGGGCCAAGGGACCA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.2%; Score 229; DB 33; Length 384;
Best Local Similarity 86.3%; Pred. No. 1.56e-142;
Matches 271; Conservative 0; Mismatches 43; Indels 0; Gaps
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Search completed: Tue Feb 24 09:01:01 1998 Job time: 62 secs.

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Release 2.1D John F Callins, Riccomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Twe Feb 24 08:49:27 1998: MasFar time 136.04 Seconds 689.884 Million cell updates/sec

Tabular cutput not generated.

Title: >US-08-844-215-19
Description: (1-372) from US0894421E.seq
Note: 372 | GASGISCAGITGIDAGIC
N.A. Sequence: 1 GASGISCAGITGIDAGIC

Scoring table: TABLE default Gap 6 Nmatch SID · Dbase 0; Query 0

Searched: 333433 segs, 126143548 bases x 3

Post-processing, Minimum Match 0% Listing first 45 summaries

1

Database:

Statistics: Mean 9.959; Variance 1.948; scale 5.112

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	### ### ### ### ### ### ### ### ### ##
Tescription	1 84 22.6 597 24 AA472093 Thinang ri Shares mou 2 996114 2 94 22.6 597 83 MMIZESES THIDANG RI Shares mou 2 9961114
ŭ1	597 24 AA472093 597 83 AM1262658
Sult Query No Score Match Length DR ID	100 100 100 100 100 100
Query Match	80 80 44 44 64 64 64 64 64 64
SOUP	80 G
Result	= 4

6 20.4 435 80 HSAA7475 nb76c05.81 NCI_CGAP_H I. 14.5 266 54 HS3C02138 nv47bc7 r1 Scarce con 3 8.1 236 57 HS3L27679 r445bc7 r1 Scarce con 3 8.2 238 69 HS3C044 aa53901.r1 NCI_CGAP_G 3 8.3 238 69 HS3C044 aa53901.r1 NCI_CGAP_G 4 7.8 511.7 AA504794 ax83401.r1 NCI_CGAP_G 4 7.8 511.17 AA504794 ax83401.r1 Scratace con 4.5 259 66 HS1281117 ab12f07.r1 Scratace 6.2 259 66 HS1281117 ab12f07.r1 Scratace 6.3 259 66 H	1 DMS02055 1 1 DMS02055 1 1 5.6 189 18 HS1259169 aa23c11.51 NOT_CGAP_G 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2.0 5.4 470 C. HSI244837 2W27045.11 States ova 4.750-03 5.4 540 25 AA47527 3E1005.11 States ova 4.750-03 5.4 540 24 MMI26504 3E1005.5.11 States ova 4.750-03 2.0 5.4 563 57 MMI26504 2W54407.51 Scares tot 4.750-03 2.0 5.4 597 21 AA28606 2S93al2.11 NCI_COAP_G 4.750-03 2.0 5.4 597 51 HSI184459 2S93al2.11 NCI_COAP_G 4.750-03 2.0 5.4 598 MHSI2459 2S93al2.11 Stratagene 4.750-03 2.0 5.4 736 28 AA48703 SWHFCA20525K Brudia m 4.750-03 2.0 5.4 736 45 BMI27202 SWHFCA20525K Brudia m 4.750-03 2.1 73 50 HSI16501 ZS11610 S1 NJ_COAP_G 6 30-02 2.1 73 19 HJMSNS574 human chromosome 7 ST 6.390-02 2.2 51 HSI281854 August of Stratageone 6.390-02 2.3 6 HSI281854 August of Stratageone 6.390-02	9 5.1 336 2 G03711 Annan STS WISSON AND F 5.1 353 65 HS1205924 av11905 51 G037es NhH 6 5.1 353 65 HS1205924 av11905 51 SOATES NhH 6 5.1 410 81 MM12050713 v780h12.1 SOATES mon 6 5.1 442 76 HSAA35248 nh99912.51 NOIZGAP.B 6 5.1 442 76 HSAA35248 nh99912.51 NOIZGAP.B 6 5.1 524 4 AA51374 human STS SHG7335C0. 6 5.1 836 42 AA521502 ni29a05.51 NCI_CGAP_1. 6 5.1 836 42 AA521502 ni29a05.51 NCI_CGAP_1. 6	A4472093 S97 bp mPNA EST 18-JUN-1997 Vh10805.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone 977244 % similar is gE-S6756.13 SAMMA-1 CHRIN C WITTON (WWAN). 91 L37438 Mus musculus getmiline imunicalicbulin gamma constant A472093 40.20084 EST. Nouse mouse. Nus musculus Bukaryotae: mitochondrial eukaryotes, Metazca, Chordata: Nus musculus Bukaryotae: mitochondrial eukaryotes, Metazca, Chordata: Nus musculus Bukaryotae: mitochondrial eukaryotes, Metazca, Chordata: Nus musculus Bukaryotae: Mus. 1 (Bases 1 to 597) Marra M., Hillier.L., Allen.M., Bowles.M., Dietrich.N., Dubuque.T., Gelsel.S., Kucaba.T., Lacy,M., Le.M., Martin.J., Morris.M., Schellenberg.K., Steptee.M., Tan.F., Underwood,K., Morre.B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Warrston,R. Contact: Marra M/Mouse EST Project Wishington University SPE-1 of MedicineP
		TURRESTE CONTROLLES CONTROLS C		ITION ITION SICON
00			00000 00	RESULT LOCUS DEFIN NID NID SOURCE ORGE ORGE AUTH TITH

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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lll gaagggaagettgaggagtetggaggaggettggtgcaaeetggaggateeataaaaete 170
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Vertebrata, Eutheria; Rodentia, Sciurognathi, Muridae, Murinae,
Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares mouse mammary gland NbMMG"/sex="male"
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Pred. No. 2.99e-114;
                                                                                                                                          Seq primer: -28ml3 rev2 ET from Amersham
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21-JUN-1997 (Pel. 52, Jast updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 t
                                                                                                                                                                                                                           /organism="Mus musculus"
                                                            mouseest@watson.wustl.edu
                                                                                                                                                              High quality sequence stop: 440
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/lab_host="DH108"
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                                                                                                                                                                                                                                              /strain="C57BL/6J"
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|larity 69.4%;
|Conservative
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314 286 1810
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                                                            Email:
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/note="Vector: pT713D-Pac (Pharmacia) with a modified boylinker; Site_1, Not 1, Site_2, Eco RI, 1st strand CDNA was primed with a Not 1 - oligo(d1) primer [5' briner forthy and the strand spanning with a strand-spanning spanning boyling b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 3/1; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by Dr. Minery Ko, Wayne State Univ Library constructed an
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LoTU-1997 (Rel. 52, Last updated, Version 2)
nh76-05 s1 NCT_GGAP_RT1 Home sapiens cDNA clone 964424 similar to
gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION (HUMAN);.
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                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of ModicineP 4444 Forest Park Fathway, Box 8501, St. Louis, MO 63109 Fel: 314 286 1800 Fax: 414 286 1810 Fax: 414 286 1810 Fax: 414 286 1810 Fax: 414 286 1810 Faxily mouseest@wasson wustl edu fhis clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image lnl gov) for further information MGT-514504 Seg primer "28m13 rev2 ET from Amersham High quality sequence step.
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                              Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schelleherg K., Steptoe M. Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson
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/clone_lib="Soares mouse mammary gland NbMMG"
/sex="male"
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0; Mismatches 84;
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                           "The WashU-HHMI Mouse EST Project";
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Matches 204; Conservative
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                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                                   Unpublished.
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Query Match
Best Local Similarity 83.5%;
Matches 132, Conservative
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Unpublished (1997)
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92056386
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                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                      FEATURES
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                                                    COMMENT
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nh76c05.s1 NCL_CGAP_Brl 1 Home sapiens cDNA clone 964424 similar to
gb.X14.884 IG HEAVY CHAIN PRECUPSOR V-III PEGICN (HUMAN);...
AASO7475
                                                                                                                                                                                                                                                                                                                                                                                                                                /note=Vector: privates
/note=Vector: privates
polylinker: lst strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
olgo dff) primer. Double-stranded cNNA was ligated to Eco
PI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified privateror. Library is not normalized. (The normalized version
of this library is NCI_CGAP_Br2.) Library was constructed
by Rento Soares and M. Fatima Bonaldo."
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Eukaryotae: mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata: Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                       Contact: Fobert Strausherq, Ph D Tel: (301) 495-1550 Email: Robert_Strausherg*Lih.gov lissue Procurement: Christopher Meskaiuk, M. D. Ph D. Michhael P. Emmert. Ruck. M. D. Ph D. Punhael P. Emmert. Ruck. M. D. Ph D. Punhael P. Emmert. Ruck. M. D. Ph D. Annallbrary Preparation: M. Bento Soares, Ph.D. cDNA library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I M. A. G. E. Consortium/LLNL atwaw-bloolling-gov/bbrp/image/Annage.html Insert Length: 558 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saps
                                                                                                                                       "National Cancer Institute, Cancer Senome Anatomy Project (CSAP),
Tumor Gene Index";
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Pred No 1 18998;
0, Mismatches 20, Indels
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/sex="female, pooled"
/tissue_type="breast"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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us 132, Conserved
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NCI-CSAP.
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                Homo sapiens (human)
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                                                                                                                        NCI - CGAP:
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/organism="Homo sapiens"
/organism="Homo sapiens"
/note="Vector: p1713D-Pac (Pharmacia) with a modified
polylinkor; lst strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I
coligo(dT) primer. Double-stranded cUNA was ligated to Prepare the Not I and coligo (dT) primer. Double-stranded cUNA was ligated to Prepare the Not I and CDO RI sites of the modified p1713
vector Library is not normalized version of fils library is NOLLOSAP_ET2.) Library was constructed by Bento Soares and M. Fatima Bonaldo."
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome sequencing Center
Clone distribution
Clone distribution NII-CSAP clone distribution information can br
found through the I M. G. G. Chonsortium/LINI at:
                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberginih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael H.
Emmert-Buck, M.D., Ph.D.
National Gancer Institute, Cancer Genome Anatomy Project (CGAP).
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22-MAY-1997 (Pel, S2, Last updated, Version 2)
22-MAY-197 (Pel, S2, Last updated, Version 2)
224MA07 r1 Scares ovary timer NHOT Home sapiens CDNA clone 741161
5' similar to qb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.
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Vertebrata: Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76: DP 40: Length 4-1. Pred. No. 1.188-98: wirms-hes 20, Indels
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Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jos
Kucaba T., Lacy M., Le N., Lencon G., Marra M., Martin J.,
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/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
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HS1202138 standard; RNA: EST; 266 BP.
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25-MAY-1997 (Rel 52. Last updated, Version 1)
2v40b02.rl Soares ovary timor NBHOT Rome sapiens CDNA clone 755939
5' similar to qb:M87789 is GAMMA-1 CHAIN C RESION (HUMAN):
                                                                                                                                                             School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel. 314 286 1800 Fax. 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       School of Medicine 4444 Forest Park Pařkway, Box §501, St. Louis, Me 5108 Tel: 314 284 180; Fax: 314 284 181; Email: estëwatson wustl equ This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK WashU-Merck EST Project Washington University
                                                                                                                              Contact: Wilson RK WashU-Merck EST Project Washington University
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                                                                                                                                                                                                                                                         LLNL; contact the IMAGE Consortium (info@image.lln1.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham. 
Location/Qualifiers
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Moore B., Schellenberg K., Steptoe M., Tan F., Theising B. White Y., Wylie T., Waterston R., Wilson R.; "WashU-Merck EST Project 1997";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 266;
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Pred. No. 3.39e-57;
0; Mismatches 59
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                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Local Similarity 66.5%;
es 119; Conservative
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                                                                                                   Unpublished.
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/note="Vector: pT713D-Pac (Pharmacia) with a medilied popylinker, Site_1 Not 1. Site_2 = Esc Rt. Ist strand TRNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M.Schudt (WT), fr. Havid Allman (NCI) and Dr. Gerald Marti (CBRP). CNNA synthesis was primed with a Not 1 - oligo(dT) primer.
                                                                                                                                              Gaps
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Robert_Strausberg@hl.gov Tissue Procurement: Louis M. Staudt.
M.D., Ph D., David Allman, Ph.D., caraid Marti. M. P. ChNA Library
Preparation: M. Bento Soares, Ph D. M. Fatima Bonaldo Ph D. ChNA
Library Arrayed by: Greg Lennes, Ph.D. DNA Sequencing Ph D. ChNA
Mashington University Genome Sequencing Center Clone distribution:
UNICGAPP clone distribution information can be found through the
I.M.A.G.E. Consortium/LNM at:

www-bio.llni.gov/bkrp/image/lmage.html Traps considered overall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUL-1997 (Pel. 52, Created)
64-JUL-1997 (Rel. 52, Last updated, Version 1)
aa65g01 r1 NCT CGAP GCB1 Home sapiens CINA clone 825648 5' similar
to SW-HV05_McGSE POIT4e IG HEAVY CHAIN PPECHESOP V PECTON :
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Tumor Gene Index";
Unpublished.
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Seq primer: -28ml3 revl ET from Amersham High quality sequence
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Vertebrata; Mammalia, Eutheria, Primates, Catarrhini, Hominidae:
further information. Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib~"Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 230 RP, 40 A; 84 C, 70 G, 36 T, 0 other;
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                                                                                                                                /organism="Homo sapiens"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
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Local Similarity 100.0%;
nes 34; Conservative
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Sequence 511 RP: 105 A:
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DNA Sequencing by: Washington University Senome Sequencing Center
Clone distribution: NII-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNI
                       31. Double-stranded cDNA was ligated to Eco PI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTP3 vector. Library wen
                                                                                                                                                     through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA505044 238 bp mRNA EST 02-JUL-1997 aa53901.rl NCI_CGAP_GCB1 Homo sapiens CDNA clone 825648 5' similar to SW.HV05_MOUSE P01749 IG HEAVY CHAIN PRECUPSOR V REGION ;
National Cancer Institute, Cancer Geneme Anatomy Project (CGAP),
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 eccggggggtetetgaggateteetgtgagaettetggataeagetttaceagegaetgg 79
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Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tue, mitochoodilal vakaryotes. Metazoa, Chordata:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 238,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                             /tissue_type="germinal center B cell" /lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                          57 A: 69 C: 66 G: 46 T: 0 Other;
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Pred, No. 3.45e-21;
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                                                                                                                                                                                                                 /clone="925648"
/clone_lib="NCI_CGAP_GCB1"
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Rest Local Similarity 66.34.)

Matches 67. Conservative
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Unpublished (1997)
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3.) Double-stranded cDNA was limited to Eco RI adaptors
(Pharmacia), digested with Not I and cioned into the Not
and Eco RI since so if the modified pill? vector: Library
went through one round of normalization, and was
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                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo."
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278-JUN-1997 (Pel. 52, Last updated, Version 1)
278-3107 rl Scares ovary tumor NeH3T Home satiens CDMA clone 410-177
5' similar to giv.L21964 16 HEAVY CHAIN V-11 PEGION (HUMAN);.
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Box 83108 Tel: 314 285 1800 Fax: 314 285 1810 Email:
LINE: contact the IMAGE Connection (info*image line dov) for further information. Seq primer: 28ml3 rev2 ET from Amersham High quality sequence stop: 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising R., White Y., Wylie T., Waterston R., Wilson R.; "Washu-Merck EST Project 1997";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson PK Washd-Merok EST Project Washington University
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Vertebrata: Eutheria, Primates, Catarrhini, Hominidae, Homo.
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O: Mismatches 34; indels
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/lab.bost="DH10B (ampicillin resistant)"
<1..>511
                                                                                                                                                                   /clone_lib-"NCI_CGAP_GCB1"
/tissue_type-"germinal center B cell"
/lab_host="DH10B"
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/clone_lib="Soares ovary tumor NbHGT"
/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                           Score 33;
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                                                                                                                                     /clone="825548"
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Rest Local Similarity 66.3%.
Matches 67: Conservative
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69 ر
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HS1258634
AA464794;
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169 C: 124 G: 112 T: U other:

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HS1281117
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5' similar to gb:L21964 IG HEAVY CHAIN V-II REGION (HUMAN);
AA454794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 revz ET from Amersham High quality sequence stop: 414.

Location/Qualifiers
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                                                                                      Gaps
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,P. and Wilson,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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        Query Match 7.8%; Score 29; DB 65; Leugum 21.8est Local Similarity 85.4%; Pred. No. 4.40e-15; Indels
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/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 4.40e-15;
0; Mismatches 6;
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es 35; Conservative
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AA488043 259 bp mRNA EST 24-JUN-1997 abilf07.rl Stratagene lung (#937210) Homo Sapiens GDNA Gloche 840613 5/ similar to gb:S55735 IG ALPHA-1 CHAIN C REGION (HUMAN);. 92215474
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/note="organ: lung; Vector: pBluescript SK++ Site_1+ FroR1
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Hillier,L., Allen,M., Rowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kuraha,T., Lary,M. Le,N. Tennon G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,R., White,Y., Wylie,T., Waterston,P. and Wilson,R. WashU-NCI human EST Project
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Vertebrata, Mammalia, Eutheria, Frimates, Catarrhini, Hominidae,
                                                                                                   27-JUN-1997 (Rel. 52, Created)
27-JUN-1997 (Rel. 52, Last updated, Version 1)
abl2f07.rl Stratagene lung (#937210) Homo sapiens CDNA clone 840613
5' similar to qb:$55735 IG ALPHA-1 CHAIN C REGION (HUMAN):.
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Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
1800 Fax: 314 286 1810 Email: estimation wistl.edu This clone is available royalty-free through LLN.: contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml? revl ET from Amersham.
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Heminidae,
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/lab_host="SOLR cells (kanamycin resistant)"
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Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,
Theising B., White Y., Wylie T., Waterston K., Wilson R.;
"Wash"-NCI human EST Project";
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/sex="male"
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standard; RNA; EST; 259 BP.
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Homo sapiens
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ECORI: Site_2: Xhoi: Cloned unidirectionally. Prime:

Olige of normal lung Average insert size: 1 0 kb;

30: 23 A AR Vector: 15 adaptor sequence: 5 SAXIGSGAGAG

Zelone-"840613"
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Submitted (15-APR-1996) Michael Ashburner, Department of Genetics,
Downing St., Cambridue CB2 3EH, England
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
Eukaryotas; mitochondril eskuryotas, Mctanku, Arthropodi,
Tracheata, Insecta, Pterygota, Diptera, Brachycera, Muscomorpha;
Ephydroidea; Drosophildas; Drosophila,
1 (bases 1 to 155)
European Drosophila Mapping, Consortium,
                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Tonsortium (info@image.ilul.gov) for further information
Seq primer: -28ml3 revl ET from Amersham.
Location/Qualiflers
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BLAST_program = BLASTX
                Machington University School of Medicine
4444 Folest Park Parkway, Box 8701, St. Louis, Mc 63108
1814 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="SOLR cells (kanamycin resistant)"
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Best Local Similarity 96 0%; Pred. No. 9.95e-07;
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/sex="male"
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/strain="Orecon-P"
/clone="3607"
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orightof_clone = Gredon-R
in_site_site_primary = 98C
BLAST_program = BLASTN
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database_version = 32.0
date_of_search = 15-12-1395.
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/organism="Neocor. FTT3D pac (Pharmacia) with a modified polylinber. Site_1: Not_2: Eco RI: Ist strand cina was prepared from human tonsiliar cells entiched for germinal center B cells by flow sorting (GD20: Id**). provided by Dr. Louis M. Staudt (NGI), Dr. Davish Allman, provided by Dr. Louis M. Staudt (NGI). Dr. Davish Allman, provided with a Not I - olive(dT) primer contact and Dr. Gerald marti (GPE). GDNA synthesis was primed with a Not I - olive(dT) primer contact and Dr. Gerald Marti (GPE). GDNA synthesis was primed with a Not I - olive(dT) primer contact and contact and closed to Eco RI adaptors (Pharmacia), digested with Not I and closed into the Not I.
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Vertekrata, Mammalla, Eutheria, Primates, Gatarrhini, Hominiday,
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This clone is available royalty-free through LINL : contact the
IMAUS Consortium (infortmagec.llnl.gov) for further information.
Seg primer: -41mil fwd. ET from Amersham.
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0: Mismatches 12; Indels
Length 156:
                                                         6; Indels
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/clone_libr"NCI_CGAF_GCB1"
/tissue_type="germinal center B cell"
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Pred. No. 1.86e-05;
23; Mismatches 6;
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Tel: (301) 496-1550
Email: Robert C
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Matches 33; Conservative
Ouery Match
Best Local Similarity 14.78,
Matches 5; Conservative
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through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." /clone="814100"
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19-JUN-1997 (Rel. 52, Last updated, Version 1)
aa23cll.sl NCI_CGAP_GCR1 Homo sapiens CDNA clone 814100 3' similar
to gb:D90209 DNA-BINDING PROTEIN TAXREB67 (HUMAN);.
                                                                                                                                                                       Confact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
Robert_Strausberg@nih.gov This clone is available royalty-free
through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Seg primer: -41ml3 fwd. ET from Amersham.
Key
                                                                                                                                    "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                    Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="germinal center B cell"
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Sequence 189 BP; 32 A; 68 C; 59 G; 30 T; 0 other;
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Pred. No. 3.13e-04;
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Best Local Similarity 73.3%;
Matches 33; Conservative
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Title: Descriptin: Perfect Score: N.A. Sequence:	
comp: Scoring table:	CGCCICGAGIGGSTTAGAGST
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90 BCT1 24:80T2 25:80T3 25:80T4 27 ROTE 29:R0T6 29:R0T7 31:R0T9 31:R0T9 32:R0T1 33:R0T11 34:R0T12 35:R0T3 35:R0T3 35:R0T1 34:R0T12 35:R0T3 35:R0T1 34:R0T12 35:R0T13 36:R0T1 37:R0T9 31:R0T9 35:R0T1 3 emblinew7 1.BCT 2:FUN 3:SEN 4:HTG1 5:HTG2 6:HTG3 7:HTG4 8:HCM1 9:HTM2 10:HGM1 11:TNV1 12:INV7 13:OPS 14:MAN 15:VPT 16:FUN 17:FPG1 19:FPG2 19:FPG 27:SYN 21:FUN 22:VIP Minimum Match 0% Listing first 4° summaries u-embl51_101 142:part1 143:part2 genbanka191 qenbankb101 114:UNA Database: Database: Database: Database: Database:

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/translation="AQLLGLLLMLPGAPCDIQMTQSPSSLSASVGDPVIITCRASQS
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Expressed humanichenian kappa genes and their hypermutation
Eur. J. Immunol. 23 (12), 3248-3262 (1993)
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DEFINITION H.sapiens rearranged immunoglobulin kappa light chain V-region
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Pred. No. 5.04e-234;
0; Mismatches 17; Indels 0; Gaps
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Submitted (01-SEP-1994) M.Welschof, University of Heidelberg,
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Vertebrata: Butheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 348)
                                                                                                                                                                              /tissue_type="spleen"
/clone_lib="lambda zap II phage library"
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/product="lg kappa light chain (VJ)"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"Ig kappa light chain (VJ)"
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                                                                                                                                        /organism="Homo sapiens"
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                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="J-Kappa 1"
                                                                                                                                                                                                                      /chromosome="2"
/clone="I.131"
                                                                                                                                                             /isolate="M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.6%;
Best Local Similarity 94.6%;
Matches 297; Conservative
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/translation="ĎIVMTQSPSSLSASVGDRVITTCRASQSISSYLNWYQQKPGKAP
KLLIYAASSLQSGVPSRFSGSSGSIDFILLISSLQPEDFAIYYCQGSYSIPKIFGQGT
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H.sapiens mRNA for Ig light chain, variable region (ID:CLL057VL).
X84346
  of Transplantation Immunology, Im
                                                                             WELSCHOF,M., TERNESS,F., Kolbinger,F., ZEWE,M., DUFRFI,S., DOERSAM,H., Hain,C., FINGER,M., Jung,M., Moldenhauer,G., Hayashi,N., Little,M. and OPELZ,G. Amino acid sequence based PCK primers for amplification of rearranged human heavy and light chain immunoglobulin variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 agiggatoigggacagaitteacicteaceateageagictgeaaceigaagaittigea 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 gcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaagceect 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 GCAAGTCAGAGTATTAGCAGGAACTTAAATTGGTATCAGCAGAAACCAGGGACAGCCCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 aageteetgatetatgetgeateeagtttgeaaagtggggteeeateaaggtteagtgge 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 acceagtetecatectecetgtetgeatetgtaggagacagagteaceateaettgeegg 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="immunoglobulin kappa light chain variable
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1 (bases 1 to 322)
Hashimoto,S., Dono,M., Wakai,M., Allen,S.L., Lichtman,S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="peripheral B-cell"
/clone_lib="immunoglobulin cDNA library"
/clone="49"
Institute of Immunology, Dept of Transplantati
Neuenheimer Feld 305 69120 Heidelberg, Germany
2 (bases 1 to 348)
                                                                                                                                                                                                                     region genes . In Immunol. Methods 179~(2),~293.214~(1995)
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/tissue_type="blood"
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                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/db_xref-"GDB:G00:128-432"
                                                                                                                                                                                                                                                         /codon_start=1
/product="Ig heavy chain"
                                                                                                                                    /organism="Homo sapiens"
/map="22q11.1-q11.2"
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/db_xref="PID:9619624"
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Matches 295; Conservative
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/db.xref="PID-9791034"
/db.xref="PID-9791034"
/transletion="bIQMTQSPSSISASVSDRVIITCRASQSISSYLNWYQQREGKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLI IYAASSI QSGVPSRESGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPPTFGQGT
KVEIK"
                            Somatic diversification and selection of immunoglobulin heavy and
light chain variable region genes in 193+ 3D5+ chronic lymphocytic
leukemia B cells
                                                                                                                                                                    Submitted (01-FER-1995) N. Chlorazzi. North Shore Universit/
Hospitai. Cornell University Medical College, 300 Community Drive,
Manhasset, New York 11036, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 giggeagiggaicigggaecagaitteacteteaceateageagietgeaacetgaagait 247
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Vertebrata; Eutheria; Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
Schulman, P. Vinciquerra, V.P., Ferrarini, M., Silver, J. and
                                                                                                                                                                                                                                                                                     /cell_type="B lymphocyte"
/cell_line="CLL057 x HMMA 2.1 heterohybridoma"
/chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Prod No. 4 220-272,
0: Mismatches 18; Indels
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M74019
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Homo sapiens
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Chiorazzi, N.
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                   Chiorazzi, N.
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                                                                                                                                      AUTHORS
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                                                                                                                      REFERENCE
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                                   TITLE
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Silberstein, L.E., Tefferies L.C., Goldman, J., Friedman, D., Moore, J.S., Nowell, P.C., Roelcke, D., Pruzanski, W., Poudior, T. and Silverman, G.J., Variable region gene analysis of pathologic human autoantibodies to the related Land I red blood cell antiqens. Blood (1991) In press.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MMMRVPAQLLGLLLMHPGAPCUIQMIGSPSSLSASVGDRVIIT
GRASGSISSYLMWYQQRPGKAPKLLIYAASSLQSGVPSPFSGSGSGIDFILIISSLUF
EDFATYYCQQSYSTPWTFGQGTKVEIKRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="bigmigspssisAsVgnRVTITGPAS@SISSY:\WY@@KPGKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLLIYAASSLQSGVPSFFSGSGSGIDFILLISSLQPELFALYYOLOSYSIPWIFGLGT
KVEIKRTVAAPSVFIFPPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"This CDS feature is included to show the translation of the corresponding V_region, Presently translation qualifiers on V_region features are illegal."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="immunoglobulin light chain variable region" /db_xref="PID:g186043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 agatgacccagtctccatcctccctqtctqcatctgtaggagacagaatcactcaccatrarit 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 geogggdaagteagageattageagetatttaaaattggtatkageagaaaeeadugaaag 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GCGGGGAAGTCAGAGTATTAGGAGAATTTAAATTGGTATCAGGAAAAGAAGAAGAAGAAGA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 occetaagetectgatetatgetgeatecagtttgeaaagtgggteeeateaaysttea 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 CCCCIAAGGICCTGAICTAFGIGCAICCAGTIGGAAAGIGGGGICCCATCGAGGIICA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 SIGGEASTGSAIGTESSACASATTTCACTCTCACCACCACCACCTCAACATT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 tigoaactiactactgtcaacagagttacagtaceccatggacgtioggcoaagguace 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="lmmunoglobulin light chain variable region"
67...>429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 19: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unmutated 15P3B3 V kappa 1 gene"
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301 aagctggagatcaaa 315 ||| ||| ||| ||||| 304 AAGGTGGAAGTCAAA 318

Dp 53

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/db_xref-"PID=g567158"
/translation-"ELTGSPSSLSASVGDRVTITCRASQSISSYLNWYQUKPGKAPKL
LIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSFPQTFGGGTKL
EIKRIVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation of the corresponding V\_region. Presently translation qualifiers on V\_region features are illegal."
                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 328)
Collet, T A, Poben, P, O'Kennedy, R., Rarbas, C.F. III., Burton, D P and Lerner, P A binary plasmid system for shuffling combinatorial antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ċ
                                                                                        immunoglobulin gamma chain; immunoglobulin heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 gecectaageteetgatetatgetgeatecagtttgeaaagtggggteecateaaggtte 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 agtggcagtggatctgggacagatttcactctcaccatcagcagtctgcaacctgaagat 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 tgccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 GOGGCTAAGSIGGIGATGIAGGGGATGCAGITIGGAAAGIGGGGTGCCATGGAGGTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 AGTGGGAGTGGATTTTGGAGAGATTTGACTTTTAACTATCACAATCTGAAACTTGAAGAT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 tttgcaacttactactgtcaacagagttacagtacccctcagacttttggccaggggacc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (tissue library: BMHIV) adult bone marrow cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 gageteacceagtetecateetectettgeatetgtaggagagaeagagteaceateaet 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 274, DE 99, Length 328,
Pred. No. 2.690-227;
0; Mismatches 21; Indels 0; Gaps
  09-NOV-1994
HUMIGHHC 328 bp mPNA PRI 09-NOV-19
Human Ig rearranged gamma-chain mRNA V-region, partial cds
                                                                                                                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A. 89 (21), 10025-10030 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="This CDS feature is included to show the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="bone marrow"
/tissue_lib="BMHIV"
/lab_host="XL1-Blue"
/map="14q32.33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="T-cell"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="IGHV@"
/note="G00-128-528"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 9
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Best Local Similarity 93.3%;
Matches 294; Conservative
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88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /partial
                                                                                                                   processed gene
                                                                                                                                                                                   Homo sapiens
                                                                                           V-region;
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                      DEFINITION
                                                                                                                                                                                   ORGANISM
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                                                 ACCESSION
                                                                                                                                                                                                                                                      REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
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                                                                                        KEYWORDS
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                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                         SOURCE
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/note="V kappa 1 segment, close to germline gene KL 02/012 (Acc.No. X59315)"
                                                                                                                                autoantibody-related; constant region; immunoglobulin;
immunoglobulin light chain; joining region; kappa chain; variable
                                          H sapiens rearranged mPNA for polyreactive natural autoantibody (Igk VJC region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="peripheral blood B-lymphocytes"
/cell_type="EBV transformed b-lymphocytes, fused with
heteromyeloma cell line CB.F7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 agatgacccagtctccatcctcctgtctgcatctgtaggagacagagtcaccatcactt 75
                       27-FFR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-DEC-1995) H. Eibel, Klinikum der
Albert-Ludwigs-Universitaet Freiburg, Klin. Forschergruppe f.
Rheumatologie, D-79108 Freiburg, FRG
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             Production and molecular characterization of a monoclonal, bylyeactive 19Mk natural autoantibody with rheumatic factor activity: A highly cross-reactive natural autoantibody uses germline VH and VL segments which are frequently found in
                                                                                                                                                                                                        Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Pertebrata; Eutheria; Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 346)
Eysenbach, G. and Eibel, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /isolate="patient EFK with rheumatoid arthritis"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 86.1%; Score 273; DB 91; Length 346; Loral Similarity 93.3% Frod No. 2.450-226. es 293; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="J kappa l segment (unmutated)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult (69 years old)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="rearranged VJ region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PCR primer VK1BACK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PCR primer HVKFOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="c kappa region"
1 96 c 82 g
                                                                                                                                                                                                                                                                                                                                                                                                                   high-affinity autoantibodies
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="CDR1 region"
156..176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="CDR2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"CDR3 region"
                         PNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="G1.B6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rearranged
                         346 hp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 346)
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autoantibody; Iq J-seqment; Iq kappa light chain; Iq subgroup I; Ig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning of a human autoimmune response: preparation and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"IqG1/K anti-thyroid peroxidase autoantibody Fab"
/product-"Iq Kappa light chain variable region, subgroup
I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.R.,
Colls,J.C., Peege,C.A.S., Peege-Smith,R., and Burton,D.R.
Probing the human anti-thyroid peroxidase repertoire of a
Hashimoto's thyroiditis patient using combinatorial phage display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a human anti-thyroglobulin autoantibody using a cembinatorial
188 atggragtggatetggggaeagattteaeteteaecateageagtetgeaaeetgaagatt 247
                                                                                                                                                248 tigoaactiactactgicaacagagitacagtaceceteggagittiggecaggggacea 307
                                                                                                                                                                                        Furmaniak, J., Pegg, C., Burton, D.P. and Smith, B.P.
                                                                                                                                                                                                                                                                                                                                                             30-MAR-1995
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Submitted (25-77N-1993) J Hexham, Toly of Sheffleld, Dept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata: Butheria; Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 321)
                                                                                    Colls.J.C. Pegg.C. Bees Smith, B. and Burton.D.R. Cloning and characterisation of TPO autoantibodies using combinatorial phage display libraries Autoimmunity 17 (3), 167-179 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae: mitochondrial eukaryotes: Metazoa; Chordata;
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Score 268; DB 91; Length 321; Pred. No. 1.55e-221;

94.58; 92.48;

Best Lonal Similarity

Query Match

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/db_xref="PID:9567136"
/translation="BLTQSPSSLSASVGDPVTITCPASQSISSY:NWYQQKPGKAFK;
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                                                                                                                        61 tgoogggoaagtoagagcattagcagotatttaaattggtatcagcagaaaocogggaaa 120
                                                                                                                                                                  64 TGCCGGCAAGTCAGAGTATTAGCAGGAACTTAAATTGGTATCAGCAGAAACCAGGGACA 123
                                        1 gageteaeceagtetinnatnetinentatintginatetgiaggagagagagteaecateaet 60
                                                            (); Saps
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Vertebrata: Eutheria: Primates, Catarrhini: Hominidao: Homo.
1 (bases 1 to 322)
Collet I.A. Poben.P., O'Kennedy.P., Barbas.C.F. III., Burtos and Lerner,R.A.
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93066172
0; Mismatches 24; Indels
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/tissue_lib="BMHIV"
/lab_host="XL1-Blue"
/map="14q32.33"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain;
                                                                                                                                                                                                                                                                                         181 agtggcagtggatctgggacagatttcactctcaccatcagcagtctgcaacctgaagat 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (tissue library: BMHIV) adult bone marrow cDNA to
                                                                                                                                                                                                                                             tgccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaa 120
                                                                                                                                                                                121 gecectaageteetgatetatgetgeatecagtttgeaaagtggggteecateaaggtte 180
                                                                                                                                                                                                                                                                                                                         184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCACCAGTCTGCAACCTGAAGAT 243
                                                                                                                                                                                                                                                                                                                                                      241 tttgcaacttactactgtcaacagagttacagtaccccgtacacttttggccaggggacc 300
                                                                                             1 gageteacceagtetecatectecetgtetgeatetgtaggagagagagagteaceateact 60
                                                                                                            09-NOV-1994
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A binary plasmid system for shuffling combinatorial antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION Human Ig rearranged gamma-chain mRNA V-region, partial cds. ACCESSION L03160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
93066172
                                                              0;
                            Score 268, DB 99; Length 322;
Pred. No. 1.55e-221;
0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="T-cell"
/dev_stage="adult"
/tissue_type="bone marrow"
/tissue_lib="bMHIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /partial
/gene="IGHV@"
/note="G00-128-528"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 bp
                            Ouery Match
Best Local Similarity 92.4%;
Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      301 aagctggagatcaaa 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 AAGGTGGAAGTCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   processed gene.
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ORIGIN
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/translation="ELTOSPSSLSASVGURV111CRASQS1SSYLNWYQQKPGKAPKL
LIYAASSLQSGVPSRFSGSGSGTUFTLLISSLQPEDFATYYCQGSYSTPYTFGGGTKL
EIKRTVA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01.SEP-1994) M.Welschof, University of Heidelberg, Institute of Immunology, Dept. of Transplantation Immunology, Im Neuenhelmer Feld 305 69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WELSCHOF,M., TERNESS,P , Kolbinger,F , ZEWE,M , DUEBEL,S., DOFRRAM,H., Hain,C., FINGER,M , Jung,M , Moldenhawer,G , Hayashi,N., Little,M. and OPELS.G. Amino acid sequence based PCk primers for amplification of rearranged human heavy and light chain immunoglobulin variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSIGVKC47 348 bp DNA PRI 19-OCT-1995
H.sapiens rearranged immunoglobulin kappa light chain V-region
                                                                                                                                                                                                                                                                                                                                                                                                            181 aqtggcaqtggatctgggacagatttcactctcaccatcagcagtctgcaacctgaagat 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 tttgcaacttactactgtcaacagagttacagtaccccgtacacttttggccaggggacc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 tgccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaaa 120
                                                                                                                                                                                                                                                                                                    4 GAGCICACCCAGTCICCATCGTCCTGCATTGINGGAGACAGAGTCACCATCACT 63
                                                                                                                                                                                                                                                                        1 gagotoaccoagtotocatoctocotgtotgcatotgtaggagacagagtoaccatcact 60
                                                                                                                                                                                                                      Gaps
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Vertebrata; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 348)
WELSCHOF,M.
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                                                                                                                                                               Score 268; DB 99; Length 326; Fred. No. 1.55c-221;
                                                                                                                                                                                                                    0: Mismatches 24: Indels
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/clone_lib="immunoglobulin cDNA library"
/clone="47"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin kappa chain; variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region genes
J. Immunol. Methods 179 (2), 203-214 (1995)
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/tissue_type="blood"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                  6 97
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<1..>340
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                                                                                                                                                             Query Match
Best Local Similarity 92.4%;
Matches 291; Conservative
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//rodon_start=1
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YCQUSYNIPWIFGGTTKVEFFFVA"
52 ?35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-APP-1993) H.G. Zachau, Institut fuer Physiologische
Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 363)
Klein P Jaenichen.R. and Zachau.H.G.
Expressed human immunoglobulin kappa genes and their hypermutation
Eur. J Immunol. 22 (12), 2248-3262 (1993)
94080891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSIGKLV56 383 bp RNA PRI 31-JAN-1994
H.sapiens mRNA for rearranged Ig kappa light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-region: immunoglobulin; J-segment; kappa light chain; V-region
                                        76 googgoaantoagagoattagoagotatttaaattggtatoagoagaaaooagggaaag 135
                                                                                     65 nonggarasteasantattaseasaasttaaattaatataaasaas 124
                                                                                                                                   136 recetaageteetgatetatgetgeateeagtttgeaaagtggggteeeateaaggttea 195
                                                                                                                                                                           125 occetaadgieeigaietalgergeafocagitigeaaasiggsgieeearesaagiida 184
                                                                                                                                                                                                                           196 giggcagiggateigggacagatitcantnicaceatcagnagicigcaaceigaagati 255
                                                                                                                                                                                                                                                 256 ttycaacttactactgtcaacagagttacagtaccccgtggacgttcggccaagggacca 315
                                                                                                                                                                                                                                                                                                                                                               245 TIGGAACTIACTATIGICAACAGAGITACACAACCCCICGGACGITGGGCCAAGGGACCA 304
5 AGC#CACCCA67C10CA1GG1GCGTG1CFGATT1G1NGGASACA3AGTCACCTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Eutheria, Primates, Cararrhini, Hominidae, Homo
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Pred. No. 2.45e-226;
0: Mismatches 21, Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib*"lambda zap II phage library'
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Ig kappa light chain (VJC)"
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7achau, H S
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Best Local Similarity 93 3%:
Matches 293, Geoservative
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FEATURES
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/product="limunoglobulin kappa chain"
/db_xref="PID:g397792"
/translation="BLVMTQSPSSLSASVGPPVTITCPASOSISSYINWYQOKPGKAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION Human 19K (thyroid peroxidase-specific Fab fragment) mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae: mitochondrial eukaryotos: Metaroa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini: Hominidae: Homo.
1 (bases 1 to 325)
Portolano, S. McLachian, S. M. and Papoport; B.
High affinity, thyroid-specific human autoantibodies displayed en
the surface of filamentous phage use V genes similar to other
239 giggcagiggaictgggacagaittcacicicaccaicagcagictgcaaccigaagait 298
                                                                                                                                                                                                                                                                                                                                                             299 tigoaactiactacigicaacagagitacaataccccgiggacgitrogoccaagqgacca 358
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                                                                                           119 geogggeaagteagageattageaactatttaaattggtateageggaaaceagggaaag 178
                                                                                                                                   179 cecetaageteetgatetatgetgeateeagtttgeaaqtgqggqteegateaaqqttea 238
                                                                                                                                                                                                                         125 CCCGTAAGGTCGTGATGTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCGAGGTTCA 184
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Best Local Similarity 93.9%: Pred. No. 2.246-225:
Matches 290: Conservative O: Mismatches 19: Indels
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/note="clone TR1.23"
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Homo sapiens
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Submitted (12-JUN-1996) P.S. McIntosh, Univ. of Sheffield, Dept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="lymph node B cells"
/clone_lib="lmmunoglobulin phage display combinatorial
library (HT131 lymph node)"
121 aageteetgatetatgetgeateeagtttgeaaagtggggteesteaaggtteagtgge 180
                                                                                193 agtggatetgggacagattteaeteteaceateageagtetgeaaeetgaagattttgea 252
                                                                                                                      190 AGIGGAICIGGGACAGAIIIGACIGICACCAICAGTAGIGGAAGGIGAAGAIIIIGGA 249
                                                                                                                                                              253 acttactactgtcaacagagttacagtaccccgtggacgttcggccaagggaccaaggtg 312
                                                                                                                                                                                                  250 ACTTACTATTGTCAACAGAGTTACACAACCCCTCGGACGTTCGGCCAAGGACCAAGGTG 309
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1 (bases 1 to 311)
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/clone-"121TP5K,131TP7K,131TP8K,131TP15K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily; joining region; variable region.
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121TP5K,131TP7K,131TP8K,131TP15K)
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Best Local Similarity 93 5%;
Matches 289; Conservative
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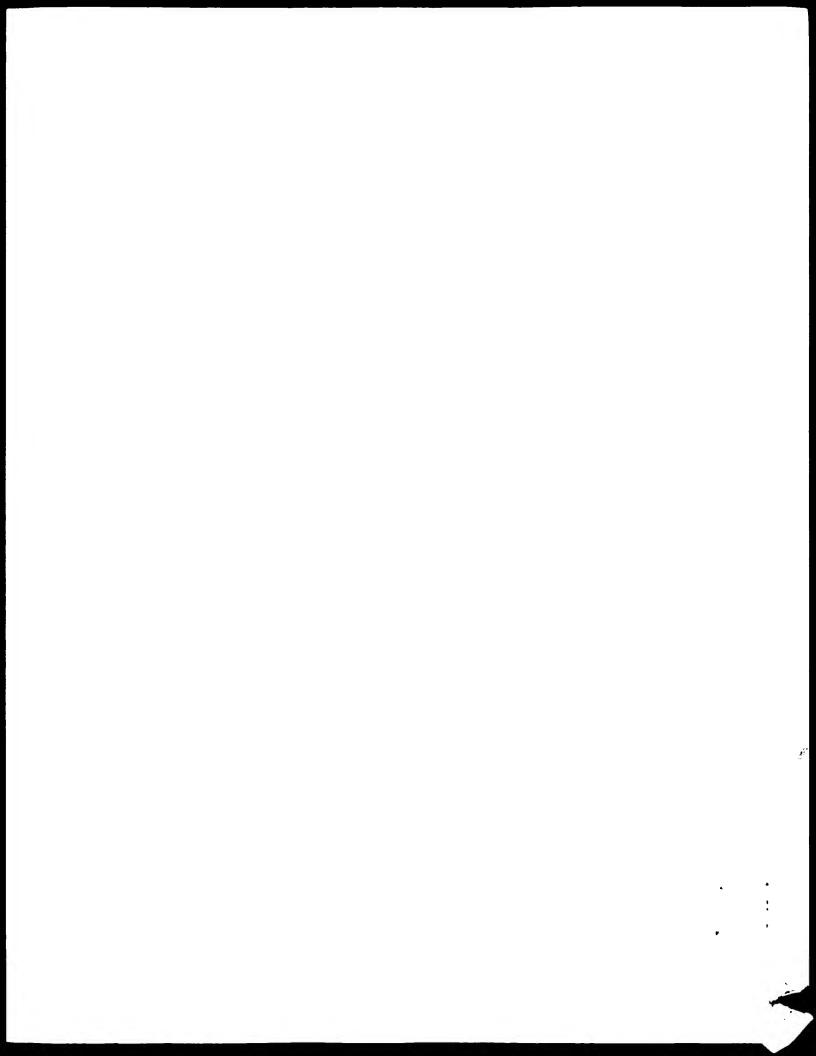
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Somatic diversification and selection of immunoglobulin heavy and light chain variable region genes in 193+ CD3+ chronic lymphocytic
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                                                                                                                                                                                                                                                                                                                                                                                    HSIG039VL 322 bp RNA PRI 27-APR-1995
H.sapiens mkNa for lg light chain, variable region (ID:CLL039VL).
X84343
                                                                           241 acttactactgtcaacagagttacagtacccogtggacgttcggccaagggaccaaggtg 300
130 AAGGTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCGAGGTTCAGTGGC 189
                                                   181 agtggatotgggacagathacachtchancatnagcagh ignaanchgaagaifflgca 240
                                                                                                                                                                                                       68 gccgggcaagtcagagcattagcagctatttaaattggtatcagcagaaaccagggaag 127
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Vertebrata, Eutheria, Frimates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 322)
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Schulman,P., Vinciguerra,V.P., Ferrarini,M., Silver,J. and
Chiorazzi,N
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92.7%; Prod No 1.706-222;
Vativo 0; Mismatches 23; Indels
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/chromosome="22"
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/db_xref*"PID: 9587330"
/translation="DIVMT9SPSSLSASVGDPVIITCPASQS1SSY:NWYQQKPGKAP
KLLIYAASSLQSSVPSPFSGSGSGTDFTLIISSLQFEDFAIYYOQQSYSIRLIFGGG1
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CI2R21,708.A61K19/395.A61K29/395,CI2N5,24,CI2NI5/07,CI2NI5/13,
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Vertebrata; Mammalia: Eutheria: Primates; Catarrhini; Hominidae;
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LOCUS
LOCUS
DEFINITION DNA encoding VL region of human monoclonal antibody that
Specifically acts against lung cancer cell,breast cancer
cell,stomach cancer cell and colon cancer cell,but not against
normal fibroblast.
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/cell_type*'hybridoma'
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Patent: JP 1994153984-A 2 03-JUN-1994;
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Releas Copyri	e 2.15 John F. Collins, Biocomputing Research Unit. aht [7] Yaar 1944, 1944 milyeraity of Pdinburgh, V.K. Distribution rights by Intelligenetics. Inc.
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
Run on: Tabular ontput s	Tue Feb 24 09:46-37 1999: MasPar time 134-06 Seconds 782-593 Million cril updates/sec ot generated.
ption:	>US-08-844-215-19 (1-372) from Uspgg44215 seq 3-2
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Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, T.M., Morene-Palanques, R.E., McCendd. A., Nguyen, D.T., Pelligrino. S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, D.M., Shiley, R., Small, K.V., Spriggs, T.A., Interback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Konsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weil, Y.F., Wing, J., Li, H., Meissner, P.S., Olsen, H., Enser, C.M. and Venter, J.C., Procen, C.A., Haseltine, W.A., Fields, C. Fraser, C.M. and Venter, J.C., Procen, C.A., Haseltine, W.A., Fields, C. Initial assessment of thuman gene diversity and expression patterns based upon 83 million nucleotides of chNa sequence
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White, O., Sutton. G., Blake, T.A., Brandon, P. C., Man-Wai C., White, O., Sutton. G., Blake, T.A., Brandon, P. C., Man-Wai C., Clayton, R.A., Cline, T.P., Cotton, M.D., Barle-Hughes, J. Fine, L. D., Fitzgerald, L.M., Fitzhugh, W.M. C., Hedblom, C.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hannan, M.C., Hedblom, E., Hinkle, P. S., Kelley, T.M., Kelley, T.G., Liu, L. L., Marmaros, S.M., Merrick, J.M., Mornen, Palanques, F. F., McDonald, L.A., Nguyen, D. L., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Naviden, D. L., Pelligrino, S.M., Phillips, C.A., Pepeda, M.A., Coleman, T.A., Collins, F. J., Dimke, D., Keng, D.-F., Ferrick, A. Fischer, C., Hastings G., W. Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melsen, S.M., Paymond, L., Weily, F., Wing, J., Xu, C., Yu, G.L., Puben, S.M., Pallino, P.J., Pannon, M. P., Posen, C. A., Haseltine, W.A., Fleids, C., Fraser, C.M., and Venter, J.C., Pasen, C.A., Haseltine, W.A., Fleids, C., Fraser, C.M., and Venter, J.C., Pasen, C.A., Pasentine, W.A., Fleids, C., Fraser, C.M., and Venter, J.C., Pasen, C.A., Pasentine, W.A., Fleids, C., Fraser, C.M., and Venter, J.C., Pasen, C.A., Pasentine, W.A., Fleids, C., Fraser, C.M., and Venter, J.C., Pasen, C.A., Pasentine, W.A., Fleids, C., Fraser, C.M., and Venter, J.C., Pasen, C.A., Pasentine, W.A., Fleids, C., Pasen, C.M., Pasen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST30467 Colon I Homo sapiens CDNA 5' end similar to immunoqlobulin mu heavy chain, VDJC regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/note="Organ. lymph node. Vector. pBlueStript SK., Site_1:
EcoRI: Site_2: XhoI"
/clone_lib="Lymph node, subtracted"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse.
Location/Oualifiers
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Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldher, R.A.,
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Tel: 3018699056
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S Address M D. Kerlavage A.P. Fleischmann P. D. Fuldher P. A.
Rulitc's Librage A.P. Fleischmann P. D. Fuldher P. A.
Rulitc's Librage A.P. Fleischmann P. Man-Wals.
Glayton F. A. Cine, T. B. Cotton M D. Earle-Hughes, J. Fine, L. Fitzqerald, L.M. Fitzhugh, W.M. Fritchman T. Googhagen, N. S.
Glodek, A., Grehm, C. L., Hannah, M.C. Hachlow, E. Hinkle, P. S. Tr.
Kelley, J. M. Kelley, J. C. Liu, L. I. Marmaros, S. M., Marrick, J. M.
Moreno-Falanques, P. F., McDonald, L. A. Naywen, P. T. Pelligrinn, S. M.
Moreno-Falanques, P. M. McDonald, L. A. Suddek, D. M., Shirley, R. Small, K. V. Spriggs T.A. Hterback, T. P. Weidman, J. F. Ll, Y. Bednarik, D. P. Ferrie, B. A. Cott, J. L., Saudek, D. M., Shirley, R. Bednarik, D. P. Ferrie, M. Fischer, C. Hastings G.A.
He, W. H., T. S. Greene, T. M. Gruber, T. Hudson P. Kim, A. Kozak, D. L. Kunsch, C. Hunglun, J. L. H. Meissener, P. S. Glsen, H. Raymond, L. Weil, Y. E., Wing, J. L. H. Weissener, P. S. Glsen, H. Baymond, L. Weil, Y. E., Wing, J. L. H. Weissener, P. S. Glsen, H. Dillion, P. J. Farnon, M. P. Posen, C. A. Haseltine, M. A. Fields, C., Dillion, M. A. Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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For chome availability, additional sequence and expression
information related to this ESI, please theck the IIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi html)
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ECORI; Site_2: XhoI"
/clone_lib="Colon I"
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                              dukaryotae: mitochondrial eukaryotes: Metazoa: Chordata:
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Tel: 3018694055
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89.2%; Pred. No. 2.22e-174;
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Adams.M. D. Kerlavage.A. P., Eleischmann.R.D., Fuldner.R.A., Radams.M. D. Kerlavage.A. P., Eleischmann.R.D., Fuldner.R.A., Eddams.M. D., Sutton. B. Eidake.J. A., Brandon. R. C., Man-Wai C., Cline,T. D., Cotton.W. P., Earlo-Hughes. J. Efine...... Glodek.A. Gnehm.C.L., Hanna.M.C., Hedblom.E., Hinkle.P. S., Glodek.A. Gnehm.C.L., Hanna.M.C., Hedblom.E., Hinkle.P. P. Fine...... Kellay. J. M., Reilay.J. C., Liu.L. - I., Marmarcas.S. M., Marrick.J. M., Moreno-Palanques.R.E., McDonald.L.A., Nuuyen.D.T., Pelligrino.S.M., Phillips.C. A., Pyder.S. E., Scott.J.L., Saudek.P. M., Shridey.R., Small.K.V., Spriger.T.A. Utterhack.T.P., Weidman.J.E.J.Y., Rednarik.D.P., Cac.I., Cepeda.M.A., Coleman.T.A., Ollins.F. I., Medarik.D., Feng.D.-F., Perrie,A., Fischer.C., Hastings.G.A., He.W.W., Hu.T.S., Green.H.M., Gruber.J., Hudson.P., Kin,A.K., Kozak.D.L., Kunsch.C., Hundjun.J., Li.H., Meissner.P., Sien.H., Raser,C.M., and Venter.J.C.
Fraser,C.M. and Venter.J.C.
Fraser,C.M. and Venter.J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For clone availability, additional sequence and expression, information rate of this EST please there the Tick Human Chen Index (http://www.tigr.org/tdb/hgi/hgi/html) Seq primer: M13 Reverse.
                            Eukaryotae, mitooboobiid eukaryotes. Motozoo: Stordata:
Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidae:
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/note="Organ: testis: Vector: pBlueScript SK-: Si'e_::
EcoRI; Site_2: XhoI"
/clone_lib="Testis tumor"
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Nature 377 (6547 Suppl), 3-174 (1995)
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Tel: 3018699056
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Pred. No. 5.02e-164;
0, Rismatches 23; Indels
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Best Local Similarity 84.9%;
Matches 129, Conservative
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                                                                                                                                                 Adams, M.D., Kerlayage, A.R., Pleischmann, R.D., Fuldner, R.A., Kanas, M.D., Kerlayage, A.R., Mirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C., Mariaros, S.M., Merley, J.M., Moreno-Palanques, R.F., Mronald, L.A., Nguyen, D.T., Pelligino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bednarik, D. P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D. Fenge, D. Frentie, A. Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Raymond, L., Wai, Y.F., Wing, T., Xu, C., Yu, G.L., Ruben, S.M., Fleids, C., Fraser, C.M. and Venter, J. Graber, J., Haseltine, W.A., Fields, C., Frisis, J. E. Ruben, S.M., Fields, C., Frisis, J., Man, M.A., Fields, C., Frisis, J., Man, M.A., Fields, C., Fraser, C.M. and Venter, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Fred No 2.20e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
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Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Reverse.
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Best Local Similarity 84.6%
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LOCUS AA291381 379 bp mRNA EST 16-MAY-1997 DEFINITION #144902 rl Soares ovary tumor NEHOT Home sapiens cDNA clone 725224 5' similar to qb-M18812 IG HEAVY CHAIN PPECHPSOR V-I PEGION

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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco PI sites of a modified pTTT vertor (Pharmacia) Library constructed by Rento Soares and M.Felina Bonaldo."
                                                                                                                                               Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL: contact the IMAGE Consortium (infoaimage.llnl gov) for further information. Seq primer: -28ml sev2 ET from Amersham High quality sequence stop: 361.
                                                                                                                                                                                                                                    1 (bases 1 to 379)
Hillier L., Allen, M., Rowles, L., Dubuque, T., Geisel, G., Jost, S., Kudaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, P., and Wilson, P., Theising, B., Wash U-Merck EST Project 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 19.4%; Score 72; DB 99; Length 379; Best Local Similarity 64 8%; Pred. No. 3.09e-93;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel·314 286 1800
Fax. 314 286 1810
Email: est@watson wustl edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 C
                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                         Homo sapiens
                                  q1939359
AA291381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 gaga 327
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                                                                                             human.
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122 CASSCAASSSCIEGASTSSSCASSCIAT 152

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Adams, M. D., Replayage, A. P., Fleischwann, P. D., Fuldner, P.A.,
Adams, M. D., Replayage, A. P., Fleischwann, P. D., Fuldner, P.A.,
Bult, C.J., Lee, N. H., Rirkness, F. F., Wannstock, R. G., Gorayne, J. D.,
White, D., Sutton, G., Blake, J. A., Randon, P. C., Man-Wai, C.,
Claylon, R.A., Cline, T. R., Cotton, M. D., Earle-Hughes, J., Fine, L. D.,
Pitzgerald, L. M., Fitzhugh, W. M., Eritchham, J. L., Geograpen, S.,
Roley, C.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R. F., McDonald, L.A., Nauyen, D. T., Pelligrino, S. M.,
Phillips, C.A., Pyder, S. E., Sooft, J. L., Saudek, D. M., Shirley, P.
Small, K.V., Spriggs, T. A., Utterback, T. P., Weidman, J. F., Li, Y.
Bednarik, D. P., Gerene, J. M., Gruber, C., Hassings, G. A.,
He, W.W., Hu, J.S., Greene, J. M., Gruber, C., Hassings, G. A.,
He, W.W., Hu, J.S., Greene, J. M., Gruber, C., Hassings, G. A.,
Bullion, P. J., Fannon, M. P. Posen, C. M., Rissner, C. M., Rusch, C., Hungjun, J. L., Messner, C. M., Rusch, C., Hungjun, J. L., L., Puben, S. M.,
Bullion, P. J., Fannon, M. P. Posen, C. A., Hassitine, W. A., Fields, C.,
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleocides of cpNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
ESILIĞEL Testis tumor Homo saplens cDNA 5' end similar to similar to immunoglobulin mu heavy chain, VPIC regions (GR:M18512).
AA300571
                                                                                                                                                                                                                                                                     Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: testis: Vector: pBluescript SK-; Site_1:
EcoRT: Site_2: XhoI"
//clone_lib="restis tumor"
/sex="maile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 ortgcaaggottotggatacacettcaceggetactatatgeactgggtgegacaggee 209
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Prod No 5 48e-70:
0: Mismatches 46: Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AGGIGCAGTIGITGAGTGIGGGGGAGGGGIGGIGGAGGTTGGGAGGIGGGTGAGAGTGT 61
                                                                                                                                                                                                                                         Eukaryotae: mitochondrial eukaryotes: Metazoa: Chordata:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MU 20850 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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q
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<1..>279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav?tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_ESTs: THC166571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 59.5%:
Matches 105; Conservative
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                                                                                                                                                                                                                Homo sapiens
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                                  DEFINITION
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ORIGIN
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MEDLINE
                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                     KEYWORDS
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A dues M. Rerlavage A. P. Fleischmann, B.D., Fuldhor, R.A.,
Bull, C. J. Lee, N. H. Kipkness, E. F. Weinstrock, W. G. Gocayne, J. D. Lee, N. H. A. Brandon, F.C., Man-Kail, C.,
Clayton, R. A. Cline, T. P., Cotron, M. D., Earle-Hughes, J. E.,
Fliggerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geodhagen, N. S.,
Glodek, A., Ghoeh, C.L., Hanna, M. C., Hedblom, E. Hinkle, P. S. Jr.,
Kelley, J. M., Kelley, J. C., Hanna, M. C., Hedblom, E. Hinkle, P. S. Jr.,
Moreno-Palangues, P. F., McDonald, L. A., Nouyen, D. T., Pelligrino, S. M.,
Phillips, C. A., Pyder, S. E., Scott, J. L., Saudek, D. M., Shirloy, R.,
Redarik, D. P., Caci, L., Cepeda, M. A., Coleman, J. F., J. Jr.,
Rozak, D. L., Kunsch, C., Hungjun, T., Li, H., Melson, P. Kim, A.K.,
Raymond, L., When, Y. Funnon, M. M., Fischer, C., Hastinds, G.A.,
Playmond, L., Welly, Fannon, M. M., Pischer, C., Hastinds, G.A.,
Playmond, L., Welly, P. Rosen, C. A., Haseltino, W. A., Fischer, C.,
Playmond, L., Welly, P. Rosen, C. A., Haseltino, W. A., Fischer, C.,
Fraser, C.M., and Venere, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial assessment of human wene diversity and expression patherns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     indecords availability additional sequence and expression information related to this EST, please check the TIGK Human Generator (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: small intestine: Vector: pBiwescript, SK::
Site_1: EcoRI: Site_2: Xhol"
/clone_lib="Small intestine :"
/dev_stage="adult"
                                                                                                                                                                                                                                                    Eukaryotae, mitochondrial eukaryotes, Metazoa: Chordata:
Vertebrata: Mammalia, Eutheria; Primates, Catarrhini; Horinidae:
                  LOCTS AA37761 219 bp mPMA EST 21-App-1097
DEFINITION ESTB9641 Small intestine I Homo sapiens cDNA 5° end similar to immunoglobulin mu heavy chain, VDJC regions.
ACCESSION AA377661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caps
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Pred. No. 3.44e-66;
"immatches 7: Indeis 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research
9712 Medical Center Drive, Pockville, MD 200459 USA
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Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                        (bases 1 to 219)
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nes 69; Conservative
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RESULT
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima_Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: ovary: Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I, Site_2: EG: PT: Ist strand cDNA was primed with a Not I - oligo(dT) primer [5' GITROCAATUTGAGGAGGGGGGGGGTITITITITITITITITITITITI
AA402547 266 bp mRNA EST 16-MAY-1997 2u47h07.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 741181 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS AA352777 267 bp mPNA EST 21-AFP-1997
- DEFINITION EST50916 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, VDJ regions (GB:233899).
                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 266)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,P. and Wilson,R.
                                                                                                                                                                                                                                            Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Mammalia, Eutheria, Frimates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Constrtium (infolimage lini gov) for further information Seq primer: -28ml3 rov2 Er from Amersham.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 AGGGCCGATTCACCGTCTCCAGAGACAATTCCAGAACACGCTGTTTCTGCAAATGAACA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 geetgagatetgaggacaeggeeetgtattaetgtgegagagetttaeeagetegteaa 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 80; Length 266;
Pred. No. 1.13e-58;
0; Mismatches 59; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashDumerck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, My 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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Local Similarity 66.5%;
nes 119; Conservative
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                                     DEFINITION
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bull, C.T., Lev, N.H., Kikhess, E.F., Weinsteck, K.S.,
Bull, C.S., Lev, N.H., Kikhess, E.F., Weinsteck, K.S.,
Grayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Ghomh, C.L., Hanna, M. C., Haddlome, E. Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.L., Marmaros, S. M., Merrero-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriey, R.,
Small, K. V., Sprigs, T.A., Interback, T.R., Weidman, T.F., Li, Y.,
Bednarik, D.P., Gepeda, M.A., Coleman, T.A., Collins, F.J.,
Dimke, D., Fengy, D.-F., Ferrie-A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.W., Gruber, J., Hiddson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Weil, Y.F., Wing, J., Xu, F., Yu, G.L., Ruben, S.M.,
Fraser, C.M., and Venter, J.C.,
Initial assessment of human gene diversity and expression gatterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                    Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata:
Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Rominidae;
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0; Mismatches 12; Indels 0: Gaps
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Nature 377 (6547 Suppl), 3-174 (1995)
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9712 Medical Genter Prive, Forkvillo MD 20850 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 84.6%;
Matches 66; Conservative
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                                                                                                                                                                                          Adams M.D. Korlayage, A.P., Fleischmann, P.D., Fuldner, P.A.,
Bult, C.J. Lee, N. H. Kirkness F.F. Weinstock, K.G., Gorayne, J.D.,
White, O., Sutton, G., Rlake, J.A., Brandon, P.C., Man-Wall, C.,
Clayton P.A., Cliber, T.P., Cotton, M.D., Earle-Hughes, J. Fine, L.D.
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, T.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S., Jr.,
Kelley, J.M., McAlley, J.C., Lin, L.T., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, P., Moronald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, P.M., Shiley, P.,
Small, K.V., Spriggs, J.A., Otterback, T.P., Weishen, J.H., Y.,
Budnarik, D.P., Carl, C.P., Cepene, J.M., Griber, C., Hastings, G.A.,
Hey, W.M., Hu, J.S., Greene, J.M., Griber, C., Hastings, G.A.,
Kozak, D.L., Kansch, C., Hungjun, J., Ju, Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Puben, S.M.,
Pandon, M., Sandon, M.R., Rosen, G.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For clone availability, additional sequence and expression information related to this EST, please check the 11GF Human Gene Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: MI3 Peverse.
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                                                                                Eukaryotae, mitochondrial eukaryotes: Metazoa: Chordata:
Vertebrata; Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 atamaanigalamaathtuaagantaagalgaagagannaagagaganntaaathottolgtaaaaqtoton 134
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Pred. No. 1.13e-58;
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Best Local Similarity 67.8%;
Matches 191; Conservative
                                                                                                                                                                           (bases 1 to 291)
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                                                        ORGANISM
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                                                                                                                                                                                                       AUTHORS
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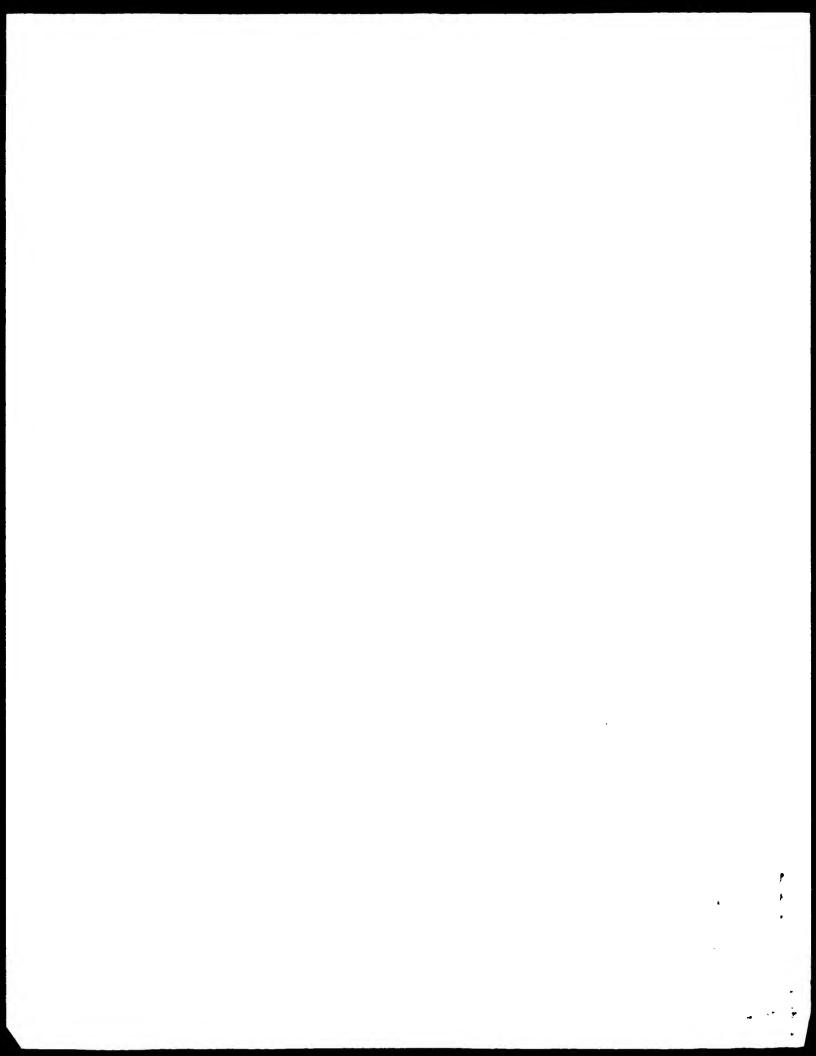
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Adams, M. D. Retlayage A. P. Floischmann, P. D. Puldher, R. A., Brander, M. D. Lee, N. H. Kirkness, E. F. Weisstock, K. G. Googyne, J. E. Bult, C. J. Lee, N. H. Rizknes, E. F. Weisstock, K. G. Googyne, J. C. Layton, R. A., Cline, T. R. Parke, J. A. Brander, M. C. Man-Wai, C. D. Elizagerald, L. M. Fitzhugh, W. M. Fritchman, J. L. Groghagen, N. S. Glodek, G. Gheher, E. Hanna, M. C. Heddrom, E. Hirkis, P. S. H. Kelley, J. M. Kelley, J. M. Kelley, J. M. Morror-Palanques, P. F. McDonald, L. A. Nuyen, D. T. Pelligrino, S. M. Phillips, C. A. Pyder, S. E. Scott, J. L. Sandek, D. M., Shriey, R. Bedlarik, D. P. Gavil, Cepeda, M. A. Culeman, F. Li, Y. Bednarik, D. P. Gavil, Cepeda, M. A. Culeman, R. Collins, E. J. Dimke, D. Fengil, P. Perrie, A. Fischer, C. Hastings, G. A. Fischer, G. Hastings, G. A. Kozak, D. L., Kunsch, C. Hungjun, J., Li, H. Meissner, P. S. Olsen, H. Raymond, L. Weil, Y. Wing, J. Xu, C. Yu, G. L. Ruben, S. M. Fisser, C. M. and Venter, J. C. M. Parker, C. M. Bastino, M. A. Fischer, G. M. Sander, C. M. and Venter, J. C. M. Sander, G. M. Sander, G. M. Sander, C. M. and Venter, J. C. M. Sander, G. M. Bastino, R. A. Fischer, G. M. Sander, C. M. and Venter, J. C. M. Sander, G. M. Bastino, R. A. Fischer, G. M. Sander, G. M. Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl). 3-174 (1995)
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                                                                                      Eukaryotae, mitochondrial eukaryotes. Metazou. Ghordata:
Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidam:
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XhoI"
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ND 32012573
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Tel: 3018699056
Fax: 3018699423
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/dev_stage="aduit, 20 yrs"
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Prod No. 1.13e-58;
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/sex="female"
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The Institute for Genomic Pesearch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerlavage, AR
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                                                                                                                                     Adams, M. D., Kerlavage, A.P., Fleischmann, P. D., Fuldner, P. A.,
Adams, M. D., Kerlavage, A.P., Fleischmann, P. D., Fuldner, P. A.,
Bult, C.J., Lee, N. H., Kirkness, E. F., Weinstock, K.G., Gocayne, J. D.,
White, O., Sutton, G., Blake, J.A.,
Elagrald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, J. Fine, L.
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Ghehh, C., Hanna, M.C., Hedblom, E., Hinkle, P. S. Jr.,
Kelley, J. M., Kelley, J. G., Liu, L. -1., Maynen, D. T., Pelligrino, S. M.,
Moreno-Palanques, P. F., McDonald, L.A., Wayyen, D. T., Pelligrino, S. M.,
Philips, C. A., Fyder, S.E., Scott, J.L., Saudek, D. M., Shirley, P.,
Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y.,
Bednarik, D. P., Cao, L., Cepeda, M. A., Collman, T. A., Collins, E. J.
Dimke, D., Feng, D. F., Reriet, A., Fischer, C., Hastings, G. A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, M., Meissner, P. S., Clsen, H.,
Paymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Fuben, S. M.,
Dillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/note="organ: lymph node; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/clone_lib="Lymph node I"
/dev_stage="adult"
<1. > 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.rigr.org/tdb/hgi.html)
                                                                                                Vertebrata: Mammalia: Eutheria. Primates. Catarrhini. Hominidae:
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                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Pred. No. 8.17e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: arkerlav@tigr.org
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                                              OPGANISM
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A dames M D. Kerlavage, A P., Fleischwann P D. Fuldner P A.
Bult, C T. Lee, N. H. Kirkness, E. F. Wehnstock, K. G. Gocayne, J.D.,
White, C., Sultron.G., Blake, J. A. Brandon R C. Man-Wai C.,
Clayton, R.A., Cline-T.P. Cotton, M D. Berle-Hughes, J. Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W N., Fritchman, J I., Geoghagen, N.S.,
Glodek, A., Geneho, C.L., Hanna, M. C., Hadblom, E. Hinte, P. S.J.T.,
Kellay, J M., Relley, J C., Liu, L. H. Marmaros, S. M., Merrick, J.M.,
Morenc-Palangues, R F., McDonald, L.A., Nguyen, D T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S. E., Soctt, J. L., Saudek, D M., Shirley, R.,
Small, K V., Spriggs T A, Interback, T R., Saudek, D M., Shirley, R.,
Bednarik, D. P., Cao, L., Cepeda, M.A., Coleman, T A., Collins, E.J.,
Dimke, D., Perrie, A., Fischer, C., Hastings, G.A.,
He, W. M., Hu, J.S., Greene, J M., Gruber, J., Hudson, P., Kim, A. K.,
Raymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G.L., Rhen, S. M.,
Pillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, M.A., Fields, C.,
Fraser, C.M., and Venter, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlar@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGE Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="organ: small intestine: Vector: pBluescript SK-:
Site_1: EcgRI: Site_2: XhoI"
/clone_lib="Small intestine I"
/dev_stage="adult"
                                                                 Eukaryotae, mitochondrial aukaryotes, Matazoa, Chordata:
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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Tel: 3018699056
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Pred. No. 1.888-49;
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Rest Local Similarity 65 6%;
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human
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A Gadas I. Consider A L. Fleischmann, P.D., Fuldher, P.A., Bradas, M.D., Kerlavag, A P., Fleischmann, P.D., Fuldher, P.A., Bradas, M.D., Bull, C.T., Lee, N. H. Kirkness, E.F., Weinstrock, K.G., Gocayne, J.D., Man-Wall, C., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wall, C., Inne, T.P., Coffon, M.D., Earle-Hughes, J., Fine, L.D., Flitzerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E.P., Brinch, L.D., Kelley, J.M., Kelley, J.G., Liu, L.T., Marmaros, S.M., Merrick, J.M., Moreno-Polanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, P.M., Shiley, P., Small, K.V., Spriggs, T.A., Htt-rrhark, T.P., Weidman, J.F., I.i, Y., Bednarik, D.P., Ferrie, A., Fischer, C., Hastings, G.A., Low, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melsner, P.S., Olsen, H., Fraser, C.M. and Venter, J.C., Yu, G.L., Ruben, S.M., Fraser, C.M. and Venter, J.C., Yu, G.L., Ruben, S.M., Fraser, C.M. and Venter, J.C., Hastings, M., Fraser, C.M. and Venter, J.C., Mark, Sequence and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For clone availability, additional sequence and expression information related to this ESI, please check the IIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                             Eukaryolae, mitochondrial eukaryotee: Metazoa: Chordata;
Vertebrata: Mammalia; Eutheria: Primates; Catarrhini; Hominidae;
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EcoR: Site_2: Xhor"
/clone_lib="Testis tumor"
/sex="male"
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Pred. No. 1.24e-47;
0; Mismatches 48; Indels 0; Gaps
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Location/Qualifiers
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<1..>304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
Bioinformatics
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Contact: Kerlavage, A
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Best Local Similarity 65.7%;
Matches 92; Conservative
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Search completed. Tue Feb 24 08:49:04 1998 Job time : 147 secs.



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179-EST179 180-EST180 181-PST181 182-PST182 183-EST183
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189:EST189 190-PST190 191-PST191 102-PST192 193:EST19*
144-EST144 145-EST195 146-EST195
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Statistics: Mean 9.966; Variance 1.896; scale 5.256

Pred No is the number of results predicted by chance to lave a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

32-0CT-1995	lar to gl.:M62726					etal liver spieen.
EST	yslibbl.rl Home sapiens obna clone 214441 5' similar to ql: M62726	(AN):				numan clone=214441 primer=M13RP1 library=Soares fots] liver spiece.
419 bp mPNA	apiens cona clo	III PECION (HUM				1 primer=Ml3EP1
H73 <u>8</u> 15 419	slib01.rl Home s	IG HEAVY CHAIN V-III REGION (HUMAN);	H73816	91046750	ST.	uman clone=21444
RESULT 1	DEFINITION ;		ACCESSION	DIN	KEYWORDS E	SOUPCE

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Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata,
Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes;
Sarcopterygii, Choanata, Tetrapoda, Amuicta, Mammalia, Theria,
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image lin| gov) for further information.
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1 (bases 1 to 419)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Piffin, L., Pohlfing, T., Scares, M., Tan, F., Trevaskis, E., Waterston, P., Williamson, A., Wohldmann, P. and
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Source: IMAGE Consortium, LLNL
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DEFINITION yjqlhnq rl Homo sapiens onna clone 154141 5' similar to gb:M6272A IG HEAVY CHAIN V-III REGION (HUMAN):

mRNA

430 bp

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RESULT

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ACCMESION NID

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DEFINITION mak7gin it Soares mouse and musculus cona chope 61894 5'
similar to gb:X14584 IG HEAVY CHAIN PRECIREOR V-TIT REGION (HUMAN);
gb:V00821 Mouse mRNA fragment for immunoglobulin mu encoding the
                                                                                                                                               double-stranded cDNA was ligated to book I adaptors (Pharmacia), digested with Not I and cloned into the Not I and Book II sites of modified pT/T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230 Library constructed by Bento
                                             Deuterostomia, Chordata, Vertebrata, Gnathostomata, Csteichthyes:
Sarcopterygii: Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                     human clone=156161 library=Soares breast 2NbHBst vertor-pT7T3D
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                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

[ [bases 1 to 430]
[ Hillier, L. Clark, N. Dubuque, T. Elliston, K., Hawkins, M.,
Holman, M. Holtman, M. Kuraba, T. Le, M., Lennon, G., Marra, M.
Parsons, J., Kifkin, L., Hohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, P., Williamson, A., Wohldmann, P. and
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Tel: 314 286 1800
Fax: 314 286 1810
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Matches 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra.M. Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg, K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wilson,R., Lennon,G., Soarce,B., Wilson,R., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson wustl.edu
This clone is available royalty-free through LLNL : contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                      Vertebrata; Euthería; Rodentía; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 macgigaagotggtggagtotggggaaggottagtgaagcotggagggtoootgaaaoto 177
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                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                Washu'HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 285 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse 3NbMS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector to vector length is 867
Seq primer: -28M3 rev2 from Amersham
High quality sequence step: 492
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Mus musculus"
/strain-"C57BL/6J"
                                                                                                                                                                                                                                                                               Waterston, R.
The Washu-HHMI Mouse EST Project
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/dev_stage="4 weeks"
/lab_bost="DH108"
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ilarity 77.3%;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.
1 (bases 1 to 330)
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/tissue_type="smail intestine"
/clone_lib="directionally cloned cona in X!!-blue MkF'"
/clone="cidlo"
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Pred. No. 3.08e-274;
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Mamm Genome 7, 509-517 (1996)
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Adams, M. J., Lee, N. Kirkease, E. F., Weinstock K. G., Gocayne, J. D., Lee, N. Kirkease, E. F., Weinstock K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brandon, P. C., Chiu, M.-W., Clay, Y. C., Clay, M.-W., Clay, M.-W., Clay, M.-W., Clay, M. C., Gocayne, J. L., Gocayne, J. L., Gocayne, J. L., Gocayne, D. FitzGerald, L. M., FitzHugh, W. M., FitzChman, J. L., Hinkle, J. T., Forlock, J. M., Moreno-Palanques, R. P., Liu, L. I., Marmarros, S. M., Meriden, S. M., Moreno-Palanques, R. P., Sordt, J. L., Nguyen, D. T., Pellegrino, S. M., Phillips, R. S., Scott, J. L., Nguyen, D. T., Nelegrino, S. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. E., Li, Y., Rednarik, D. F., Gollins, E. J., Dimke, D. Ferrie, A., Fischer, C., Hastings, G. A., He, M.-W., Hu, J.-S., Greene, J. M., Gollins, E. J., Dimke, D. Ferrie, A., Fischer, C., Hastings, G. A., He, M.-W., Hu, J.-S., Greene, J. M., Meisener, P. S., Gleene, J. M., Meisener, P. S., Willen, W. J. Fannon, M. P., Rosen, C. A., Haseltine, M. A., Fields, C., Fraser, C. M., and Venter, J. G., Littial Assessment of Human Gene Diversity and Expression Patterns Engand Theory M. J. Standon, M. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: tdbinfo@tdb.tigr org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
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IG HEAVY CHAIN V-III REGION (HUMAN);
                                                                                                                                                                                                                                                        Eukaryotae, Metazoa, Eumetazoa, Bilateria; Coelomata,
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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T27868 ESP-1995
EST18962 Home sapiens CDNA 5' end similar to inmunoglobulin mu
heavy chain V.D.7' redicors (GR:MI8617) (HI:3226).
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Local Similarity 92.1%; Fred. No. 7.38e 253;
les 163; Conservative 0; Mismatches 14; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGCTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                           Fuldner, P. A.
                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 297)
Adams,M D , Kerlavage,A P , Fleischmann P D
                                                                                                                                                                                              human primer=Ml3 Reverse library=Human Lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
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YOTOGOS I'I HOMO SAPIONS ODNA CIONO 181320 5' eimilar to obsessas
IG ALPHA-1 CHAIN C REGION (HUMAN);
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Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes,
Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Iheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                    human cione=187156 library=Scares breast 3NbHRst vector-pT7T3D
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Local Similarity 83.9%; Pred. No. 1.41e-231;
Nes 161; Conservative 0; Mismatches 31; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                            Eutheria: Archorda Primates: Catarrhini: Hominidae: Homo I (bases 1 to 303)
Hillser, C., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulthan, M., Pohlejng, T., Fe, M., Lennon, G., Marra, M., Parsons, J., Piffkin, L., Pohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and
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/clone="187156"
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Fax: 314 286 1810
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resistant) primer*M13RP1 Rsitel=Not I Rsite2=Eco FI Adult human. Ist strand CDNA was primed with a Not I - Olgo(dI) primer [5' TGTIAC7AROIG5AA3C95C9A5C9CIIIIIIIIIIIIIIIIII 3'). double-stranded cDNA was ligated to Eco EI adaptors (Phaimacia). digested with Not I and cloned into the Not I and Eco PI sites of a modified prif3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20; Library constructed by Pento Soares and M.Patima Bonaldo.
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                                                                                                                                                                                                                                                          Eukaryofae: Metazoa: Eumetazoa: Bilateria: Coelomata: Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osteichthyes: Sarcopteryqii: Choanata: Tetrapoda: Amniota: Mammalia: Iheria: Eutheria: Archoota: Primates: Catarthini: Hominidae: Homo. 1 (bases 1 to 422)
Hillier. L. Clark N. Dubuque.T. Elliston.K. Hawkins.M., Holtman.M., Rucaba.Tr. ElM., Lennon.G., Marra.M., Parsons.J., Ritkin L. Pohlfing.T. Sares.M., Tan.F. Trevaskis.E., Waterston,R., Williamson.A., Wohldmann.P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. [ncation.juailflars
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 90; DB 69; Length 422;
Pred. No. 2.10e-129;
0; Mismatches 34; Indels 3; Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
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Source: IMAGE Consortium, LLNL
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Matches 141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
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Fax: 314 286 1810
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double-stranded cDNA was ligated to Ene PI adaptors (Pharmacia), didested with Not I and cloned into the Not I and Ene BI sites of a modified piTl3 verter (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento

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Library constructed by Rente Source
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Hillier! Clark.N. Putbag.e.T. Filisten.K., Hawkins.M., Hollman.M., Hullman.M., Kucaba.T., Lo.M., Lennon.G., Marra.M., Parsens.J., Pifkin.I. Pohlfing.I. Scares.M., Tan.F., Trevaskis,E., Waterston,F., Williamson.A., Wohldmann.P. and
                                            Eukaryojae, Metazoa, Eumetazoa, Bilateria, Goelomata,
Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichtnyes,
Sarcopterygii: Choanata, Tetrapoda, Amniota, Mammalia, Thoria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LINL : contact the IMAGE Consortium (info@lmage.llnl gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 TATTCAGACTCCGIGAAGGGGGGGAITGACGGIGIGCAGAGACAATTCCAGGAACACGCGG 237
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                                                                                                                        Eutheria; Archonta; Primates: Catarrhini: Hominidae; Homo.

1 (bases 1 to 485)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,K., Frit, J., Pohlfing,T., Soares,M., Tar,F.
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Washu-Merck EST Project
Washington University School of Medicine
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Source: IMAGE Consortium, LLNL
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Spares and M.Fatima Benaldo.
                                                                                                                                                                                                                                                                                              Wilson, R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
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larity 81.5%;
Conservative
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Fax: 314 286 1810
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                              Homo sapiens
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Best Local Similarity
Matches 97: Consent
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Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteir)thyes,
Sarcopterygii: Choanata: Tetrapoda, Amniota; Mammalia: Theria;
                                                                                                                                                                                                               High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (Info@image.llnl.gov) for further information.
Trace considered overall poor quality.
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Robbert,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soaree,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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                                                                                                                  Washington University School of Medicine
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Fred. No. 1.23e-77;
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                                                                                                                                                                                                    Email: est@watson.wustl.edu
Wilson,R.
The WashU-Merck EST Project
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WashU-Merck EST Project
                                                                                                 WashU-Merck EST Project
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Local Similarity 84.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76; Conservative
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Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, R.A., Mirkness, E.F., Weinstock, Y. G., Gorsyne, J.D., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, Y. G., Gorsyne, J.D., Bult, C.J., Lee, N., Cine, P.T., Cotton, M.D., Earle-Hophes, J. Fine, J.D., Flizgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S., Kelley, J.M., Moreno-Palanques, P.F., McDhonald, J. A., Moreno-Palanques, P.F., McDhonald, J.A., Ngyen, D.T., Pelley, J.M., Moreno-Palanques, P.F., McDhonald, J.A., Wilmek, K.M., Phillips, C.A., Ryder, S.F., Gott, J.L., Saudek, D.M., Shirley, P., Small, X.V., Spriggs, T.A., Titchhark, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, H., Titchhark, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, H., Titchhark, T.R., Weischer, C., Hassings, G.A., He, W.W., Hull, T.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Ku, G.L., Ruben, S.M., Dillon, P.J., Pannon, M.R., Rosen, C.A., Hassilfor, W.A., Frisher, C., Meits, J., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
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Deuterostomia: Chordata, Vertebrata, Gnathostomata, Osteichthyes:
Sarcopterygii: Choanata: Tetrapoda: Amniota: Mammalia: Theria:
                                                                                         High quality sequence stops: 177
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNI : contact the
                                                                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov) for further information.
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1 (bases 1 to 209)
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932 Clopper Rd, Gaithersburg, MD 20
Tel: 3018699056
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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932 Clepper Fd. Saithersburg. MC LC
Tel: 3018699056
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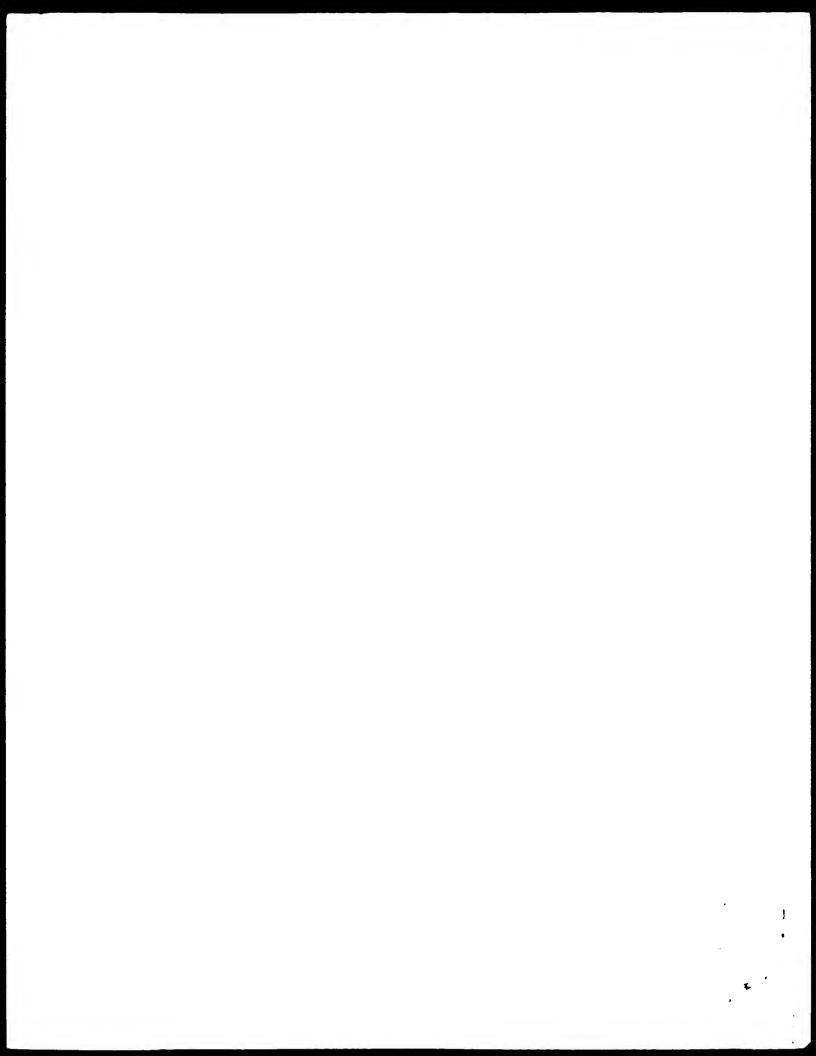
1 (Dases 1 to 238)

2 Adams, M.D., Kerlavage, A.P.; Fleischmann, P.D.; Fuldher, P.A.;
Bult, C.T., Lee, N., Kirkness, E.F., Weinstock, K.G.; Gocayne, J.D.; White, O.; Sutton, G.; Blake, J.A.; Farandon, R.C.; Chiu, M.-W.;
Clayton, R.A.; Cline, R.T.; Cotton, M.D.; Barle-Hughes, J.; Fine, L.D.;
Fitzgerald, I.M.; Fitzhugh, W.M.; Fritchman, T.L.; Geoghagen, N.S.M.;
Kelley, J.M.; Klimek, K.M.; Kelley, J.C.; Liu, L.-T.; Marmaros, S.M.;
Meridek, D.M.; Shirley, R.; Small, K.V.; Spriggs, T.A.; Utterback, T. Relley, J.M.; Shirley, R.; Small, K.V.; Spriggs, T.A.; Utterback, T. Relley, J.M.; Shirley, R.; Small, K.V.; Spriggs, T.A.; Utterback, T. Rellem, J.E.; Liiv, D. Bednarik, D.; Feng, P.; Ferrie, A.; Fischer, C.; Hastings, G.A.; He, M. W.; Hu, J. G.; Greene, J.M.; Kim, A.; Kozak, D.L.; Kunsch, C.; Ji, H.; Meissner, P. S.; Olsen, H.; Maymond, L.; Wung, J.; Kung, J.; Kannon, M.R.; Posen, C. A.; Haseltine, W.A.; Fields, C.; Fraser, C.M.; and Venter, J.G.; Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon S. Million Basepairs of CDNA Sequence
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chain V region (GB:X61012) (HT:3230).
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932 Clopper Rd, Gaithersburg, MD 20
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia), Library went through one round of normalization to a Cot \tau 20. Library constructed by Benth Shares
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Sarcopterygii; Choanata; Tetrapoda, Amniota; Mammalia; Theria;
Butheria; Archonta; Primates; Gafarrhini; Hominidae; Homo.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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11.8%; Score 44; DB 51; 1
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Matches 96; Conservative 0; Mismatches 48
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Fax: 314 286 1810
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Comp: CICCAGGTGGAGGTGAG

Scoring table: TABLE default Gap 6 Searched: 87531 seqs, 22995021 bases x 2

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 7.705; Variance 4 193; scale 1 838

Statistics:

SUMMARIES

Pred. No.	1,356-167	3 300-155	2 63e-141 1 88e-137	6 540-136 2 270-134		3 256-128	1.12e-126	1.12e-126	1.12e-126	3 866-125 7 796-123
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20 185 49.7 360 7 US-08-264- Sequence 13, Application 194 49.5 360 11 PCT-US93-1 Sequence 31, Application 22 184 49.5 360 11 PCT-US93-1 Sequence 31, Application 24 49.5 376 11 PCT-US93-1 Sequence 23, Application 24 49.5 376 11 PCT-US93-1 Sequence 3, Application 25 179 48.1 39.3 7 US-08-468- Sequence 3, Application 27 176 47.3 1347 1 Sequence 3, Application 27 176 47.3 1347 1 Sequence 3, Application 39 167 44.9 Sequence 26, Application 30 167 44.9 357 7 US-08-207- Sequence 26, Application 31 166 44.6 752 1 US-08-207- Sequence 26, Application 31 166 44.6 752 1 US-08-207- Sequence 26, Application 37 163 43.8 33.9 417 7 US-08-398- Sequence 21, Application 37 163 43.8 33.9 417 7 US-08-398- Sequence 21, Application 37 163 43.8 756 105-07-398- Sequence 21, Application 37 163 43.8 756 7 US-08-398- Sequence 29, Application 37 163 43.8 756 7 US-08-398- Sequence 29, Application 43 156 43.5 7 US-08-398- Sequence 29, Application 43 156 43.5 7 US-08-398- Sequence 29, Application 44 15 7 US-08-398- Sequence 31, Application 45 45 7 77 7 US-08-398- Sequence 31, Application 45 159 42.7 772 7 US-08-331- Sequence 33, Application 45 159 171 154 174 155 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174 156 174	\$\text{App \(\text{App \) \endots App \(\text{App \(\text{App \(\text{App \(\text{App \(\text{App \) \endots App \(\text{App \) \app \} \endots App \(App \) \\ App \) \\ \endots App \(\text{App \) \	.22e-10 04e-10 04e-10
186 49 7 360 7 005-08-264 49 5 360 11 pcrt. (98.33-1) 22 11 pcrt. (98.33-1) 23 11 pcrt. (98.33-1) 24 11 pcrt. (98.33-1) 25 11 pcrt.	13. Applica 2.4 Application 2.4 Application 3. Application 3. Application 3. Application 2.5 Application 2.5 Application 2.1 Application 2.1 Application 2.2 Application 2.2 Application 2.3 Application 2.4 Application 2.5 Application 2.6 Application 2.7 Application 2.8 Application 2.9 Application	6. 5455030. 8. Applicat 11. Applicat 33. Applica
22 188 4 4 4 9 9 7 4 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9	PTT-108-20-20-20-20-20-20-20-20-20-20-20-20-20-	5455030-8 5455030-8 PCT-0892-0 08-08-331-
012042067890011884886789001128440	00000000000000000000000000000000000000	3.0 711 1 2.7 712 1 2.7 738 2
	0120-4207 2000 1120 421 42 600 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	12645 10655 10655

ALIGNMENTS

PROFUCTION OF HUMAN MONOCLONAL ANTIHUGGES SPECIFIC FOR HEFAILLS B SURFACE ANTIGE COMPUTER: IEM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PT-DOS/MS-DOS
SOFTWARE: PT-DOS/MS-DOS
CURRENT APPLICATION DATA:
AFFLICATION NUMBER: TS/TS/259.372A
FILING DATE: 14 TIN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21.4PF-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: NUMBER OF SEQUENCES: 16
CORPESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLF
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco J. 1 US-08-259-372A-1 STANDARD: DNA: UNC: 423 BP. APPLICATION NUMBER: US 07/676,036 FILING DATE: 27-MAP-1991 PRIOR AFFLICATION DATA: PAPLICATION NUMBER: US 07/528,796 FILING DATE: 15-JUN-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/192,754 FILING THE 11-MAY-1988 PRICH APPLICATION DATA: 18 06/925,196 APPLICATION NUMBER: US 06/925,196 01-JAN-1900 Sequence 1, Application US/08259372A. Sequence 1, Application US/08259372A Patent No. 5565384 GENERAL INFORMATION: APPLICANT: Ostberg, Lars G. ZIP: 94111-3834 COMPUTER PEADABLE FORM: MEDIUM TYPE: Floppy disk TITLE OF INVENTION: TITLE OF INVENTION: USA Q U STATE: CA RESULT

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STREET:
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VENTION: PRODUCTION OF HUMAN MONOCLONAL
VENTION: ANTIRODIES SPECIFIC FOR HEPATITIS R SURFACE ANTIGE
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                                                                                                                                                                                                                             LOCATION: 1..423
Sequence 423 BP; 87 A; 100 C; 131 G; 105 T; 0 other;
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                                                               11823-50-7
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08468511. Sequence 1, Application US/08468671 Patent No. 5648077
                                            NAME: Smith, William M.
REGISTRATION NIMBEP: 30,223
REFERENCE/DOCKET NUMBEP: 1182
TELEFORMUNICATION INFORMATION:
TELEFORM (415) 325.2400
TELEFAX: (415) 575-2400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                LENGIH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                  ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: PEI-1
                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 90.8%;
Matches 275, Conservative
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                                                                                                                                                   CDNA
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                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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01-JAN-1900
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Townsend and Townsend and Crew LLP

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Best Local Similarity 90.8%; Pred. No. 1.35e-167;
Matches 275; Conservative 0; Mismatches 28; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-NOS/MS-DOS
SOFTWARE: Patentin Pelease #1.9, Version #1.30
CUPRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..423
Sequence 423 BP; 87 A; 100 C; 131 G; 105 T; 0 other;
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11823-50-7 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APP-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/676.036
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 07/192,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 05/925,196
                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/7
FILING DATE: 11-MAY-1988
PRIOR APPLICATION NUMBER: US 05/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM-
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE: Hybridoma CELL LINE: PE1-1
                   San Francisco
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: singl
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                                                         USA
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                                                                                                                                     COMPUTER:
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                                                         COUNTRY:
                                 STATE
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TITLE OF INVENTION: VACCINATION WITH A R-CEIL SUPERANTISEN AND CONJUGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SILVERMAN, GREGG J.
IIILE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
                                                                                                                                                                                  191 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 191
                                                         239 GAGAGTGGGTGAAGGGGGATTGAGGACGCGCAGAGAAGAAGAAGAAGAAGGGGTTTFC 268
122 GAGGGAAGGGUTTGGAGTGGGTGGGAGTATATGGTTTGATGGAAGTAATGAATATATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.4PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1..339
Sequence 339 BP: 75 A: 89 C: 98 G: 77 T: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 232; DB 11: 1
Pred No 5 56e-156.
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1880 Century Park Past - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JT 3
PCT-US93-10555-45 STANDARD: DNA; UNC: 339 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCI/US93/10555
FILING DAIE: 29-001-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45, Application PC/TUS9310555.
Sequence 45, Application PC/TUS9310555
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FD-2530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5100
INPURMATION FOR SEO ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEFEPENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 339 base pairs
TYPE: nucleic acid
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Best foral Similarity A9 5%;
Matches 25%; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STAIE: California
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CLONE: 0-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION.
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112 CRESCARSESCETESARISESTOSTASTIGIAISGAISGARCIACIANGIAÇIAIS 181
                                                                                                 122 CAGGCAAGGGGCTGGAGTGGGTGGCTATGGTTTGATGGAAGTAATCAATACTATT 181
                                                                                                                          182 CASACTOGGISCASSGCGSATTCACCATCTCASASACAACTCCSASAACACCCTSTATC 243
2 ASSIGNANTATIONASITIONS NAMED STOCK AND CITCARA AND CITCARA AND CONTRACTOR (FI
                                                                                                                                                                           242 IGCAAATGAACAGCCTGAGAGTCGAGGACACGGCTGTCTATTACTGTGCGAAAG 295
                                                                                                                                                                                       APPLICANT: HARFELDT, Elisabeth
APPLICANT: LAKE, Philip
APPLICANT: OTTAGE, Barbara
APPLICANT: GYBERG, Lars G.
TITLE OF INVENTION: MOUNCLOAL ANTIBODY TO HERPES SIMPLEX
WINDOW OF CONTROL OF SAME
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORPESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /product= "HSV863 heavy chain
OTHER INFORMATION: variable region"
Sequence 426 BP: 86 A; 101 C: 141 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9. Version #1.25
                                                                                                                                                                                                                                                     US-08-305-683A-1 STANDAPD: DNA; UNC; 426 RP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURPENT APPLICATION DATA: APPLICATION NUMBEP: US/08/305,683A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPFRATING SYSTEM: PC-F05/MS-D0S
                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09305683A.
Sequence 1, Application US/09305683A
Patent No. 5646041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IELEPHONE: (415) 326-2400
INFORMATION FOR SEC ID NO. 1. SEGUEPOS. CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13 SEP-1994
CLASSIFICATION: 424
PRIOP APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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AITORNEY/AGENI INFORMATION:
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MEDIUM IYPE: Floppy
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STREET: 3/2 _,
CITY: Palo Alto
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01-JAN-1900
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VACCINATION WITH A R-CELL SUPERANTIGEN AND CONJUGA
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                                                       59 AGGIGCAGCIGGIGGAGICGGGGGGAAGACGICGICCAGCCIAAAAAGGICCCIGAAAACIIT 118
                                                                                                                                                                                                                                         119 CCTGTGCAGCSPCFGGATTCACCTFGAGIAGGCATGTCATGCATTGGGTCCGGCCAGGCTC 178
                                                                                                                             179 GAGGCAAGGGGCTGCASTGGCTGGCAGTTACATGGTACGATGGAAGTAACAAAGCTATG 23%
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                                                                                  2 AGGIGCAGCIGCICGAGICIGGGGGAGGCGIGGTCCAGCCIGGGAGGICCTGAGACICT 61
                             Gaps
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 Length 426;
                          0; Mismatches 33; Indels
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Score 231; DB 7; Le
Pred No 3 30e-155;
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STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                    PCT-US93-10555-37 STANDARD; DNA; UNC; 369 BF.
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FILING DATE: 29-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37, Application PC/TUS9310555.
Sequence 37, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGS J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEFERENCE/DOCKET NUMBER FD-2630
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GIASSIFICATION:
ATTORNEY/AGENT INFORMATION:
WAME: HOWELLS, Stacy L.
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IBM PC compatible
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 37-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 369 base pairs
nucleic acid
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Query Match 62.1%;
Best Local Similarity 88 9%;
Matches 264; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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STATE: California
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TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA
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                                                                                                                                                                                                                                                                                                                                                                          122 CAGGGAAGGGGGGGGGGGGGGGGGGGGGGTAITAGTGGTAGTGGTGGTAGCAGATACTACG 181
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                                                                                                             Z ASSIGAAACISTICSAGICTOSOGGAAAACIIGGIAAAAAAGAGAGGAGAGIATICAAAACIET 61
                                                                                                                          Sabs
                                                                                                                                                                                                                                                                          METHOD FOR STIMULATING PRODUCTION OF
                                                            Score 213; DR 11; Length 369;
Pred. No. 2.53e-141;
                                                                                     Indels:
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CHRRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
                                    Sequence 369 RP; 79 A; 97 C; 115 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3. Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 6
PCT-US93-10555-47 STANDAPD; DNA: UNC: 294 BD.
                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 47, Application PC/TUS9310555. Sequence 47, Application PC/TUS9310555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
PEGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                             57.38;
                                                                         Best Local Similarity 80.2%;
Matches 296; Conservative
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                         369
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APPLICANT: SILVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
              NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                               361 ACCGTCTCC 369
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                         LOCATION
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FEATURE:
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                                                             Query Match
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TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA
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Sequence 41. Application PC/TUS9310555
GENERAL INFORMATION:
APPLICAT: SILVERMAN, GREGG J.
ITILE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
ITILE OF INVENTION: VARIABLE PROTON GRNE PAMILY PESTFICIED ANTIHODIES
                                                                                                                                                                                                                                                                                                                                            121 CCAGGCAAGGGGCTGGAGTGGCAGGTATATGGTTTGATGGAAGTAATGAATACTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GRAGACTOOGTGAAGGGCGGTTCACCATCTCCAGAGATTTCCAAGAAGACGTGTAT 240
                                                                                                                                                                                                                                                                                                                                                                                                     121 CCASSSAASSOSSSTSSASSTSSSSTSTCASSTATIASTSSTASTSSTSSTASTASTASTAS
                                                                                                                                                                                                                                                                                                      Score 208; DB 11; Length 294;
Prod No 1 88e-137;
0, Mismatches 42; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC COMPALIBLE
OPERATING SYSIEM: PC-LUGS/MS-LUGS
SCETWARE: PATENTIN PCLEASE #1.0, Version #1 25
CURRENT APPLICATION DATA:
                                                                                                                                                                                         LOCATION: 1..294
Sequence 294 BP: 53 A: 71 C: 96 G: 64 T: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Spensley Horn Jubas & Lubitz
1880 Century Park Bast - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCI-USGR-17555-41 STANDARD, DNA, UNIT 345 HP
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29-0CT-1993
TELECOMMUNICATION INFORMATION TELEPHONE: (519) 455-5100 TELEPAX: (519) 455-5110 INFORMATION FOR SED ID NO: 47: SEQUENCE CHARACTERISTICS:
                                                                                                          TOPOLÓGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: THEREOF
                                                                   LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  55.98;
85.78;
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             Conservative
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FILING DATE: 29-0CT
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STATE: California
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                                                                                                                                                                              NAME/KEY CDS
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nes 250, Conser
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VACCINATION WITH A B-CELL SUPERANTISEN AND CONJUGA
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Sequence 43, Application PC/TUS9310555
Sequence 43, Application PC/TUS9310555
GENEPAL INFORMATION:
SILVERAN GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VAPIABLE PEGIGN GENE FAMILY PESTPICTED ANTIBUTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 CASACTOST SASSOSSSTOSTOSTOTOCARACACANTITOARACACACTOTATO 241
| HTTL: | HTTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 206: 08 11; Length 345; Pred. No. 6.54e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTGTALIACTGTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM IYPE: Floppy disk
COMPUTER: TEM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 345 BP, 74 A: 88 C. 108 G, 75 T, 9 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUT-US93-10555-43 SIANDARD; DNA; UNC; 372 BP
                                                                               FEEFERMANICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FR SECTION INFORMATION:
TELEPHONE: (619) 455-5110
INFORMATION FOR SECTION: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYRE: nucleic acid
                          NAME: Howells, Stacy L. PEGISTPATION NUMBER 34,842
                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THEPEOF
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 85.8%;
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1880 Centu
CIIY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
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                                                                                                                                                                                                                                                                                                                                         242 TGCAAATGAACAGCCTGAGAGGGGGGGGGGGGGTGTCTACTGTGGGGAGAGAGTG 303
                                                                                                                                                                                                                                                                                                                                                                                                   242 TSCAACTSAACAGTSTSASASSSSAAGAAGAGGGTGTGTATTACTSTGCAAGAGGGGAAT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                     302 IGCGACGGCCCAAIGSITAIGCIAAGGGGGGTGAGIAGIGGGGGGAGGGAACCCIGG 361
                                                                                                                                                                                                                                                                                             62 CCTG1GCASCCTC1GGATTCACCTTCAGTAGTTACTGGATGCACTGGGTCCSCCAASCTC 121
                                                                                                                                                                                                                                                                    2 AGGIGAAACIGCICGAGICIGGGGGAGGCIIAGIICAGCCIGGGGGGIGCCIGAGACITT 61
                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                      Query Match 54.8%; Score 204; DB 11; Length 372; Best Local Similarity 79.5%; Pred. No. 2.27e-134; Matches 295; Conservative 0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE TITLE OF INVENTION: SECRETINS ANII-GANGLIGSIDE ANTIROLY
                                                                                                                                                                                                       Sequence 372 BP; 82 A; 103 C; 109 G; 79 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
CURRESPONDENCE FORESS.
ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-026-320A-1 STANDARD; DNA; UNC; 432 BP
   UMBER: PCT/US93/10555
29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1900
Sequence 1, Application US/08026320A
Sequence 1, Application US/08026320A
Patent No. 5419904
                                                          REFERENCE/DOCKET NUMBER: FD-26
TELECOMUNICATION INFORMATION-
TELEFAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                        CLASSIFICATION:
ATTORNEY/AERT INFORMATION:
NAME: HOWELLS, STACK, 84,842
                                                                                                                                                MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE.
CLONE: SPA1-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reiko F
CUPRENT APPLICATION DATA: APPLICATION NUMBER: PC
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APPLICANT: Irie, F
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                                                                                                                                                                                      NAME/KEY: CDS
                 FILING DATE:
                                                                                                                                                                                               LOCATION.
                                                                                                                                                                             FEATURE:
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/function= "Heavy Chain"
/product= "Immunoglobulin Variable Region"
/standard_name= "HuMat LGI2 Heavy Chain Variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 CCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGTAGTACTAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels Or Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /function= "Complementary determining OTHER INFORMATION: region 3 (CPP3)" Sequence 432 BP: 88 A; 99 C; 138 G; 107 1; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epstein Barr Virus Transformed B cell
1612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 271.300
OTHER INFORMATION: /function= "Complementary
OTHER INFORMATION: determining region 2 (CDR2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 203; DB 5; Lei
Pred. No. 1.34e-133;
0; Mismatches 46;
                                                                                                                                                                                            APPLICATION NUMBEP: US/OR/O25,320A FILING DATE: 26-FEB-1993 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/609803 FILING DATE: 05-NOV-1990 NATORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region Sequence"
                                (Y: United States of America 90067
                                                                       COMPOUTER PEAGRALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                        NAME: Oldenkamp, David J
PEGISTRATION NIMBER: 29421
REBERDAC-FOCKET NUMBER: 94
TELECOMMINICATION INFORMATION-
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAONE: 3107885046
TELEPAX: 310271297
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS.
LENGTH: 432 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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LOCATION: 397.429
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                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
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nes 249; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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Los Angeles
                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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               STATE: C
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VACCINATION WITH A R-CELL SUPERANTIGEN AND CONJUGA
                                                                                                                                                                                                                                                                                                            APPLICANT: SILVERMAN, GREGG 3.
IIILE OF INVENTION: METHOD FOR STIMILATING PRODUCTION OF
IIILE OF INVENTION: VARIABLE REGION GENE FAMILY PESTRICTED ANTIHOLIES
                                                                                           122 (ASSCANGSSSCTSSASTSSTESTATSCITTGALSCANGLANISAATANTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.8%; Pred. No. 3.256-128;
Matches 243; Conservative 0; Mismatches 47; Infels (
                                                                                                                                                 242 IGCAAAIGAACAGCCIGAGAGGGGAAGAGAGGGCGIIAIAIIACIGIGGG 291
                                                                                                                                                                           242 TSCARATSRACASSCITCASASSCESSGACASSGCTSTSTTATTASTSSSS 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                  JT 11
PCT-US93-10555-19 STANDARD: DNA; UNC; 360 BP
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                                                                                                                                                                                                                                                                    Sequence 19, Application PC/TUS9310555.
Sequence 19, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTOPNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
PEGISTPATION NUMBER: 34,842
PFEHENNIF/DWIKEI NUMBER - FU
IELECOMMUNICATION INFORMATION:
IELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER - FILING DATE: 29-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: USA
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MOLECULE TYPE:
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ZIP: 90057
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                                                                                                                                                                                                                                                        01-JAN-1900
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                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTISEN AND GONJUGA
                                                                                                                                                                                                                                                                      METHUD FOR STIMULATING PRODUCTION OF VAPIABLE REGION GENE FAMILY RESIRICTED ANTIHODIES
 181 TCAGACTCCGTGAAGGGGGATTGACCGTCTCCAGAGAGAAT(CGAGGAAGAGGCTGTTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 COTGIGORGESTICISSALIGACILIASENSENIGGENIGACIASSICESSENSEN 121
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Prod No. 3 250-129:
0. Mismatches 47: Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Pelease #1 0, Version #1 25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                     IIILE OF INVENTION: THEKEOF
NUMBER OF SEQUENCES: 51
COPPESPONDENCE ADDRESS: 5A
ADDRESSEE: SPENSIBY HORN Jubas & Lubitz
STREET: 1380 Century Park East - Suite 500
                                                                                                                                                              T 10
PCT-US93-10555-21 STANDAPD: DNA; UNC: 360 PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WUMBER: PCT/US93/10555
29-0CT-1993
M.
                                                                                                                                                                                                                  Sequence 21, Application PC/TUS9310555. Sequence 21, Application PC/TUS9310555 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2: Floppy disk
IBM PC compatible
3YSTEM: PC-DUS/MS-FUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: HOWELS R 4 dy I
RECISTATION NUMBER: 34,842
REFERENEY/FORKE INMHER: F0-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5110
INFORMATION FOR SEC 110 NOT 21:
SEQUENCE CHAPACIERISTICS:
                                                                                                                                                                                                                                                          SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENA (Genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loral Similarity 83 88;
sec. 243: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
SIMANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC (PERATING SYSIEM)
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TITLE OF INVENTION:
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CLONE: SPA3-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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TOPOLOGY - linear MOLECULE TYPE: DNA (genomic) IMMEDIATE SOUPCE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 360 base pairs
TYPE nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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CITY: Los Angeles
GTATE: California
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                                                                                                                                                                                                                                                                                                                            METHOD FOR STIMULATING PRODUCTION OF VAPIABLE REGION GENE FAMILY RESTPICTED ANTIRODIES
                                                                        122 CAGGGAAGGGCCTGGAGTGGGTCTCAGATATTAGTGCCAGTGGTGGTAGTAGGATATTATG 181
                                                                                               122 CAGGCAAGGGGCTGGASTGGGTGGCAGGTATATGGTTTGATGGAAGTAATCAATACTATT 181
                                                                                                                       182 CAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATT 241
                                                                                                                                              182 CAGACTCCGTGAAGGGCCGATTCACCGTCTCCASAGACAATTCCASGAACAGGGTGTTTC 241
2. ASSISSANSCINSTICANSSONAS AND SOCIAL CONTROL OF ASSISSAND CONTRACACTOR AT
                        62 CCTGTGCAGGSTCTSGATTGAGGTTGAGTAGTTATGGCATGGGAGTGGGTCGGCCAGGGTC
                                                                                                                                                                      242 IGCAAATGAACAGCCTGAGAGCCGAAGACACGGCCTTATATTACTGTGCG 291
                                                                                                                                                                                   52.2%; Score 194; DB 11; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Belease #1 0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                         E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                           PCT-US93-10555-27 STANDARD; DNA; UNC; 360 RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US93/10555 FILING DATE: 29.0CT-1993 CLASSIFICATION:
                                                                                                                                                                                                                                                                              27, Application PC/TUS9310555.
27, Application PC/TUS9310555
INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLEEMAIDNE: (619) 455-5100
TELEFAX: (619) 455-5110
TNPORMATION FOR SEQ. 10 NO: 27.
SEQUENCE CHARACIERISICS:
LENGTH: 360 back
                                                                                                                                                                                                                                                                                                                APPLICANT: SILVERMAN, GREGG J. IIILE OF INVENTION: METHOD FOR TITLE OF INVENTION: VAPIABLE PI
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NAME: Howells, Stary L
PEGISTPATION NUMBER: 34,842
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California
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IMMEDIATE SOUPCE:
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Sequence 27,
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TITLE OF INVENTION: VACCINATION WITH A R-CELL SUPERANTICEN AND CONTIGA
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                                                                                                                                                                                                                                                                                                                                                 182 CASACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATT 241
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                                                                                                                                                                                                                                                                                                                    122 CAGGGAGGGGCCTGGAGTGGGGTCTCAGATATTAGTACCAGTGGTGGTAGCAACATATTATG 181
                                                                                                                                           2. AGGTGAAAC PGCTCGAGTCTGGGGGGAAGATTGGTACAGGCCTGGGGGGTCTCTGAGACTCT 61
                                0. Gaps
                                                                                                                                                                                                         62 OCTGTGGAGGGTGTGGATTGAVGTTTAGGAGGGATGGATGAGGTGGGGTGGGGTGGAGGTG
                                                                                                                242 ISCAAATGAACAGCCTGAGAGGCGAAGACAGGGCCTTAJATTAGJGTGGG 291
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Best Local Similarity 83 48, Pred No. 1 120-126,
Matches 242, Conservative 0: Mismatches 48.
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 13
PCT-US93-10555-25 STANDARD; DNA; UNC; 360 BP.
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APPLICANT: SILVERMAN GREGG J.
TITLE OF INVENTION: WERHOD FOR STIM TITLE OF INVENTION: VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
PREPERCY_COCKET NUMBER: EF.26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
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IMMEDIATE SOURCE:

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAPIABLE PEGION GENE FAMILY PESTPICTED ANTIRODIES
                                                                                                                                                                                                                                                                                             | 62 | 001615648001016441110401111486444166641648410364048410 | 121 | 121 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 CAGACICCGIGAAGGGGGGGIICAGCAIGÍGGAGAGAATIGCAAGAAGAAGAGAII 241
                                                                                                                                                                                       2 AGSIGAAACIGGIGGASIGIGSSGSGAGSAIIGSIACAGCGIGGGGGGGCCGIGAGACIGI 61
                                                                                                                                                                                                                    Gaps
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                                                                            Score 1947 tH 11: Length 350:
Fred. No. 1.12e-126.
0: Mismatches 48: Indels '
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CURRENT APPLICATION DATA:
LOCATION: 1.,360
Sequence 350 RP: 73 A; 97 C; ill G: 77 I: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 14
PCT-9893-10555-23 STANDARD: DNA: UNC: 360 BP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       771/US93/104
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOU-SW/SOU-DA
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COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC:DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Howells, Stary L
REGISTRATION NUMBER: 34,842
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LENGTH.
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TELEFAX: (619) 455-5110
INFORMATION POF SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THEREOF
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TYPE: nucleic acid
STRANDFDNESS: single
                                                                            Overy Match
Best Local Similarity 83.4%,
Matches 242; Conservative
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MEDIUM IYPE: Floppy
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STREET: 1880 Centu
CITY: Los Angeles
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USA
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TITLE OF INVENTION:
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TILLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTISEN ANS CONTISA
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBACIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 CAGACTOCGIGAAGSSCOSGITCACCAIGICASAGACAAIICCAAGAACAACACCICIAII 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 APATGABANTENTOGRETINGESSABBATTESTANAGOTNESPARANTOGRENGT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 194; DB 11: Length 369;
Pred. No. 1.12e-126;
6; Mismarches 48; 1000!s 9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 ISCAAATGAACAGCCTGAGAGCCGAAGACACGGCCTTATATTACTGTGCG 291
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COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                           Sequence 360 BF; 75 A; 97 C; 111 G; 77 T; 0 other;
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1880 Century Park East - Suite 500
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PCT-US93-10555-33 STANDAPD DNA: HNC: 340 BP
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Sequence 33, Application PC/TUS9419555
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
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INFORMATION FOR SEQ ID NO: SEQUENCE CHAPACTERISTICS: LENGTH: 360 base pairs
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APPLICATION NIMBER: PCI
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.4%:
Matches 242; Conservative
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MEDIUM IYPE: Floppy
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CITY: Los Angeles
STATE: California
COUNTRY: USA
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SpA3-13
                                                                                        NAME/KEY: CDS
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                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                        Query Match 52.2%; Score 194; DB 11; Length 360; Best Local Similarity 83.4%; Pred. No. 1.12e-126; Matches 242; Conservative 0; Mismatches 48; Indels (
                                                                                      LOCATION: 1..360
Sequence 360 BP; 75 A, 96 C, 111 G, 78 T, 0 other;
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: SPA3-37
                                                                             NAME/KEY: CDS
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Search completed: Tue Feb 24 14:30:27 1998 Job time : 60 secs.

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Release 2.12 July F. Jullins. Biocomputing Research Sait Copyright (c) 1993, 1994, 1995. University of Edinburgh, U.K. Distribution rights by IntelliGenetics. Inc.

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Psrch_no n.a. · n.a. database search, using Smith-Waterman algorithm

Publion: The Peb 24 09:40:37 1998: MasPar time 62:05 Seconds 691 924 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-19
Description: (1-372) from US08844215.seq
Perfect Score. 32
N A. Sequence: 372
Comp.

. GCCTGGTGACGGTGTGCTGA 372

Scoring table: TABLE default Gap 6 Searched: 159651 segs, 57698962 bases x 2

Dbase 0; Query 0

Mmatch STD:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: n-qen

n-geneseg30 light12:part2 3:part3 4:part4 5:part5 5:part5 7:part18 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21 part21 2:part22 23:part23 24:part24 25:part25 25:part26 27:part27 28:part38 29:part29 30:part30 31:part31 30:part32 33:part33

Statistics: Mean 8.102: Variance 4.826; scale 1.579

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*					
Result No.	Score	Query Match	Query Match Length DR	D.B.	ID	Description	Pred. No.
-	253	7.0.7	583	13	078971	Human immunoglobulin	5.69e-163
C1	257	1 69	345	٤,	もりとしら L	Anti-TGF beta-2 SCFV	α51.010.
3	257	59.1	512	6	078968	Human immunoglobulin	1.01e-158
4	253	68.0	369	۴.	TEARRO	Anti-TGF beta-1 scFv	6.820-156
V۱	250	67.5	698	(5)	T60381	Anti-TGF beta-1 seft	9 040-154
Ş	249	e u	L. C.1	ra	01100	٠.	4 500-153
7	1.	56.4	423	33	TRUBARA	Monoclonal antibody P	1 195-151
œ	C4	56.4	423	Ċ	T46128	Monoclonal antibody F	1,196.151
·(3*	247	56.4	429	ं	054050	Sequence of the VH re	1 140-151
10	543	66.4	904	۲.	S43772	Sequence encoding the	
11	246	66.1	436	(7	011957	Anti-human Php HAM-B	6 0RP-151
12	245	65.9	339	7	011956	Anti-human PhD REG-A	3 100-150
13	(1 17 (1	65.1	698	33	T60382	Anti-IGF beta-1 scFv	4.086-148
14	0.45	64.5	0.0	a) C	160122	Coding sequence for h	1 066-146
15	er C	ः १ ३	01	5	015031	Anti-Tak hora-2 segu	07 C C C C

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55 S S S S S S S S S S S S S S S S S S		. C1 O C C C C	കെയയയെയുന്ന സെക്കേഷ്	014000 01400 01400 01400 01400 01400 01400 01400 01400
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ALIGNMENTS

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DNA fragment comprising human immunoglobulin Wh genes for the production of human immunoglobulin in mammalian hosts production of human immunoglobulin in mammalian hosts of Jair 41 Page 72-731 137pp. Japanese.

A series of genes (1299.7972) encoding human immunoglobulin variable heavy chains. The genes were selected and closed from a series of osmid constructs: V202, V203, V21, V6, V24, 3-37, M84, M18 and M131, by HCH amplification using primers QP8917-38. The genes are subdivided into 5 families of VM genes. The fragments cover a region of 800 kb. The Invalidation cutyme. The Invalidation high molecular weight PNA from human prime families of VM was partially disested with Tagl restriction cutyme. The fragments were separated by quelelectrophoresis and 35-45 kb fractions were collected. The fragments were ligated with 1301-131setcd cosmid vector P'841. The ligation profices were in citro pived and interted
                                                                     03-AUG-1995 (first entry)

Human immunoglobulin Vh gene #33.

Human immunoglobulin Vh gene #33.

Human immunoglobulin: variable: heavy chain: cosmid: placenta; vector: pJBB1: E.coli: mammalian: ds.

Homo sapiens
                                                                                                                                                                                                            /*tag= a
/product= human immunoglobulin variable heavy chain
                                                                                                                                                                                                                                                                                                          /*tag= c
//note= "miscellaneous siganl, does not conform to
terminator or splice site sequence"
WO9426895-A.
                                                                                                                                                                     Location/Qualifiers
20 .472
LT 1
Q78971 standard; DNA; 583 BP.
Q78971:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1994.
10-MAY-1993; Jüü603.
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                                                                                                                                                                                                                                                                                 240 cetgigaagegictggalicaceticagtagetatggaaigcaetgggiceggeeaggeic 299
                                                                                                                                                                                                                                                                                                                                                                     360 cagaetecqeqaaqqqeeqatteaceatetecaqaqaaaattecacqaacacqctqttte 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts. Sequence 583 BP; 136 A; 127 C; 186 G; 134 T;
                                                                                                                                                                                                                                      2 AGGTGCAGGTGCAAGTCTGGGGGGAGGGTGGTCAAGCTGGGAAGTCCTGAAGCTCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune and inflammatory disease
Example 1: Fig 2a(1): 184pp; English.
This DNA sequence comprises the gene encoding the VH domain
This DNA sequence comprises the gene encoding the VH domain
(W1552) of human servantibody. Av.H1 (also know; as 6H1), which
is specific for transforming growth factor (TGP) beta-2. It was
isolated by panning a phage antibody library produced from cloned
quemine V genes and synthetic CDPs. The antigen-binding domains
of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can
be used to counter the adverse effects of TGF beta-1 and/or beta-2 can
promotion of fibrosis (in dermal, ocular or keloid scarring, lung
fibrosis, arterial injury, proliferative retinopathy, retinal
detachment, adult respiratory distress syndrome, liver cirrhosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis,
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 tgcaaatgaacagcctgagagccgaggacacggctgtgtattactgtgcgagaga 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-TGF beta-2 serve antibody 2A-H11 VH gene.
Transforming growth factor beta-2; TGF beta-2; human;
antibody engineering; serv; phage display; lung fibrosis;
arterial injury; proliferative retinopathy; retinal detachment;
adult respiratory distress syndrome; liver cirrhosis;
post myocardial infarction; post-angioplasty restenosis;
scleroderma; vascular didease; cataract; glaucoma; scarring;
glomerulonephritis; ost-aboprosis; immune disease; inflammation;
rheumatoid arthritis; macrophage deficiency disease;
macrophage pathogen infection; therapy; ss.
                                                                                                                                                  .
                                                                                                            Length 583;
                                                                                                                              Pred. No. 5.69e-163;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        post myocardial infarction, post-angioplasty restenosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams AJ:
                                                                                                                            5.69e-163;
                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Bacon L, Green JA, Jackson RH, Johnson KS,
Tempest PP, Thompson JE, Vaughan TJ, Willia
                                                                                                          Score 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T60369 standard; DNA; 345 BP.
                                                                                                                            Local Similarity 94.6%;
les 279; Conservative
                                                                                                            70.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-0CT-1996; 020920.
19-JAN-1996; GB-001081.
06-0CT-1995; GB-020486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric synthetic.
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                                                                                                          Query Match
                                                                                                                                                       Matches
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DNA fragment comprising human immunoglobulin Vh genes - for the production of human immunoglobulin in mammalian hosts

Droduction of human immunoglobulin in mammalian hosts

A scries of genes (979, 1399, 2490)

A scries of genes (979, 120, 120, 120)

A scries of genes were isolated and cloned from a series of cosmid constructs; Y20; Y103, Y21; Y5;Y44; 3.31; M84; M18 and M131, by DCR amplification using primers (78917.38. The genes are subdivided into 5 families of Vh genes. The fragments gover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with Taql restriction enzyment. The fragments were separated by gel electophoresis and 35-45 kb fractions were collected. The fragments were ligated with Clai-digested cosmid
                                                                                                                                                                                                                                                               Ö
                                                                                                                                                                                                                                                                                                                                                                                           61 teetgtgeagegtetggatteaeetteagtagetatggeatgeaetgggteegeeagget 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGGTATGGTTTGATGGAAGTAATCAATATTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TCASACTCCSTSAAGGGCCSATTCACCSTCTCCAGACAALLCCAGGAACACOGTGTTT 240
                                                                                                                                                                                                                                                                                                       1 gaggtgcagctggtggagtctggggggaggcgtggtccagcctgggaggtccctgagaactc 60
                                                                                                                                                                                                                                                                                                                                                1 GAGGIGCAGCIGCICSAGIDISGGGGAGGCGIGGICCAGCCIGGGAGGICCCIGAGAGTTC 60
scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephitis, also (not claimed) osteoporosis), or (11) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be
                                                                                                                                                                                                                                                            O: Gaps
                                                                                                       used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low ICSOs for neutralisation. 112 G; 74 T; Sequence 345 BP; 76 A; 83 C; 112 G; 74 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin; variable: heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccaggcaaggggctggagtgggtggcagttatatggtatgatggaagtaataatactat
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                                                                                                                                                                                                                 Length 345;
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                                                                                                                                                                                                                                                            0; Mismatches 16: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cosmid; placenta; vector, pJB81; E.coli; mammalian; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= human immunoglobulin variable heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "miscellaneous signal, does not conform to terminator or splice site sequence"
                                                                                                                                                                                                                                        Pred. No. 1.01e-158;
                                                                                                                                                                                                                 DB 33;
                                                                                                                                                                                                                 Score 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1995 (first entry)
Human immunoglobulin Vh gene #30.
Primer; PCP; amplify; human; immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q78968 standard; DNA; 512 BP.
                                                                                                                                                                                                                                      Local Similarity 94.5%;
nes 273; Conservative
                                                                                                                                                                                                                 69.18;
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(NISB ) JAPAN TOBACCO INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09426895-A.
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vector pUBB1. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human [munneylobulin in mammalian hosts sequence. 512.8F. 127.4]. 100A.71. 159.03. 125.75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 aggidopagoidgidagagididagagagagagagagagagagagoodagagadioodagagactot 228
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This DNA sequence comprises the gene conding the VH domain this DNA sequence comprises the gene conding the VH domain this DNA sequence comprises the gene conding the VH domain sequence comprises the gene conding the VH down as 7A3), which is specific for transforming growth factor (TGF) beta-1. It was solicited for transforming growth factor (TGF) beta-1. It was solicited by panning a phase autibroly library produced from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, occurring, lung librosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis,
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transforming growth factor beta 1 or 2 - and nucleic acid encoding
it, used to neutralise effects of TGF, e.g. for control of fibrosis,
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Anti-TGF beta-1 scFv antibody 1-B2 VH gene.
Transforming growth factor beta-1: IGF-beta-1: human:
antibody endineering; scFv: phage display: lung fibrosis.
arterial injury; proliferative retinopathy: retinal detachment;
adult respiratory distress syndrome: liver cirrhesis:
post myocardial infarction: post-andioplasty restenosis:
scleroderma: vascular didease, cataract, glaucoma, scarring;
qlomerulonephitis: osteoporosis: immune disease: inflammation:
rheumatoid arthritis: macrophage deficiency disease:
macrophage pathogen infection; therapy; ss.
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                                                                                                                                                                                                                                                                              Length 512;
                                                                                                                                                                                                                                                                     Match 69.1%; Score 257; DB 13; Length 512
Local Similarity 93.6%; Pred. No. 1.01e-158;
es 276; Conservative 0; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160380 standard: DNA: 369 BP.
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06-0CT-1995; GB-020486.
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                                                                                                                                                                                                                                                                         Query Match
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post myocardial infarction, post-angioplasty restenosis,

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122 caggcaaggggctggagtgggtggcagttatatatcatatgatggaagtaataautactatg 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 cagaeteegigaagggeegatteaceateteeagadaeaatteeaagaaeaegeigiate 241
                                                                                                                                                                                                                                                                                                 2 aggigobbotggagagicigagagagagagagagagogib
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This DNA sequence comprises the gene encoding the VH domain.
This DNA sequence comprises the gene encoding the VH domain.
(W15535) of human scFv antibody 3169, which is specific for transforming growth factor (TGF) beta-1. It was isolated from a large single chain Fv library. The antigen-binding domains of human antibodies (see W15522-40) to TGF beta-1 and/or behavior promotion of fibrosis (in dermal, coular or keloid scarring, lung
scleroderma, vascular disorders, cataract, glancoma, or exp. neutal scarring and glomerplenephritis, also (not claimed) estopporosis), or (ii) immune and inflammatory diseases (e.g. rheumator) arthritis, macrophage deficiency diseases to macrophage pathosen infection). Nucleic acids encoding human antibody VH and VL can be
                                                                                                       used for prodn. of recombinant antigen-binding domains. Those are highly specific, have low dissociation constants (pref. less than 5 nM) and low 1050s for neutralisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.NOV-1997 (first entry)
Anti-TGF beta-1 sefv antibody 3169 VH gene.
Transforming growth factor beta-1; TGF-beta-1; human;
antibody enqineering, sefv, phase display, lung fibrosis:
arterial injury; proliferative retinopathy: retinal detachment;
adult respiratory distress syndrome; liver cirrhosis:
post myocardial infarction; post-andioplasty restenosis;
scleroderma; vascular didease; cataract; glaucoma; scarring;
glomerulonephritis; osteoporosis; immune disease; inflammation;
rheumatoid arthritis; macrophage deficiency disease;
macrophage pathogen infection, therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 PSCAAATGAACASACTIGASACCOGASAACAACAACAACAATGATATAACTATACTATTACTATAACTATACAA 292
                                                                                                                                                                                                             Length 369:
                                                                                                                                                                                                                                                     indels
                                                                                                                                                                       8; T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson KS, Pope AR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams AJ
                                                                                                                                                                                                                                 Best Local Similarity 93.5%; Pred. No. 6.82e-156;
Matches 272; Conservative 0, Mismatches 19.
                                                                                                                                                                     138 6
                                                                                                                                                                                                             DB 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaughan IJ,
                                                                                                                                                                                                             Score 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAMR-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T
T60381 standard; DNA; 369 BP.
                                                                                                                                                                 87 A;
                                                                                                                                                                                                             58.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacon L, Green JA, Jackson
Tempest PR, Thompson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1997,
07-OCT-1996; 020920.
19-JAN-1996; GR-001081.
06-OCT-1995; GB-020486.
                                                                                                                                                                     369 RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97-215360/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; W15535
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                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                      62 octytycaycetetygaiteacetteagiageiatygeaigeaetygyteegeeayyete 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 CAGGCAAGGGGCTGGAGTGGGTGGCAGGTATATGGTTGATGGAAGTAATCAATACTATT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 CAGNETGCGTGAAGGGCCGATTCACCGTCTCCAGAGACAATTCCAGGAAGACACTTTT 241
                                                                                                                                                                                                                                                                                    Indels 0: Gaps
                 detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty restencesis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid
                                                                                                             arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be used for prodn. Of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low 1050s for neutralisation. Sequence 369 RP. 83 A. 117 G. 81 T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 44: Fig 18: 104pp; English.

The leader peptide and the L'V region are encoded in different reading frames. The L'V region corresponds to the last three amino edids of the leader peptide and the variable region gene.

See also 011878 and 011879.

Sequence 1521 BF, 349 A, 376 G, 425 G; 371 F.
                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CCTGTGCGAGCGTCTGGATTCACCTTCAGTGCTTATGGCATGCACTGGGGTCCGGCTAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of \lg 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (first entry)
Encodes heavy chain variable region for 4B9 human monoclonal Ab.
immunoglobulin G, heavy chain, variable region, duplication;
passive immulty; group B streptococt; ss.
fibrosis, arterial injury, proliferative retinopathy, retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 TGCAAATGAACAGCCTGAGACCCCAGGACACGGCTGTCTATTACTGTGC 291
                                                                                                                                                                                                                                                Length 369,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 tgcaaatgaacagcotgagagctgaggacacggctgtgtattactgtgcg 291
                                                                                                                                                                                                                                            Score 250, DB 33, 1
Pred. No. 9.04e-154;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/product= heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1989; 05-432700.
(BRIM) BRESICL MYERS SQUIB.
Shuford WW. Harris LJ, Raff HV;
WPI; 91-163947/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R12132, R12133, R12134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q11880 standard; DNA; 1521 RP.
                                                                                                                                                                                                                                            67.2%;
illarity 93.1%;
Conservative
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06-NOV-1990; U06426.
                                                                                                                                                                                                                                                              Local Similarity
nes 270; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "octamer"
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/note= "leader"
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08-DEC-1997 (first entry)
Monoclonal antibody PE1-1 Vh region coding sequence.
Heavy chain, light chain: variable region; human monoclonal antibody;
immunisation; hepatitis b virus; HBV; vaccine; mouse; fusion; xenogeneic;
peripheral blood lymphocyte; surface antipen; cell culture; ion exchange;
chromatography; size separation; primer: PCR: polymerase chain reaction;
amplification, hybridoma, infection, immunosuppression, hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the nucleotide sequence encoding the heavy chain variable (Vh) region from the human monoclonal antibody (MAD) PET-1. The MAD was generated by immunishing humans with a hepatitis B virus (HBV) vaccine, isolating peripheral blood lymphocytes (PEL) and fusing them with a mouse/human xenogeneis cell line SPAR-4.
                                                                                                                                                                                                                                                                                                                      1042 gtagtgg-igg--ta-gitgc--iactoctitgactaciggggocagggaacontggina 1095
                                                                                                                                                                                                                                                                                                                                                                                                     742 aggigeageiiggiggiggiegieiiggggggaggeggegieeniggieenigggaaggieenigaagaeiet 801
                                                                                                                                                             G.
                                                                                                                                                                                           862 caggraaggggctggagtggctgcgttatatcatctgatggcagtgttgatactactg 921
                                                                                                                                                                                                                          122 CASSCAASSSSCTSSASTSSSTASSTATATSSTITSATSSAASTAATCAATAATT 181
                                                                                                                                                                                                                                                          981
                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                        301
                                 Gaps
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                                                                                                                                                                                                                                                          922 cagantocogigaagggcogatinaccatoiccagagacaaticcagggatatgcigiatg
                                                                                                                                                             62 CCTGTGTGCAGCGTCTGGATTCACCTTCAGTTTATATGCTTATGCACTGGAGTCGGGTCGGCTA
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                                                                                                                                                Longth 1521;
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                                 0; Mismatches 40; Indels
Score 249; DB 2; L
Pred, No. 4.60e-153;
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66.98;
                  Best Local Similarity 87.6%;
                                    325; Conservative
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US-904517.
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15-JUN-1990; US-538796.
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14-JUN-1994; US-259372.
06-JUN-1995; US-468671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1096 ccgtctcctca 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           liver transplant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 CCGTCTCCTCA 372
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 Query Match
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                                   Matches
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exchange throman graphy on Eastward. The heavy and light chains of the MAbs were isolated and their amino acid sequences determined. Primers were encrated and used to amplify cDNA synthesised from RNA purified from each bybridona cell line. The sequences of the heavy and light chains (nucleic acid and amino acid) from MAbs PEI-1, ZMI-1, ZMI-2 and MDN-4 are shown in TPSR38-45 and W2494-4! The Mabs can be used to treat HBV infections in immunosuppressed patients or patients with chronic active hepatitis, especially liver transplant patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  # Match 65.4%; Score 247; DB 33; Length 423; Local Similarity 90 8%: Prod No 1 196-151; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
PEI-1, ZMI-1, ZMI-2, MD3-4 and LD3-3. The cell lines were then tested for production of an anti-hepatitis F wirus surface antigen antibody by ELISA. The MAS are then purified from large scale cell culture by protein A chromatography and see separation on Sephacryl S300 gel and ion exchange thismatography on G Sephacrace. The heavy and light chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MRR-1997 (first entry)
Monoclonal antibody PEI-1 heavy chain variable region cuding Sequence.
Monoclonal antibody diagnosis, treatment, infection hepatitis B;
Kenodeneic hybriddoma, SAR 4; PEI-1, ZMI-1, ZMI-2, MD3-4;
IgGl class; heavy chain; light chain; variable region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 agatgcagotgatgaatotgagggagaggtggtccaggottggaggtccctgagactct 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 caggenagggyotggagtgggtggcagtgatateateatgatggaagtaatagaatggtatg 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 caqacteogiqaaagggeogaticaccateteeagagaeaaticcaagaacactetgiiic 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 igeaaaigeacageetgagagetgeggacaegggtgiataitaetgigegaaagaicaae 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119^\circ cetatgeagectetagatteacetteagtaaggtatggeatgeaetgagteeggeete 178^\circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 octoficiadatriosatricacificastecitarioscalidaactiosoficialegaete 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GAGGGAAGGGGGTGGAGTGGGTGGGTAIAIGGIIIGAIGGAAGTAATGAAAGTAIT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 GAGACICOSTGAAGGGGGALICACOGICICCÁGAGAGAAIICCAGGAACACGCIGTÍIC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human more long antipodies specific for bepatitis B surface antigen - are used to treat or prevent infection or in diagnostic assays claim 9; Column 27:28; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AGGIGCAGCIGCICGAGITTGGGGGAGGGGGTGCTGAGGGTGGGAGGTGCTGAGAGICT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/note= "leader seguence"
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US-925196.
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31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-1990:
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14 - JUN - 1994;
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diseases caused by infection with hepatitis's have been prefared from cell line obtained by fusing a xenogeneic hybridoma designated SPAN 4 with blood cells of a patient immunised with hepatitis B varcine. Specific antibudies are PEI-1, ZMI-1, ZMI-2, MDA-4 and 103-4, each of these being of the 1961 class. The present sequence encodes the heavy sequence (423 BP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 aggigeageiggiggagieiggggggaaggegiggieeageeigggaagaicenidadaeint 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 cotytycayoctotyyattoacottoaytayytatyyoatyoactyyytooyoonyyote 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 caggicaaggggctggagtgggtggcagtgatatcatatgatgqtagaagtaataaatq;tatq 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 CCTGIGGABGGIGIGGAIIGAGGIIGAGIGGIIAIGGGA)GGAGTIGGGICGGGGAGGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 CAGACTOOGIGAAGGGGGGAIICAGGGIGIGGAGAGAAGAAITGGAGGAAGAAGAGIIIG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luman volutheers were liminised with hepatitis B vaccine. MD3-4, ZM1-1 and PE1-1 hybridoma cell lines were derived from lymphocytes of individuals immunised with Heptavax (Morre & CO). Antibodies PE1-1, ZM1-1, MZ1-2 and XM3-4 belong to the 1751 clas. The cell lines producing PE1-1, ZM1-1 and ZM1-2 were deposited as ATCF HR923, 9191 and 9192 respectively. The cell lines all behave as typical (mouse x human) x human hybridomas and produce their respective Abs in concs. ranging up to 25 mg/l in standard suspension culture. The heavy variable (VH) and light variable (LH) chains of Abs FE1-1, ZM1-2 and MD3-4 were isolated and shapened 104a1 PNA was axiral ted film (MC) hybridoma cells of each cell line, ss DNA was synthesised using AMV-reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 Addiscreated and the second additional content of the content of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Gaps
Monoclonal antibodies effective for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 cagactocatgaagggoogattoacaatctocaaactocaaacactotto
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Sequence of the VH region of monoclonal antibody PEI-1 against
Sequence of the VH region of monoclonal antibody; therapy:
Hepptlits B virus; surface antigen; monoclonal antibody; therapy:
HBSAG; diagnosis; HBV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CASSCAASSSSCISSAGISSSISSCASSIAIAISGIIIGAISGAASIAAICAAIACIAII
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.8%: Pred. No. 1.19e-151;
Matches 275; Conservative 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
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06-NOV-1992; U09749.
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P-PSDB; R54047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CCTGTGCAGCGTCTGGATTCACCTTCAGTGCTTATGGCATGGGACTGGGTCCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 caggcaaggggctggagtgggtggcagtgatatcatatgatggaagtaataaatggtatg 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
transcriptase and oligo-dT as primer PCPs were performed and amplified DNA was size selected, ss DNA for sequencing was isolated from each positive clone after superinfection with M13K07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence encoding the heavy chain variable region (VH) of human immunoglobulin G3 (1gG3) produced by transformed human B-cell line 88BV59, ATCC CRL 10624.
                                                                                           Sequencing was by the dideoxy chain termination method (Sanger
                                                                                                                                                                                                                                                                             0, Mismatches 28, Indels 0;
                                                                                                                                                                                                              Length 429;
                                                                                                                                                          106 T;
                                                                                                                                                                                                              Score 247; DB 10; I
Pred No 1 19e-151;
                                                                                                                                                          132 G;
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IDS 148..204
                                                                                                                                                          103 C;
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                                                                                                                                                          88 A;
                                                                                                                                                                                                              Match 66.4%;
Local Similarity 90.8%;
Nes 275, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q43772;
01-0CT-1993 (first entry)
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09-DEC-1992; 203827
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EP-545634-A.
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142. 88BV59 uses VHIII and a D region which may have resulted from intra D-D recombination and/or gene conversion along with somatic unitation. It is radically different from any germ line D region. It utilises germ line JH3. It is of note that a cysteine at AA posn. 59 (AA No. 78 in R38161) is present within the 88BV59 VH. No other kabat posn 59.
                                                                                                                                                                                                                                                                                                                                                                                         59 aggtgcagctggtggagtctgggggaaggcgtggtccagcctgggaaggtccctqagaactct 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 cetgigeagectetggaiteacetteagiagetatggeaigeacigggieeggeeaggete 178
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                                                                                                                                                                                                                                                                                                                                                                                                          2 AGGESCASCIGOTOGASIONAGESCAGESCAGOSCIGOSCAGIOCOTOGASCICI 61
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                          Disclosare, Fig 2, 18pp; English.
043772 encodes the complete heavy chain from the leader through AAs
                                                                            Transformed human B cell line for monoclonal antibody prodn. for cancer diagnosis - prepd from peripheral blood B-cells of cancer patients actively immunised with autologous tumour antigen, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 tgcaaatgaacagcetgagagetgaggacaccgetgtetattactgtgtgtgaaaya 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                   / Match 66.4%; Score 247; DB 7; Length 909; Local Similarity 91 9%; Pred No 1 19e-151; hes 271; Conservative 0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                           194 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding complementary determining regions – of human anti-rhesus D antibodies, useful in produ. of monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; rhesus D; blood-typing; CDR;
                                                                                                                                                                                                                                                                                           245 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemolytic disease of the newborn; HDN; ss.
                                                                                                                                                                                                                                                                                       279 €:
                                Haspel MV, Kobrin BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-1991 (first entry)
Anti-human RhD HAM-B MAb (VH chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                         189 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r 11
Q11957 standard, DNA, 336 BP
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13-DEC-1991; HS-807300.
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13-NOV-1990; E01964
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WPI; 91-178104/24.
P-PSDB; R12275.
                             Crichton VZ, Hasp
WPI; 93-190019/24.
                                                                                                                              treating cancers
               (ALKU ) AKZO NV.
                                                               P-PSDB; R38161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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'label= CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                         Query Match
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antibodies and for passive immunisation
Disclosure. Fig 14, 32pp. English.
The DNA sequence of elever more lends antibodies are
the presented in ULINAS S. Synthetic genes, for both heavy and
lith chains may be created by combining selected CDR 1, 2, and 3
regions, which may be selected from different antibody mods having
varied binding specificity. The chimaeric anti-hic antibodies can be
vised for diagnosts and therapy, and are capable of providing blood-
typing reagents of high specificity and reliability. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The DNA sequence of eleven monoclonal antibodies are represented to 01945 T Synthatic genes. for both heavy and light chains may be created by complining selected DNB 1. 2 and 3 regions, which may be selected from different antibody mois having varied binding specificity. The chimaeric anti-Khb antibodyses can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 GCCAGSTATAIGSTIIGAIGSAASIAATGAATACTAIICASACIGGTGAAGGGCGGAIT 203

    cttcagtagctatggcatgcactgggtccgccaggctccaggcaaggggctggagtgggt 120

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 CIICAGIGCIIAISGCAIGCACIGGGICCCCCCAGGCICCAGGCAAGGGGCTGGAGTGGGI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 caccatotocagagagagasticoaagaacacqotqistotycaaatgaacayootqagago 240

    gagragestagteragestaggaaggtesetgaagastetestgtgeagegtetggatteas 60

                                                                                                                                                                                                                                                                                                                       be used in passive immunisation to prevent haemolytic disease of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 66.1%; Score 246; DB 2; Length 336; Local Similarity 94.2%; Fred. No. 6.08e-151, nes 260; Conservative 1; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding complementary determining regions - of human anti-rhesus D antibodies, useful in produced in encoding antibodies and for passive immunisation Disclosure: Fig 13, 32pp. English
                                                                                                                                                                                                                                                                                                                                                                                                74 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-1991 (first entry)
Anti-human PhD PEG-A MAN (VH chain).
MONOGIORAL ANTIBODY: Thesus D: blood-typing: CDR:
haemolytic disease of the newborn: HDN, ss.
                                                                                                                                                                                                                                                                                                                                                                                                108 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24] cyaggacacacqctqtqtattactgtqcqagagaqqt 275
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                                                                                                                                                                                                                                                                                                                                                                                                77 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                75 A;
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Hughes- Jones N:
WPI: 91-178104/24.
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                                                                                                                                                                                                                                                                                                                                                                                                336 BP;
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immune and inflammatory disease

Example 1: Fig 1c(i): 184pp: English.

This DAN sequence comprises the gone encoding the VH domain

(M15536) of human scfv antibody 3169, which is specific for

transforming growth factor (TGF) beta-1. It was isolated from

a CPR3 spiking experiment. The autique tinding downers of

chuman antibodies (see W1552-40) to TGF beta-1 and/or beta-2 can

be used to counter the adverse effects of TGF beta-3 such as (i)

promotion of fibrosis (in dermal, ocular or keloid scarring, lung

fibrosis, arterial injury proliferation retinged

detachment, adult respiratory distress syndrome, liver cirrhosis,

post mycorardial infarction, post angioplasty restences;

scieroderma, vascular discrebers, catalact, giaucoma, or esp. genral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 GGCAGGTATATGGTTTGATGGAGTAATCAATACTATTCAGACTCCGTGAAGGGCGGATT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 caccatetecagagacaattecaagaacaegetgtatetegcaaatgaacageo1qagage 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 GACCGTCTCCASASACAATTCCABSAACACTGTTCTGCAAATGAACGGCCTGAGACC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 otteaataattatggeatgeactqqjteegeeaggeteeaggaaagggagetggagtgggt 128
used for diagnosis and therapy, and are capable of providing blood-typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic discuss of the newborn.
                                                                                                                                                                                                                                                                                                                                                                                                              1 gggaaggegiggiccageelgagaaqiceelgagaacieiceigigeagegiegicgicigaaiicae 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 GGGAGGCGTGCTGCAGCCTGGAGGTCCCTGAGACTCTCTGTGCAGCGTCTGGATTCAC 83
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transforming growth factor beta 1 or 2 - and nucleic acid encoding
it, used to neutralise effects of TGP, e.g. for control of fibrosis,
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 CITCAGISCITATGGCATGCACTGSGTCCGCCAGGCTCCAGGCAAGGGGGTGGAATGGGT
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Transforming growth factor beta.1: TGF-beta.1: human:
antibody engineering: serv: phage display: lung fibrosis:
arterial injury, profilerative retinopathy, retinal detachment:
adult respiratory distress syndrome: liver cirrhosis:
post myocardial infarction: post-angloplasty restenosis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scleroderma; vascular didease; cataract; gláucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease;
                                                                                                                                                                                                                                                                                                                                       :
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                                                                                                                                                                                                                                                    Length 339;
                                                                                                                                                                                                                                                                                                                               0; Mismatches 14; Indels
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Tempest PR, Thompson JE, Vaughan IJ, Williams AJ:
                                                                                                                                                                                                                                            65.9%. Score 245. Lb 2. L
94 9%: Pred. No. 3 10e-150:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 CGAGGACACGGCTGTCTATTACTGTGCGACAGA 296
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                                                                                                                                                                          85 A:
                                                                                                                                                                                                                                            Goery Match
Best Local Similarity 94 98:
Matches 259: Conservative
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06-001-1995: GB-000486
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GB1305921-A.
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of the invention preferably contains the sequence represented by Wi3912 in the complementarity determining region-1 (CDR-1) of the heavy chain variable region. The antibody of the invention also contains the sequence represented by Wi3913 in the CDR-3 of the light chain variable region. The antibody is capable of binding to adr type hepatitis B (HB) virus antigen. A human anti-HB virus monoclonal antibody preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; heavy chain; light chain; variable region; human; monoclonal; complementarity determining region; human; adr type hepatitis B virus; HB virus; CDR: virus antigen; anti-HB antibody; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T60116-T60123 represent the coding sequences for the heavy and light chains of the human monoclonal antibody of the invention. The antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 cagccaaggggctggagtgggtggcagttatatatcatatgatggaagtagtaaatactatg 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 cagactecgtgaagggeegatteaceatetecagagaeaattecaagaaeacgetgtate 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 CAGACTCCGTGAAGGGCCGAFTCACCGFCTCCAGAGACAATTCCAGGAACACGCTGTTTC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        confit the contragation of the contragoration of the contragoratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 aggigcaaciggiggagiciggggggggggggcgiggiccagccigggaggiccigagactci 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGGTGCAGTTGCTTCAGTCTGGGGGAGGGTGGTGGTGCAGCCTGGGAGGTGCCTTGAGAGTTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Gaps
scarring and glomerulonephritis, also (not claimed) osteoporosis), or (1i) immune and inflammatory diseases (e.g. rheumicin arthritis, macrophage defliciency diseases or macrophage pathogen infection) Nucleic acids encoding human antithody VH and VL can be used for prodn. of recombinant antiqen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low 1650s for neutralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 CASGCAAGGSGCTGGACTGGGTGGCAAGATATATATGTTTGATGGAAGTAATGAATAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to adr type HB virus can be
Jy. It can also be used as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human anti-Hepatitis B antibody - used in a adr type HB virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 33; Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 28; Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.5%: Score 240: DB 28; I
Best Local Similarity: 91.7%: Pred No 1 06e-146;
Matches 264, Conservative 0, Mismatches 24.
                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.08e-148;
                                                                                                                                                                                                                                                                115 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which is highly safe and is effective to provided, using the monoclonal antibody, vaccine against HB infection.
                                                                                                                                                                                                                                                                                                                                         Score 242;
                                                                                                                                                                                                                                                                91 (;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coding sequence for heavy chain #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Page 17; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T60122 standard; cDNA; 357 BP
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11-JUL-1995; DY-174752.
(ASAH) ASAHI KASEI KOGYO KK.
WPI; 97-140911/13.
                                                                                                                                                                                                                                                            85 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 A,
                                                                                                                                                                                                                                                                                                                                     Query Match 65.1%;
Best Local Similarity 91.7%;
Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                369 RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 BP,
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P-PSDB; W13927
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J09020798-A.
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                                                                                                                                                                                                                                                                   Sequence
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This used to incutantity disease

Example 1: Fig 2a(ii); 184pp; English.

This DNA sequence comprises the gene encoding the VH domain

This DNA sequence comprises the gene encoding the VH domain

(W1552) of human scftv antibody 2A-96 (also known as 11E6), which

is specific for transforming growth factor (TGF) beta-2. It was

solated by panning a phage antibody library produced from cloued

germine V genes and synthetic CDPs. The antigen-binding domains

of human antibodies (see W1552.40) to TGF beta 1 and/or beta-2 can

be used to counter the adverse effects of TGF beta, such as (i)

be used to counter the adverse effects of TGF beta 2 and 3 (i)

c promotion of fibrosis (in dermal, ocular or keloid scarring, lung

fibrosis, arterial injury, proliferative retinopathy, retinal

detachment, adult respiratory distress syndrome, liver cirrhosis,

post myocardial infarction, post angioplasty restenosis.
67 agcytotygattcacettcagtagtcatygcatycantyggtnogccagqntnoaggraa 125
                                                                          69 AGGSTCTGGATTCACCTTCAGTGCTTATGGCATGCAGGGCTCCGCCAGGCTCCAGGCAA 128
                                                                                                                                                        127 ggggetggagtgggtggcacttatatgggetgacggaactaataaatattatgetgaete 186
                                                                                                                                                                                                                                       129 GGGGCTGGAGTGGGTGGCAGGTATAGGTTTGATGGAAGTAATCAAJACTATTCAGACTC 188
                                                                                                                                                                                                                                                                                                                     187 egtgaagggeegatteaceateteeagagaeaattreaagaaaanargrigitatrignagat 246
                                                                                                                                                                                                                                                                                                                                                                                           189 cstgaagggcgattgacgstgtccagagacaattccaggaacacstgtttttgcaaat 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2^{\circ} and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used for prodn. of recombinant antigen binding domains. These are highly specific, have low dissociation constants (prof. loss than 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) esteoporosis) or (ii) immune and inflammatory diseases (e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arthitis, macrophage deficiency diseases of macrophage pathogen infection). Nucleic anids encoding human antibody VH and VI can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AntiTGF beta-2 scrv antibody 2A-A9 VH dene.

AntiTGF beta-2 scrv antibody 2A-A9 VH dene.

Transforming growth factor beta-2; 75F-beta-2; human;

antibody engineering; scrv. phage display, lung fibrosis,

arterial injury; proliferative retinopathy: retinal detachment;

adult respiratory distress syndrome; liver cirrhosis;

post myocardial infarction; post-angioplasty restenosis;

scleroderma, vascular didease, cataract, glaucoma, scarring;

glomerulonephritis; osteoporosis; immune disease; inflammation;

rheumatoid arthritis; macrophage deficiency disease;

macrophage pathogen infection; therapy; ss.
                                     Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 gaacageetgagageegaggacaeggetgtgtattaetgtgegagaga 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 GAACASCCTGAGACCCGAGGACACGCTGTGTATTACTGTGGACAGA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 238; DB 33;
Pred. No. 2.73e-145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jackson RH, Johns
n JE, Vaughan IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
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83 A; 87 C;
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T60370 standard; DNA; 350 BP
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89.98;
                                     Thompson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07.0CT.1996; 020920.
19.JAN-1996; GB-001081.
06.OCT-1995; GB-020486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric Homo sapiens;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nM) and low ICSOs for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Green JA,
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WPI: 97-215360/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB2305921-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacon L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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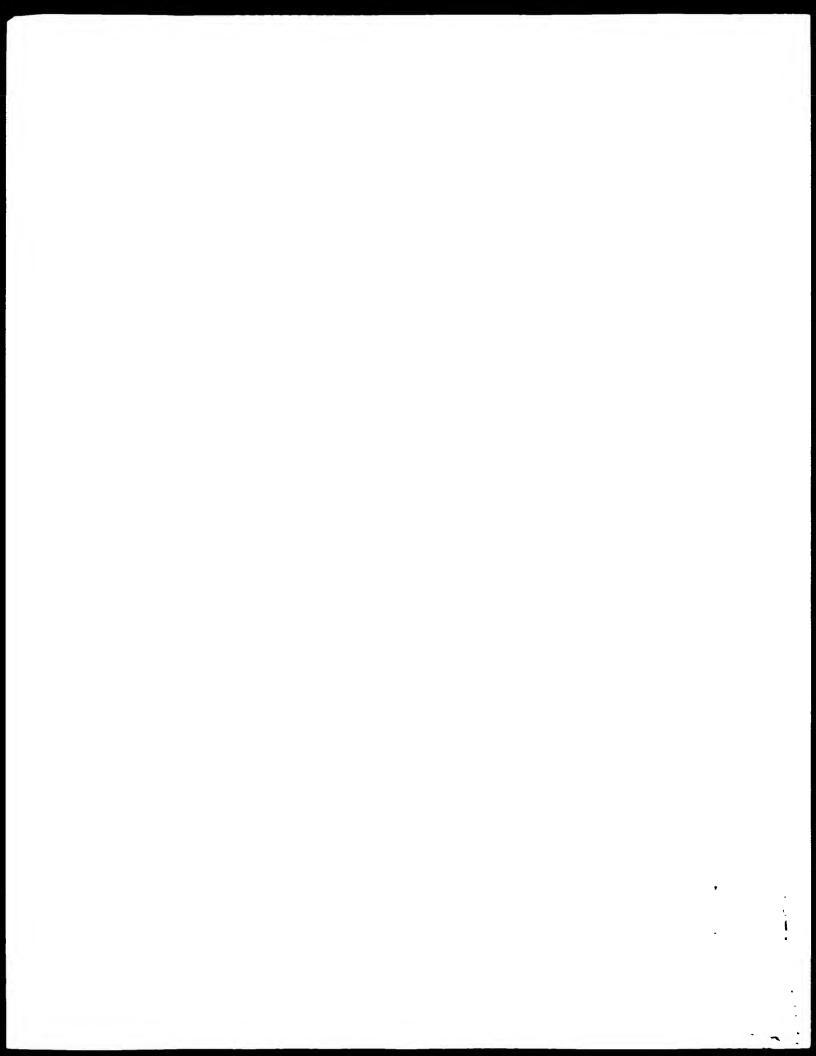
Best Local Similarity

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67	r-4	GASTE	GAPATOPARCIENTARATORARANA GEORGES CONTROLES DE CONTRA A C	- Y	- 1501505 - 1501505	 .AGCCTGC	SAGGICCE	TGAGA	CIC 60	<u> </u>
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Š	51		TOCISTOCASOSICIOSATICACCITCASTOCIANOSATOCATOS SICOSOCASOCI	701100	AGTGCTTALC	TITE		1 1 1 1 1 GCCA3		120
qc	121		ocadoraagggqotinagtgggtggcagttatatoatatgatggaagcaataatato	tageae	ittatatoat	atgatga	raagcaata	aatac 		180
ōγ	121		CCAGGCAAGGGGTGGAGTGGGTGGGTATAGGTTTGGTGGAAGTAATGATATT	1.500 A	951AIA1991	11GA193	SAAGTAATC	AAIAC		Ş.
qq	181	900900	181 geagacteogtgaaggeogatteacatetecagagaeaatteeaagaacaettgtat	200 BOI	atotocadao	acaatto	caagaaca	09019	tat 24	24 Û
0.5	181	TCAGAC	18: ICAGACICCGEGAAGGGGGGAIIGAGGETIGGAGAGAGAGAATIGGAGGAACACCGGEGAAGGGGGGAIIGAGGGGGGGGGGG	ICACC	SICICAGAGAG	ACAATIC	CAGGAACA	CGCTG	TIT 24	2 4 0
<u>م</u> 2	241		241 ctacaaatgaacagoctgagagotgaggacacaggocatgtattactgtgcaagaggg	1	i IIIIIIII	tigtatta	ctgtgcaa	1 11	9 298	
οy	241		CISCAAAISAACAGGGIGAGAGGGGAGGAGGGGIGIGITATIACIGIGGGAGAGG	COGAGO	SACACGGCIC	TCIALLA	VITGIGGGA	CAGAG	G 298	

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Cop	<pre>se 2.1D John F Tollins, Bicocmputing Research Unit ight (c) 1993, 1994, 1995 University of Edinburgh, U.E. Distribution rights by Intelligenetics, Inc.</pre>
MPsrch_nn n a	- n a database search, using Smith-Waterman algorithm
Run on:	Tup Feb 24 08 31 ft 1998; Masbar time 490 14 Seconds 1078,ekt Millian cell updates/sec
Tabular output	
Title: Description: Perfect Score N.A. Sequence: Comp:	>US-08-844-215-19 (1-372) from USO8844215.seq 372 i AABATGAAGTTGATAGATGA 372 i TECAGGTGAAGTTGATGAGTG
Secring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0: Query 0
Searched:	430261 segs, 710217276 bases x 2
Post-processing	. Winimum Match 0% Listing first 45 summaries
Database:	embl-new7 1:BCT_2.PUN_3.3EN_4.HTG1_5.HTG2_6.HTG3_7.HTG4_8.HTM1 9:HDM2_10.HTM3_11.NTN_12_11.NTW2_13-NPG_14.HM3_5.VRT 15.PUN_3.PUN_12.PUN_3.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3_5.NTM3
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Statīstics:	Mean 10.911: Variance 4.331; scale 2.312

and is derived by analysis of the total score distribution.

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EATURES	Loca	at ion,	Quali	Location/Qualifiers					
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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/cell_line="418_155_35"
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human-mouse heterohybridoma F386"
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NID # 9499609
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/map="14q32.33"
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/gene="IGH@"
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Best Local Similarity 88.18;
Matches 327; Conservative
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LRAEDTAVYYCARMEYSSGMYGEYLQHWGQGTLVTVSSASTKGPSVFPLAPSSKSTSW
                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata, Eutheria, Frimates, Catairhini, Hominidae, Homo. I hases 1 to 53.3.
Chai,S.K., Kasaian,M.T., Ikematsu,H., Kim,M.Y. and Casali,P. VH-D-JH gene sequences of mAb produced by human B-la, B-lb, and B-2
C-region, D-region, 7-region, V-region, immunoglobulin heavy chain.
Homo sapiens (individual_isolate Donor B) adult peripheral blood
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/product="inmunoglobulin heavy chain"
/db_xref="PID:g553399"
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/product="immunoqlobulin heavy chain"
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Fred No 2 966-223;
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/map="14q<sup>3</sup>2 33"
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/isolate="Donor B"
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Bost Local Similarity 88.1%;
Matches 327; Conservative
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Submitted (11-071-1991) F.M. Raaphorst, Division of Immunology, Dept. of Immunohematology and Bloodbank, Academic Hospital Leiden, Building I, E3-Q, P.O.Box 9600, 2300 Leiden, THE NETHERLANDS Enidian I, E3-Q, P.O.Box 8600, 2300 Leiden, THE NETHERLANDS Schroeder H W. Jr. et al. Proc Natl Acad Sci. 178A, 87:5149(1990) & Ichihara y. et al. Eur. J. Immunol. 18:649(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS HSVH31348 366 bp RNA PPI 02-JUN-1992
DEFINITION H-Sipiens rearranged mRNA for fetal IG heavy chain Vh3, DQ52 and ACCESSION X5367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pestricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal lymphocyte channoglobulin heavy chain rearrangements Eur. 3. Immunol. 22 (1), 247-251 (1992)
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                                                               233. cuductocogiqaaqqqqqcogaiticaccatotocaqaqacaaittocaqqqqqqqqqqqqq
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Vertebrata: Eucheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 365)
Paaphorst:F M. Timmers:F. Kenter,M.7, Van Tol,M.7. Vosse
Tenath 366,
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Pred. No. 2.75e-222;
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/isolate="Clone FL13-48"
/dev_stage="13 week old foetus"
/issuc_type="liver"
/cell_type="B lymphocyte"
/chl_type="B lymphocyte"
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/note="Jh element"
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Raaphorst,F.M.
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/product="immuseglobulin beavy chain variable region"
/db_xxef="PID:g1791923"
/translation="@VQLVESGGGVVQP3PSLRLSCAASGFTFSSYGMHWVPQAFGR:
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marrow transplant recipient 90 days post transplant; clone
8 in reference 1"

    (bases 1 to 368)
    (alas.A.M., Nottenburg.C. and Milner.E.C.B.
    Pirect Submission
    Submitted (CP-NOV-1946) Immunology, Virginia Mason Brewatch Confer-1000 Senera Street, Seattle, WA 98101, 05A

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Glas,A M., Nottenburg C and Milher,E C
Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
Glin. Exp. Immunol 107 (2), 372-380 (1997)
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                                        2 aggigcagoiggigagictggggggggggggggggiggicgaggcigggaggicciaagacici 61
                                                                                   2 AGGTGGAGCTWTTGGAGTGTGGGGAGAAGTGTGCTGCAGGTTGGGAGGTCGTGAGAGTCT
SqbS : 3
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Vertebrata; Eutheria; Primates; Catarrhini: Hominidae: Homo.
0; Mismatches 31: Indels
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/clone="3b2q3"
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Vertebrata, Eutheria: Primates: Catarrhini, Hominidae, Homo
1 (bases 1 ro 399)
Timmers.E., Kenter.M., Thompson.A., Kraakman.M.E., Berman.T.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 64471] from the original journal article. This sequence comes from Fig.la.
                                                                                                                                                                                                                                                                                           122 CAGGCAAGGGGGTGGAGTGGGTGGCAGGTATATGCTTTGATGGAAGTAATCAATACTATT 181
                                                                                                                                                                                                                                                                                                                                                               182 cagaetecegigaagggeegaiteaeeaieteeeagagaeeaaiteeaagaaeaegeigiate 241
                                                                                                                                                                                                                          62 cctgtgcagcctctggattcaccttcagtagctatggcatgcactgggtccgccaggctc 121
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                                                                                                                                                        2 aggtgcagetggtggagtetggggggagacgtggtccagcctgggaggtccctgagactet 61
                                                                                                                                                                                       2 AGGIGCAGCIGCTCGAGTCTGGGGGAAGCGTGGTCAGCCTGGGAGGTCCCTGAGACTCT 61
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/gene="immunoglobulin heavy chain V region, VH3"
                                                                                     Length 368;
                                                                                                                    0; Mismatches 38; Indels
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                                                                                     Score 267; DR 95; I
Pred. No. 2.75e-222;
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Local Similarity 88.7%;
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/product="immunoglobulin heavy chain v region"
/db_xref="PID:q236905"
//db_xref="PID:q236905"
/Lanslation="wwLVESGGSVV.vGFSELLLSCAASSFIFSSYGMHWVLGAPPRS
LEWMANIMPGSNYYADSVKGPFTISPDNSKNTLYLOMNSI,PAFDTAVYYCAPPPRE
TIAAAGNFDYWGQGTLATVSSGSRSAPTLFP"
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Verrekrata, Butheria, Primares, Catarrhini, Huminidae, Homo.
1 (bases 1 to 341)
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ACCESSION M77333
NID g185761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.5%; Score 266; DR 102; Length 349; Bost Local Similarity 87.9%; Pred. No. 2.566-221; Matches 326; Conservative 0; Mismatches 42; Indels 3
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Homo sapiens
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/map="14q32.33"
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/product="immunoglobalin heavy chain"
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//translation="Van@volvEssasavvqpaksLpEscaassHFSSYGMHWVPgAP
//translation="Van@volvEssasavvqpaksLpEsnasHFSSYGMHWVPgAP
//translation="Van@volvEssasavvqpaks"
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1. (bases 1 to 342)
Djavad.N., Bas.S., Shi,X., Schwager,J., Jeannet,M., Vischer,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comparison of rheumatoid factors of rheumatoid arthritis patients,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of individuals with mycobacterial infections and of normal controls: evidence for maturation in the absence of an autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-JUL-1995) E Boosnek, HCTS, Unite d immunologic de transplantation, 24, Rue Micheli-du-Crest, 1211 Geneva 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 cagacaaggggctggaadtgggttggcabttatatatgtatgatggaagtaataaataaatat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSIHCVDII 342 bp RNA PRI 20-JAN-1997
H.sapiens mPNA for rearranged Ig heavy chain variable domain,
cell_type RA-1-DT7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       o: Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 TOCAMATGAACAOOOTGASAOOOOASSACAGSGCCTATTACTGIGGGACAGA 296
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/cell_type="RA-1-DT7, ERV transformed R rell"
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                                                                                                                                                                                                                                                                                                                        Length 341;
                                                                                                                                                                                                                                                                                                                      Score 265: DB 99: Length 341
Pred. No. 2.37e-220;
0: Mismatches 15: Indels
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                                                                                                                                                   /note="G00-118-731"
337..>341
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/codon_start=3
                                                                                                                                                                                                              /dene="IGH9"
                                                                                                                                                /dene≖"IGH3"
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Submitted (31-071-1901) F M Paaphorst Pivision of Immunology,
Submitted (31-071-1901) F M Paaphorst Pivision of Immunology,
Dept. of Immunohematology and Bloodbank, Academic Hospital Leiden,
Building I, E3-0. P.O.Box 9600, 2300 Leiden, THE NETHERLANG
For related sequences see Xf2944-Xf972, Xf3f22-3, M7277,
Schroeder H W Jr Pt Al, Proc Natl Acad Sci.08A, 87:6149(1940) A
Ichihara y, et al, Dur. J. Immunol. 18:649(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pestricted utilization of germ-line VH3 geres and Short disease third complementarity-determining regions (CDR3) in human fotal B lymphocyte immunoglobulin heavy chain rearrangements gur. 3 Immunoglobulin heavy chain rearrangements
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 COTOTOCAGOSTCTSSATIONOCITICAGISCITATOSOATSCACISSGIOGSGCAGGGTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 caggeaaggegeiggagigggilggeagitalaiggiatgaiggaaglaaiaaaaakk 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 cagaetteegigaaagggeegaileareaheitenama, ettenagaganaaileesaaaaaaeeeeetetaie 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGIS HSVH4132 359 Mg FWA FELL IG heavy chain VK3. DDF2. DEFINITION H.Sapiens rearranged mRNA for fetal IG heavy chain VK3. DDF2. possible inverted DM2 (overlapping with D052), and JM3 (clone

    aggitgdaggtggtggtgtggggggggggggtggttccagcctggqaggtccctqaqacfirt 61

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AGGIGCAGGIGCTPGAGIGTONANANANATIGGTPPANGCIGGGAGGICCCIGAGACICI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 359)
Paaphorst, F. M., Timmers, E., Kenter, M. J., Van Tol, M. 1. Vosse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 ჩვისმმსწვისების გუნის გუნი
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Longth 312:
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                                                                                                                            /db_xref="PID:e254910"
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Pasphorst, F M
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/cell_typer"P lymphcsyte"

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/product="immunoglobulin heavy chain"
/db_xref="PID:g185727"
/translation="VQCgVgLVESGGGGVVQPGFSLFLSGAASGFTFSSYGMHWVPQAP
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Wu,J , Kozin,F , Carson.D A and Chen,P.P.
Molecular basis of an autoantibody-associated restriction fragment
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Homo sapiens (individual_isolate Nov) adult DNA.
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Olee,T., Yang,P M , Siminovitch,K A , Olsen,N.J , Hillson,J.
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                                                                                                                                                                                                                           Score 265; DB 96; Length 359; Pred No 2 37e-220;
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Human Ig germline H-chain gene V-region, clone Nov.
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/db_xref="GDB:G00-118-731"
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/map="14q32.33"
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/note="Jh element"
                                                         /note="Vh element"
/chromosome="14"
/map="14q32"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Germline variable region gene segment derivation of human monoclonal anti-TAN(D) antibodies. Evidence for affinity maturation by somatic hypermutation and repertoire shift J. Clin Invest. 90 (6), 2481-2400 (1992)
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Verrebrata; Eutheria, Primates, Catarrhini; Hominidae; Homo.
1 (bases 1 to 375)
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DEFINITION H Sapiens mPNA for HamRH heavy chain variable 1g domain.
ACCESSION X64154
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Pred. No. 2.37e.220;
0; Mismatches 15; Indels
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Bye,J.M., Carter,C., Cui,Y., Gorick.R D., So
Winter,G., Hughes-Jones,N.C. and Marks,J.D.
                                                       /note="G00-118-731"
337..343
/note="7 mer recombination signal"
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/cell_type="B-lymphocytes"
/cell_line="HAM-B"
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/note="Vh region"
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N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research,
Babraham Hall, Cambridge CB2 4AT, UK
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Vertebrata: Mammalia; Butheria: Primates: Catarrhini; Hominidae;
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Homo sapiens (human)
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Winter S., Hughes-Jones N.C., Marks J.D.;
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26-JUL-1997 (Rel. 52, Last updated, Version 6)
H.sapiens mRNA for Hampy heavy chain variable Iq demain
heavy chain, Iq heavy chain,
immunoglobulla heavy chain variable region; mariable IC3
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/5259="YPP2 region"
           /note="CDR1 region"
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Matches 324; Conservative
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"Germline variable region gene segment derivation of human monocional anti-Rh(D) antibodies. Evidence for affinity raturation by somatic hypermutation and repertoire shift";
I flim inver: 90.1440.4440(1942)
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/ordanism="Homo sapiens"
/cell_type="B-lymphocytes"
/cell_line="HAW-B"
/isolate="blood donor Ha"
                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                      IMGT/LIGM; X64154; Pelease 97,06,
See also X64148-69
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/note="CD19+ peripheral blood B cells obtained from a bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marrow transplant recipient 90 days post transplant; clone 28 in reference 1"
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LEWVAVISYDGSNKYYADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYYCAPDPNK
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-NGV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
                                                                                                                                                                            Glas.A.M., Nottenburg.C. and Milner.E.C. Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient Clin. Exp. Immunol. 107 (2), 372-380 (1997)
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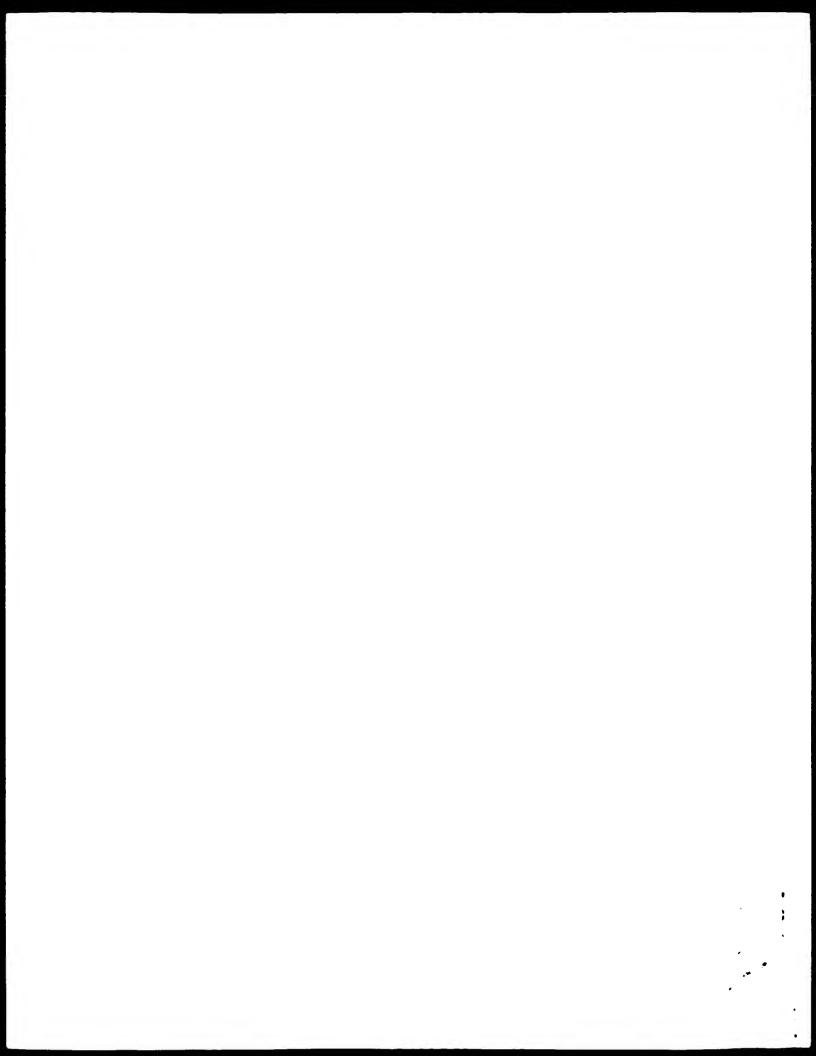
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 375)
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Best Local Similarity 87.4%; Fred. No. 2.37e-220;
Matches 327; Conservative 0; Mismatches 44;
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/clone="3c2d1"
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LEWVAVTWYPGSNKYYADSVKGRFTISPDNSKNTLYLQMNSLRAEDTAVYYCARDNYY
YDSSGYYYYYYGMDVWGQGTTVTVSS"
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-OCT-1994) Mahmoudi M., University of Western Ontario, Medicine and Microbiology and Immunology, University Hospital Room BRE-12, London, Ontario, Canada, N6A 5A5 Location/Qualifiers
                                                                                                                                                                                                                                                           Mahmoudi,M., Edwards,J., Cairns,E. and Bell,D.
Molecular characterization of natural human anti-Sm autwantihodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note"-*Author-given protein sequence is in conflict with the conceptual translation."
  HSBUD94H 384 bp RNA PRI 28-OCT-1994
HOMO Sapiens MRNA for anti-Sm antibody VH chain (VH3/DXp4/JH5).
Z46379
                                                                                                          anti-Sm antibody; diversity region; immunoglobulin heavy chain;
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1 (bases 1 to 384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="anti-Sm antibody VH chain (VH3/Dxp4/JH6)"
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                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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94.9%; Pred. No. 2.37c-220;
vative 0; Mismatches 15;
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/cell_type="B-cell"
1. >384
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325..384
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Mahmoudi, M.
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                                                                                                                                                                                               Eukaryotae: mitochondrial eukaryotes: Metazoa: Chordata;
Vertebrata: Puthoria: Primates: Catarrhini: Hominidae; Homo
1 (bases 1 to 412)
Olee, I., Yang, P.-M., Siminovitch, K.A., Olsen, N.J., Hillson, J.L.,
Wu, J., Kozin, E., Carson, B.A. and Chen, P.P.
Molecular basis of an autoantibody-associated restriction fragment
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                                                                                                                                                                                                                                                                                                              length polymorphism that confers susceptibility to autoimmune
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Homo sapiens germline 19H chain, V region, clone hviol989
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242 ISCAAATGAACAGGGGGAGGGGGAGGAGAAGGGGTGTGTATTAGTAGGAGAGA 296
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Homo sapiens adult peripheral blood DNA.
Homo sapiens
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Pred. No. 2.37e:220;
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25
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                                                                                                                                                                                                                                                                                                                                                                                         Loration/Qualifiers
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∕qen⊖="IGH9"
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101..405
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Rest Local Similarity 94.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vischer, I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comparison of rheumatoid factors of rheumatoid arthritis patients, of individuals with mycobacterial infections and of normal controls: evidence for maturation in the absence of an autoimmune
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                                                                         H.sapiens mPNA for rearranged Ig heavy chain variable demain, cell-type TB-1-P7.
X99355
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Vertebrata: Eutheria; Primates; Catarihini; Hominidae; Homo.
1 (bases 1 to 333)
Njavad,N., Bas,S., Shi,X., Schwager,J., Teannet M., Vischer,P.
Roosnek,E.
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Pred No. 2.200:219:
0: Mismatches 16: Indels (
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Host Local Similarity 94 FM;
Matches 280; Conservative
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Pelcase Copyrig	 2 1b John F Collins, Riocomputing Pescarch Unit ht (c) 1993, 1994, 1995 University of Edinburgh, Distribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a.	. n.a. database search, using Smith-Waterman alg
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adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
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gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
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Tumor Gene Index
Unpublished (1997)
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                 -28ml3 rev2 ET from Amersham High quality sequence stop: 1
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further information. Trace considered overall poor quality Seq
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Pred No 0 00e+00;
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                                                                                /organism="Homo sapiens"
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Contatt Pobert Strausberg, Ph D Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov

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CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I M A G E Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="vector" pampl0; mena made from lipnsarcoma, cDNA made by oligo-dT priming Non- directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
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A-ZTT-1947 (Pel. 52, Last updated, Version 2)
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gb:M63438 IG KAPPA CHAIN PPECHPSOP V-III PEGION (HUMAN)).
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High quality sequence stop: 413.
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/tissue_type="liposarcoma"
/lab_host="DH108"
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                                                                                                                                                                                                /organism="Homo sapiens"
/note="Vector: pAMP10: mENA made from liposarcoma, cDNA
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gol, average insert size 500 bp.
Peference: Krizman et al. (1995) Cancer Research
56:5880-5383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 gocaattoagagtatoatoagoaccoottagootggtatoagoaaaaaootggooaggot 214
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                                                                                                                                                                                                                                                                                                                                                                          Score 175; DB 71; Length 418;
Pred No 7.03e-298,
0, Mismatches 54, Indels 4; Gaps
                   Contact: Robert Strausberg, Ph.D. Tel: (701) 496-1550 Email: Pobort Strausberg*hih gov lissue Procurement. L. Jeffrey Modeiros. M.D. Michael R. Emmert-Buck, M.D. Ph.D. PobN Library Preparation-David B. Krizzen, Ph. C. EDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Secome Sequencing Center Colone distribution: NGI-GSP clone distribution: NGI-GSP clone distribution information can be told through the I.M.A.G.E. Consortium/Linia information can be www-bio linia gov/bbrp/image/image.html Insert Length- 1076 Std
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23-JUN-1997 (Rel. 52, Last updated, Version I)
2435D05.rl Soares overy timor NUHCT Homo saptens CDMA Clone 739953
5' similar to qb:x06754 IG KAPPA CHAIN PRECURSOW V-III PEGION
                                                                                                                               Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.
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Vertebrata: Butheria: Primates: Catarrhini: Hominidae. Homo
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                                                                                                                                                                                                                                                                              /clone="940044"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab.pst="DHIOB"
                                                                                                                                                           Location/Qualifiers
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Best Local Similarity 91.4%;
Matches 253, Conservative
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Tumor Gene Index";
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/note="Organ: ovary: Vector: pT73D (Pharmacia) with a modified polylinker. Site_1 Not 1: Site_2: ECO RI: 1st strand coln was primed with a Not 1: olido(d) primer [5: FITACTAATOFSAATGATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTATOTAT
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Hillier,L. Allen,M., Rowles,I., Dubuque T., Grisel,G., Jost,S.,
Krizman,D., Kucaka,T., Lady,M., Le,N., Lenter,S., Marra.M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston/R. and Wilson.R.
WashUnCI human ESI Project
Unpublished (1997)
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Vertebrata, Mammalia, Eutheria: Primates: Catarrhini: Hominidae)
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                                                                                                                                                                                                                                                                                                       confact: Wilson PK Washington University School of Medicine 4444
Forest Park Farkway, Box 8501. St. Louis, MD 6108 Tel: 314-286
BROO Fax: 314-286-1810 Bmail: estawatson wastledd This orlone is available regality fire—through LINE. Contact the IMANE Consortion (info@image iln) gov) for further information. Say primer: -28mid
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Krigman D., Kudaba T., Lacy M., Le N., Lennon G., Marra M., Martin D., Moore R., Schollenberg K., Steptoe M., Tan F., Thelsing B., White Y., Wylle T., Waterston R., Wilson R.: "Washu-NCI human EST Project";
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/clone="739953"
/clone_lib="Soares ovary tumor NDHOT"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Ero PI: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' sgrand cDNA was primed with a Not I - oligo(dT) primer [5' sgrand cDNA was primed with a Not I - oligo(dT) primer [5' sgrand cDNA was primed with a Not I - oligo(dT) primer [5'] sgrand construction of the Note of the Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded from was size selected, ligated to Ero RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Ero RI sites of a modified pT7T3 vector (Pharmacia), Library constructed by Bento Soares and M Ertima Room and
                                                                                                                                                                                                                                                           Email·est@watson wustledu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@imaqe.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 agcagggccactggcatcccagacaggttcagtggcagtgggtctgggacagacttcact 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 ACCAGAGCCACTGGTACCCCAGAGAGGTTCAGTGGCAGTGGGGTCTGGGACAGAATTCACT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 ctcaccatcatgcagactggagcctgaagattttgcagtgtattactgtcagcagtattgg 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 CICACCAICA-GCAGCCTGCAGTCTGAGGACTTTGCAGTTTATTTCTGTCAACACTATAG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 ttagcctggtaccagcagaaacctggccaggctcccaggctcctcatctatggtgcatcc 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-1997 (Rel. 52, Created)
13-JUN-1997 (Rel. 52, Last updated, Version 1)
8-SESSOG.11 Soares ovary tumor NDHOT Homo sapiens cDNA clone 810346
5' similar to ab:M12740_-0481 IS KAPPA CHAIN PRECUPSOR V-III PERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillier L. Allen M. Bowles L., Dubuque T., Geisel G., Jost S. Kucaba T., Lacy M. Le N. Lennon G., Marra M., Martin J., Moorre B., Sciellenberg K., Steptoe M., Tan F., Theising B., Wwlie T., Waterston R., Wilson P.; Washu-Merck EST Project 1997";
                                                                                                                         4444 Förest Park Parkway, Box 8501, St. Louis, Mo 63108
Tel: 314-286-1800
Fax: 314-286-1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 1;
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Vertebrata, Eutheria, Primates; Catarrhini; Hominidae: Homo.
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<1. >242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares ovary tumor NbHOT"
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Pred. No. 8.41e-267;
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                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="ovarian tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Local Similarity 87.7%;
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                                         Contact: Wilson RK
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LOCUS AA464224 324 bp mRNA EST 10 JUN 1997
DEFINITION XX83c06.rl Scares ovary tumor NCHOI Home sapiens cDNA clone 810346
5' similar to gb:M12740_cds1 1G KAPPA CHAIN PRECIPESOP V-III PFGION
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Vertebrata, Mammalia; Eutheria, Primates, Catarrhini, Huminidae;
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Hillier, Allen, M., Bowles, L., Dubuque, T., Geisel, G., Tost, S. Kucaba, T., Lacy, M., Le, N., Lencon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Materston, R. and Wilson, R. Grey Project 1997
Oppublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St Louis, Mon S108 Tel: 314 286 1800 Fax: 314 286 1810 Fmail: estGwatson.wustl.edu This Cione is available royalty-free through LLNL, contact the IMAGE Consortium (info@image lini gov) for further information Seg_primer: -28m13 Fev2 ET from Amersham High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="ovarian tumor" /lab_host="bH10b (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 324 BP; 68 A; 102 C; 82 G; 72 T; 0 other;
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Pred. No. 1.52e-258;
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="810346"
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WashU-Merck EST Project
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Local Similarity 89.2%;
les 206; Conservative
                                                                                                                                                                          quality sequence stop: 161
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/note="Grad. Ovary: Vector: p1713D (Pharmacia) with a modified polylinker: Site_1: Not I, Site_2: Ecc RI; 1st strand crnw was primed with a not I. oligodd) primer [5: TSITAMATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAATOTSAA
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Vertebrata: Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                     Email: estiwatson.wustl.edu
This clone is available royally-free through LLNL: contact the
This clone is available royally-free through LLNL: contact the
TMAGE Consortium (infoitmage.llnl gov) for further information
Seq primer: -28ml3 rev2 Fr from Amersham
High quality sequence stop: 161.
Location/qualifiers
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Hillier, Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S. Krizman, D., Krizman, T., Lary, M., Le, N., Lennon, G., Marra M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, P. and Wilson, P. Unpublished (1997)
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4444 Forest, Park Parkway, Box 8501, St. Louis, MO 63108
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TMAGE Consortium (infoalmage lln! gov) for further information.
Seq primer: -28ml3 rov2 EI from Amersham.
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2890h01 rl Scares ovary tumor Nabor Home sapiens CDNA clone B11057
5' similar to gb-M12740_cds1 iG KAPPA CHAIN PPFFURPSOP V-II1 REGION
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Vertebrata: Mammalia; Butheria; Primates: Catarrhini, Hominidae:
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               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 53105 Fax: 314 286 1810
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Contact: Wilson PK
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/note="Organ: ovary; Vector: pT713P (Pharmaria) with a
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25-MAX-1997 (Rel. 52, Last updated, Version 1)
22-W22N09 rl Scares ovary tumor UbHOT Home sapiens CENA clone 770081
5' similar to qb·M12740_cds1 IG KAPPA CHAIN PPECURSOP V-III PEGION
available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml3
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further information. Seg primer: -28ml3 rov2 ET from Amersham
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                             /clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                 54 A; 80 C; 59 G; 47 T; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 134; DB 66; I pred. No. 2.11e-213;
                                                                                                                                                                                                                                                                                                                              /tissue_type="ovarian tumor"
                                                                                                    /organism="Homo sapiens"
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                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 42.5%;
Best Local Similarity 91.9%;
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                                rev2 ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 240 RP;
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zx84a06 rl Soares ovary tumor NPHOT Homo sapiens chwa clone 810418
5' similar to gb:M12740_cdsl IG KAPPA CHAIN PRECURSOR V-III REGION
(HWAN):
AA464451
92189335
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                       (Pharmacia). Library constructed by Bento Soares and
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Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylle,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
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4444 Friest Park Parkway, Box 8501, St. Louis, MC 63108
                                                                                                                                                                                                                                                                                    Length 244;
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                                                                                                                                                                                           /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                           /clone_lib="Soares ovary tumor NbHOT"
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Hillier,L., Allen,M , Howles,L , (hibigue,T ,
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                                                                                                                                                                                                                                               Sequence 244 BF; 54 A; 82 C; 60 G; 48 T; 0 other;
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Pred. No. 2.99e-205;
0; Mismatches 15;
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                                                                                                                                                                                                                                                                                    Score 130;
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                                                                                                                        M Fatima Ronaldo
∕clone="770081"
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                                                                                                                                                                              /sex="Female"
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.6%;
Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                   Gaps
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13 JUN-1997 (Rel. 52, Last updated, Version 1)
zx84a05 rl Soares ovary tumor NbHOI Homo sapions obNA clone 810418
5' similar to dicMIZ742_cds1 is RAFPA CHAIN PRECURSOR V-III REGION
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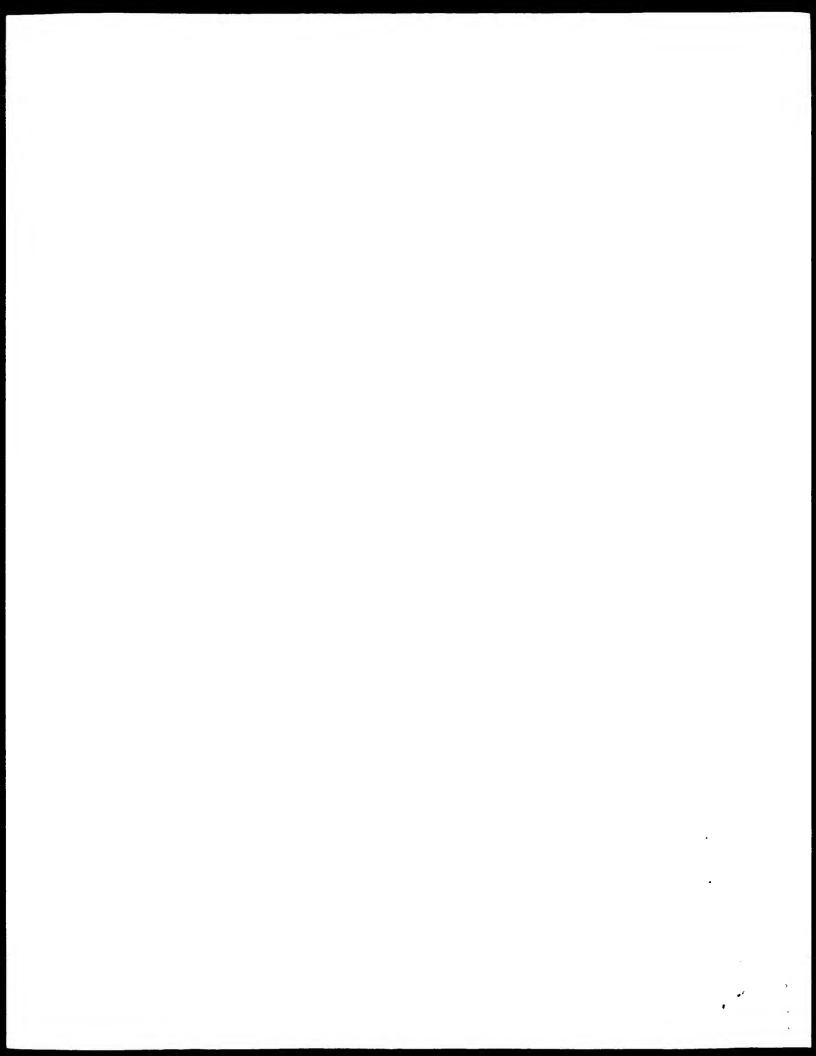
Estawatson wustliedu This clone is available loyalty-free through LLNL. Contact the INAGE Forsortium (info@image lini gov) for further information. See primer (info@image lini gov) for Locather information Contactor (info@image lini gov) for Corther information Contactor (info@image lini gov) for Locather Information Contactor (info@image lini gov) for Locather Information (info@image lini gov) for Locather (info@image lini gov)
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Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore R., Schallenberg K., Stepton M., Tan F., Theising B.,
White Y., Wylie T., Waterston R., Wilson R.;
"WashU-Merck ESI Project 1997";
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Vertebrata: Eutheria: Primates, Catarrhini, Heminidae, Homo
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HS1259291 standard; RNA; EST; 242 BP
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Unpublished (1997)
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Eukaryotae; mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata: Mammalia: Eutheria: Primates; Catarrhisis Hominidae;
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Email: est@watson.wustl.edu
This clone is available royalty-free through LUNE; contact the
IMAGE Consortium (info@image.iini.gov) for further information.
Seg primer: -28m13 rev2 ET from Amersham.
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4444 Forest Park Parkway, Box 8501, St. Louis, MC 63138
Tel: 314-286 1800
                                                                                                    Match 40.6%: Score 128: DB 43: Lenath 210: Local Similarity 91.6%, Frod. No. 3.49e 201; es 141: Conservative 0; Mismatches 13: Indels
/tissue_type="ovarian tumor"
/lat_hust="EHiOB (ampiviliin resistant)"
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/lab_host="DH10B (ampicillin resistant)"
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/sex="Female"
                                                              54 A, 82 C, 58 G, 47 T, 3 other;
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/organism="Homo sapiens"
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AA464647;
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                                                              0; Gaps
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24-JUN-1997 (Rel. 52, Last updated, Version 1)
24-JUN-1997 (Rel. 52, Last updated, Version 1)
5. Subject Soares ovary tumor NbHOT Homo sapiens cDNA clone 755051
5. Similar to qb:MI2740_cds1 IG KAPPA CHAIN PPECUPSOR V-III PEGICN (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK Washington University School of Medicine 4444
Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
BR00 Fax: 314 286 1810 Email: estGwatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer. .28mi3
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      Length 242;
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/lab_host="DH108 (ampicillin resistant)"
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Pred. No. 4.04e-197;
Score 125; DB 29; L Pred. No. 4.04e-197;
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54 A, 82 C, 59 G, 47 T, G other,
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AA482641;
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13-JUN-1997 (Rel. 52, Last updated, Version 1)
13-B5D2.r1 Soares ovary tumor NbHOT Home sapiens CDNA clone 810527
5' similar to gb-M12740_cds1 IG KAPPA CHAIN PPEGIPSP V-111 PEGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    School of Medicine 4444 Forest Park Parkway, Rox 8501. St. Fouis, MO 63108 Tel: 314-286-1800 Fax: 314-286-1810 Email: estewatson.wustl.edu This clone is available royalty-froe through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham. Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hilifer L., Ailen M., Bowles L., Dubuque T., Geisel G., Jost S.,
Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore R., Schellenberg K., Steptoe M., Tan F., Theising R.,
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Search completed: Tue Fob 24 08:31:31 1998 Job time: 131 secs.



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* SOLOCO	e 2.15 John F. Scillins, Biocomputing Research Unit. ght (c) 1993, 1994, 1995 University of Edinburgh, U.K Distribution rights by IntelliGenetics, Inc
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oatabase :	EST-D 99-EST295 100-EST296 101-EST297 102-EST298 103-EST290 104-EST300 105-EST301 106-EST302 107-EST303 108-EST304 109-EST305 110 EST306 111 EST307 112 EST308 113-EST309 114-EST316 115-EST311 116-EST312 117-EST313 118-EST314 119-EST315
Statistics.	Mean 9 884: Variance 1 931: scale 5 119

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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Kelley, J. W., Kolley, J. C., Liu, L.-1, Marmaros, S.M., Merrick, J. M., Moreno-Palanques, P. F., McDonald, L. A., Nouyen, D. T., Pelligrino. S. M., Phillips, C.A., Pyder, S.E., Scott, J. L., Saudek, D. M., Shirley, P., Small, K. V., Spriggs, T.A., Utterback, T. P., Weldman, J. F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimker, D. Fengi, D. F. Ferrie, A. Fischer, C., Hastings, G. A., He, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P. S., Olsen, H., Paymond, L., Well, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S. M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J. C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGP Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
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/note-"Organ: pancreas; Vector: pBluescript SK-; Site_1:
EGORI: Site_2: XhoI"
/clone_lib-"pancreas tumor III"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 agagigitiggiacgiticitageciggiateageacaaaacciggecaaccicecaggeice 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ctgagacagaattcactctcaccatcageggectgcagtctgaggactttgcagtatact 240
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Tel: 3018699056
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Pred No 0 00+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
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Tobases 1 to 328)

Adams, M. D. Kerlavage, A. R. Fleischmann. R. D. Fuldner, R.A.,
Bult, C.J., Leee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G. Rlake, J. A., Brandon, R.C., Man-Wall, C.
Clayton, R.A., Cline, T. P., Cotton, M.D., Earle-Hughes, J. Fine, L. D.,
Flizgarald, L.M., Flizhugh, W.M., Fritchman, J.L., Geoglanden, N.S.,
Glodek, A. Gnehm, C.L., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palangues, P.F., McChald, L. A., Ganda, D. S., Shilley, J.M., Kelley, J.W., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Phillips, C. A., Ryder, S. E., Scott, J.L., Sandek, D.M., Shirley, R.,
Bednarik, D.P., Cepeda, M. C., Cepeda, M. C., Grieman, J.F., Ll, Y.,
Bednarik, D.P., Cao, L., Cepeda, M. A., Coleman, J.F., Ll, Y.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Phymond, L., Wei, Y.-F., Wing, T. W., C., Yu, G.L., Photon, R. P., Praser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi html) Seq primer: Mil Reverse.
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                                                                              Eukaryolae, mitochondrial eukaryotes: Metamoa: Chordata;
Vertebrata; Mammalia; Eutheria, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 aggeteeteatetatggtgeateeateagggneaetggeateeeageeaggtteagtgge 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 GCCAGTCAGAGTGTGGGTAACAATTTAGTTTGTTATCAGTAGAAATTTGGCTGCC 125
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Tel: 3018699056
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Pred Nn 0 000+00;
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<1..>328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams. M.D. Kerlavage. A.R., Fleischmann. R.D., Fuldner. R.A., Bult. G. J. Loe. N. H. Kirkness. E.F., Weinstock, K. G. Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon. F. Man-Wall. C. McGlodek. A. Gnehm. C.L., Hanna, M. C., Hedblom, E. M., Kelley, J. M., Kelley, J. C. McDonald, L. A. Mayen. D. T., Gocyhagen. N. S., Kelley, J. W., Kelley, J. C., McDonald, L.A., Nguyen. D. T., Pelligrino. S. M. Phillips. C. A. Pyder. S. F. Scott, J. L. Saudek. D. T., Pelligrino. S. M. Phillips. C. A. Pyder. S. F. Scott, J. L. Saudek. D. M., Shirley, R. Bednarik. P. P. Cac. L. Sepeda, M. A., Cleman, I. A., Collins, E.J., Bednarik. P. P. Cac. L., Sepeda, M. A., Cleman, I. A., Collins, E.J., Branton, S. M., Guber, J. H., Meissner, P. S., Glsen, H. Kozak, D. L., Kunsch, C., Hungiun, J., Li. H., Meissner, P. S., Glsen, H. Raymond. L. Weil, Y. Fennon, M. P., Posen, C. A., Haseltine, W. A., Fields, C. Fraser, J. C. M., and Venter, J. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 94626280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For clone availability, additional sequence and expression information related to this ESI, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hqi/hqi.html) Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: pancreas: Vector: pBluescript SK-; Site_1:
EcoRI: Site_2: XhoI"
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
<1...370
                                                                                                                                                                                                                                                                                                                                                                          Vertebrata: Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                           LOCUS AA295093 370 bp mRNA EST 18-APR-1997
DEFINITION EST100400 Pancreas tumor I Home sapiens cDNA 5' end similar to similar to immunoglobulin kappa, variable region (GB:Y00540).
ACCESSION AA295093
NID q1947582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 decagteagagigitageageaactiageeiggiaeeageagaaaceiggeeaggeace 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 aggeteetnatetatnatgeateeaeeaagggeeactggtateeeageeaggtteagtgge 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 acgeanntheeagceaceigteegittiinis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ACCCASTCIOCASCCACCCTSICISISICICCASSSSAAAASASCICICICCISCAGG 66
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                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryotae: mitochondrial eukaryotes: Metazoa; Chordata;
Eukaryotae: mitochondrial eukaryotes: Catarrhini; Hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research
9711 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 202: DR 24;
Pred No 0 00e+00;
     247 GITIAITICEGICAACACIAIAGIAGCIGGGGGGGTCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_ESTs: THC168243
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86 08;
                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioinformatics
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                                                                                      RESULT 3
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                                                                                                                                                                                                                                                                                                                 ORGANISM
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                        KEYWOPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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double-stranded cDNA was size selected. ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco PI sizes of a modified pr773 ventor (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
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/note="Organ: ovary: Vector: pT713D (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Ero R:: 1st strand cDNa was primed with a Not I: - oligo(dI) prime: IGTIACCAATCIGAAGIGGGGGGGGGGTITITITITITITITITI 3').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 400)
Hillier, Allien,M. Bowles,L., Euthaque,T. Geisel,G., Just,S.,
Kucaba,T., Lady,M. Le.N. Lennon,G., Marra,M., Martin,J.,
Moore,R., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,P. and Wilson,R.
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa: Chordata:
Vertebrata; Mammalia: Eutheria: Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL : contact the IMAGE Censertium (infe@image link gov) for further information. Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 acgeaqtetecaggeacecetatetttatetecagggaaaaggeececetetectusagg 129
239 agtgggtetggggacagagttcaetetcaceatcagcagcetacagtetgaagattetgea 298
                                                                 187 AGTGGGTCTGGGACAGAAITCACTCTCACCAICAGCAGCTGCAGTCTGAGCACTITGCA 246
                                                                                                                                                                                                                                                                                                                                                             LOCUS AA456778 400 bp mRNA EST 06-JUN-1997
DEFINITION 2W27f11.rl Scares ovary tumer NAHOT Home sapiens cDNA clone 77
5' similar to 9b:X06764 IG KAPPA CHAIN PRECUKSOR V-111 PESTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 48: Indels 4: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Propert Park Parkway, Box R501, St. Louis, MC 63108 Tal: 314-286-1800
Fax: 314-286-1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 188; DB 116; Length 400;
Pred. No. 0.00e+00;
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/lab_host="pHIOB (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib~"Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
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                                                                                                                                              299 gtttattactgtcagcaacataagaattggcc 330
                                                                                                                                                                                                                   247 GITIATITICISTCAACACTATAGIACCTGGGG 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 c
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Homo.

Sadams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A.,

Bult.C.J. Iee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Pritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehn, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S., Ir.,

Kelley, J.M., Kelley, J.G., Liu, L.I., Marmarcs, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Fyder, S.E., Scott, J.L., Saudak, D.M., Shriey, P.,

Small, K.V., Spriggs, T.A., Utterback, T.P., Weidan, T.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Glsen, H.,

Paymond, L., Weir, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (5547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: arkerlavatior.org

For clone availability, additional sequence and expression
information related to this EST, please check the TiGP Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                 190 cccaggetecteatetatggtgeatecageagggeaaetggeateceagaeaggtteagt 249
                                                                                                                                                                                                                                                                                                                                 250 ggcagtgggtctgagacagacttcactctcaacatcggcaagactggagcctgacgattt 309
                                                                                                                                                                                                                                                                                                                                                                                           184 GGCAGTGGGTCTGGGACAGAATTCACTCTCACCATCAGCA-GCCTGCAGTCTGAGGACTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 tgcagtgtattactgtcagcagtatggtagctcaccgtggacgttcggccaagggaccca 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 gecagticacagtigtidageageageigettageetiggtaeeageagaaaeetiggeeagget 189
                                                                                                                            67 GCCAGTCAGAGTGTCGGTAACAA-T--TTAGCTTGGTATCAGCAGAAACCTGGCCAGGCT 123
                                                                                                                                                                                                                                                           124 GCCAGGCTCCTCATTTATGGTGGAAACAACGAGGACTGGTAGCCCAGAGACAAGGTTCAGT 183
7 ACGCASTCTCCAGCCACCCTGTGTGTGTCTCCAGGGAAAAAAAGCTCCCTCTCCTGCAGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1997
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/nottx="Organ. skin, Vectvr. pBluescript SK:, Site_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA379044 349 bp mRNA EST 21-APR-1
EST91999 Skin tumor I Homo sapiens cDNA 5' end similar to
immunoglobulin kappa light chain, VJ regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
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Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 SGTCGAGTTCAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 ggtggaaatcaa 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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He,W.W., Hu,J.S., Greene,J.W., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Merssner,P.S., Olscon,H... Raymond,L., Wel,Y.F., Wing,J., Xu,C., V.,G.L., Puben,S.M., Dillion,P.J., Fannon,M.P., Posen,C.A., Haseltine W.A. Fields C., Fraser,C.M. and Verter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA345486 403 bp mPNA EST 21-APR-1997
EST51505 Gall bladder II Home sapiens CDNA 5' end similar to
similar to immunoglobulin Kappa light chain, V region (GR:X06763).
AA345486
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Vertebrata, Mammalia: Eutheria: Primates: Catarrhini: Hominidae;
                                                                                                                                                                                                                                                                                               124 CCCAGGCTCCTCATTTATGGTGGAAACACCAGGGCCACTGGTACCCCAGACAGGTTCAGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                       ggcagtggggtctgggacagacttcactctcaccatcagcagactggagcctgaagatttt 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 GSCARTGGGTCTGGGACAGAATTCACTCTCACCATCAGCACTTGCAGTCTGAGGACTTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 gcagtatattactgtcaagcagtatggtagtttacccctcaantttcggccctggggacc 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 gecaetgagagtgttagcaacacetaettageetggtaecaacagaaaeetggecagget 147
                                                                                                                                                                                                                      28 acteagiciceaggeacecigicitigiciceeagggaaaagageeaceciciceigeagg 87
                                                                                                                                                                    6: Gaps
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                                                                                                                             Length 349;
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                                                                                                                             Score 185; DB 59;
pred No 0.00+00;
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ECORI; Site_2 * xhoI"
/clone_lib="Skin tumor
/dev_stage="adult"
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Bioinformatics

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Adams.M.D. Kerlavage.A.R., Fleischmann,R.D. Fuldner,R.A.,
Rult.G. J. Lee.N. H. Kirkness.E.F. Weinsrock.K.G. Gocayne.J.D.,
White.O., Sutton.G. Blake.J. Brand.B.G. Man-Wai.G.,
Clayton.P.A. Chine.T.P. Cotton.M.D. Barlo-Hughes.T. Fine.L.D.,
Fliggerald.L.M. Fizhugh.W.M. Fritchman.J. Geophagen.N.S.,
Glode,J.A., Chenna,M. C. Hendelom.E. Hinkle.P. S.Tr.,
Kelley,J.M. Kelley,J.G. Liu.L.-I. Marmarns.S.M. Merrick.J.M.
Moreno-Palanques.R.F. McDonald.I.A. Nguyen.D.T. Pelligring.S.M.
Phillips.C.A., Pyder,S.E. Scott,J.I., Saudek,D.M., Shirley,P.
Small.K.V. Spriggs.T.A. Utterback.T.R. Weidman.J.F. Lii.Y.
Bednarik,D.P. Cac.L. Cepeda,M.A. Coleman.T.A. Collins.E.J.,
Dimke.D. Fengy,D.-P. Ferfie,A.M. Fischer,G. Hastings.G.A.
He.W.W., Hu.J.S., Greener,J.M., Gruber,J., Hudson.P., Kim.A.K.,
Kotak.D. For Maching.M. A. Fischer,G. Hudson.P. Kim.A.K.,
                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.igr.org/tdb/hgi/hgi html) Seq primer: MI3 Reverse.
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Vertebrata; Mammalia: Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 agggecactggceatececagacaggtteagtggeagtgggagtetgaggacagacagaetteaetete 221
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                                                                                                                                                                                                                                                                                                     /ornanism-"Homo sapiens"
/note-"Organ: gall bladder; Vector: pbluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 44; Indels 3; Gaps
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ESI13427 Testis tumor Homo sapiens cDNA 5' end similar to immunogiobulin kappa light chain, VJ regions. AA300582 q1952925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 403;
The Institute for Genomic Research
9712 Medical Center Stive, Bockville, Mc 20955 93A
Tel: 8018649A65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 teaectaagaegtteageesaagggaeesaaggtggaaatea. 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 172; DB 73;
Pred. No. 6.54e-295;
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 €
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                                                                                                            Email: arkerlav@tigr.org
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Best Local Similarity 83.3%:
Matches 234; Conservative
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Sallion.Fig. Fanasa.M.E.) Acsem.Lih., Buseltine.Ach. Fields.C.,
Fraser,C M and Venter J C.
Initial assessment of human gene diversity and expression patterns
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For clone availability, additional sequence and expression
information related to this EST, please check the TiGP Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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/note="Grgan: testis; Vector: pBluescript SK-: Sltc_l:
EcoRI: Site_2: XhoI"
/clone_lib="Testis tumor"
/sex="male"
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                                                                                                                                                                       based upon 83 million nucleotides of cDNA sequence Nature 377 (5547 Suppl). 3-174 (1995)
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Pred. No. 8.18e-293;
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Wei, Y F , Wing. J , Xvi. C
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Raymond, L ,
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Adams, M. D., Kerlavage, A. P., Fleischmann, P. D., Fuldner, B. A.,
Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D.,
White, O., Sutton, G., Biake, J. A., Brandon, P. C., Man-Wai, J.
Clayton, R. A., Cline, T. P., Corton, M. D., Earle-Hudhes, J., Fine, L. D.,
Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoglagen, N. S.,
Clodek, A. Gnehm, C. L., Hanna, M. C., Hedbinow, E. Hinkle, P. S.T.,
Moreno-Palanques, P. F., McDonald, L. A., Mquyen, D. T., Pelligrino, S. M.,
Phillips, C. A., Pyder, S. E., Scott, J. L., Saydek, D. F., Li, Y.,
Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J.,
Dinke, D., Feng, D. F., Ferrie-A., Fischer, C., Hadson, P. Kim, A. K.,
Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Glsen, H.,
Paymond, L., Weil, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
Dillion, P. J., Fannon, R. Posen, C. A., Haseltine, W. A., Fields, C.,
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
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/organism="Homo sapiens"
/organ: Lymph node: Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
/clone_lib="Lymph node I"
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<1 ~4.05
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Fred No 2 456-282;
0. Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bloinformatics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 52.7%;
Local Similarity 83.0%;
es 219, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 c
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DEFINITION

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Adams, M.D., Kerlavage, A.R., Fleischmann, P.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstrock, K.G., Gorayne, J.D.,
Mait, C.J., Lee, N.H., Kirkness, E.F., Weinstrock, K.G., Gorayne, J.D.,
Rajton, R.A., Cline, T.R., Cotton, M.D., Farlo-Hophes I. Fine L.D.,
Ritzgarald, L.M., Fitzhigh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glode, A., Gonhm, C.L., Hanna, M.C., Heddhlow, E. Hinkler, F.S.,
Kelley, J.M., Kelley, T.C., Liu, L.-I., Marnaros, S.M., Merrick, J.M.,
Moreno-Palanques, P.F., McDonald, L.A., Nuyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Kyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.A., Colliss, E.J.,
Dimke, D., Fongo, D.-Fr, Ferrie, M.A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Praser, C.M., and Venter, J.C.,
Fraser, C.M., A., Fischer, C., Haselline, W.A., Fischlas, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the IIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi html)
                                                                                                                                                      Bukaryotae; mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata, Mammalia, Eutheria, Frimates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /nofe="nogan: thymus Vector pBluescript SK- Site_l-
ECORI; Site_1: XhoI"
/clone_lib="Thymus III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 atccaccagggccactggtatcccagccaggttcagtggcagtgggtctgggacagagtt 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 AAACACCAGAGGACTGGTADDOCCAGAJAGGTTCAGTGGGAGTGGGGTTGGGGACAGAATT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 cactotoaccatoagoagootgoagtotgaagattttnoagtttattactgtoagoagta 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 CAATITAGCIIGGIAICAGCAGAAACCIGGCCAGGCICCCAGGCICCICAIITAIGGIGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 caacttagcetggtaccagcagaaacetggecaggnteccaggeteetnatetatggtge 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 33, indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pockville, MD 20850 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 TAGTACCTGGCCGCTCACTTTCGGCGGGGGGGGCAAGGICGAGIICAA 314
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Rest Local Similarity 85.5%; Pred No 3 046-280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics
The Institute for Genomic Research
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<1..>253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                  (bases 1 to 253)
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                                                                                                               Homo sapiens
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Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A.,
Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A.,
Bull, C.J., Sutton, G., Blake, J.A.,
Bull, E.C., Sutton, G., Blake, J.A.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Googhaden, N.S.,
Glodek, A., Gnehm, C., Liu, L.I., Mammarres, S.M., Merrier, T.M.,
Kelley, J.G., Liu, L.I., Saudek, D.M., Shirley, P.,
Fhilips, C.A., Ryder, S.F., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Welley, P., Liu, Y.,
Bednarik, D. P., Gaeda, M.A., Coleman, T.A., Gollins, E.J.,
Limke, E., Feng, D.F., Ferrie, A., Fischer, T., Hastings, G.A.,
He, W.M., H., T.S., Greepa, M.A., Coleman, T.A., Gollins, E.J.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Bullion, P.J., Fannen, M.P., Rosen, C.A., Haseltine, M.A., Fields, C.,
Fraser, C.M., and Venter, J.G., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.G., Mersen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.G., Mersen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.G., Mersen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.G., Mersen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.G., Mersen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.G., Mersen, C.A., Mers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this ESI, please check the TISP Human Generator (bttp://www.tigr.org/tdp/hgi/hgi/hgi/hmi)
                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryotae; mitochondrial eukaryotes: Metazoa: Chordata:
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site_1. Ecopl. Site_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 agagitatiagcagaaactiagceiggiteeaqeagaaaeeiggeeageeteeeaggeiee 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA351678 21-APR-1997 EST 21-APR-1997 EST 7998 1-cell lymphoma Homo sapiens ctnA 5' end similar to similar to similar to immunoglobulin kappa, variable region (GR-Y00640).
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Nature 377 (5547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, Mr 20859 USA
Tel: 3018699056
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Best Local Similarity 87.3%; Pred. No. 5.99e-249;
Matches 172; Conservative 0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: palmescript_SK-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib-"I-cell lymphoma"
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Initial assessment of human gene diversity and expression puttorns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                   Pukaryotae: mitochondrial eukaryotes: Metazca: Chordata:
Vertebrata; Mammalia; Eutheria; Primates: Catarrhini: Hominidae:
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EcoRI; Site_2: XhoI"
/clone_lib="Thymus II"
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                                                                                                    AA383914 238 bp mPNA FST 21-AP EST97387 Thymus II Homo sapiens cDNA 5' end similar to immunoglobulin Kappa light chain, VJ regions.
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Pred No 1 23e-240;
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Contact: Kerlavage, AR
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Best Local Similarity 89 98:
Matches 170: Conservative
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267 ctggcacagagttcact 283
                                  194 CTGGGACACACATTGACT 210
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3. Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, P. A.,

Bult.c.J. Lee, N. H., Kirkness, E. F., Weinstock, K. Gorayne, T. D.,

White, O. Sutton, S. Blake, J. A., Brandon, P. C., Man-Wai, C.,

Clayton, R. A. Cline, T. R., Cotton, M. D., Earle-Highes, J. Fine, L. D.,

Fitzgerald, L.M., Fitzhugh, W. M., Fritchman, J. L., Geoghagen, N. S.,

Glodek, A., Gnehm, C. L., Hanna, M. C., Hinkle, P. S., Jr.,

Kelley, J. M., Kelley, T. C., Liu, L. T., Marnaros, S. M., Merrick, T. M.,

Moreno-Palanques, P. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M.,

Philips, C. A., Pyder, S. E., Scott, J. L., Saudek, D. M., Shirley, R.,

Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y.,

Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J.,

Bednarik, D. P., Ferrick, A., Fischer, C., Hastings, G. A.,

Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,

Raymond, L., Well, Y. F., Willey, M. M., Wille, M., Briben, S.,

Dillion, P. J., Fannon, M. R., Frosen, C. A., Haseltine, W. A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser, C.M. and Venter, J.C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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information related to this EST, please check the 115F Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
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EcoRI; Site_2: Xho!"
/clone_lib="Pancreas tumor III"
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                             DEFINITION EST77409 Pancreas tumor III Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region.

ACCESSION AA366461
                       GOCACTCAGAGTGTGGGTAACAATTTAGCTTGGTATCAGCAGAAAACCTGGGCGAGGCTCCC 126
                                                                                 170 aggeteetcatetatggtgeatecaecaggtecaetgetateccagecaggtteagtgge 229
                                                                                                              21-APR-1997
Score 143; DB 55; Length 294;
Pred No 2.05e-234;
0, Mismatches 21; Indels
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Local Similarity 88.3%;
Pes 181; Conservative
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.iigr.org/idp/hgi/hgi.html)
Seq primer: M13 Peverse
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EcoRI; Site_2: XhoI"
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryotao, mitochondrial eukaryotos, Metazoa, Chordata.
Vertebrata, Mammalia, Eutheria, Primatos, Catarrhini- Hominidae.
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85 acgeaatetecagecaceetgtetgtgtetecaggggaaagagecaceeteteetgeagg 144
                                                                                                                                                                                                                                                                                                                               205 occaggotoctoatctatggtatotocaccagggccagtggtgtcccagccaagttcagt 264
                                                                                                                                                                                                                                                                                                                                                                          145 gecaginagagigitaggagaaactactiageciggiaceageagaaaceiggecagaei 204
                                                                                                                                                                                                                                             67 GCCAGTCAGAGTGTC--G-GTAACAATTTAGCTTTGGTATCAGCAGAAACCTGGCCAGGCT 123
                                                                         7 ACGCAGICICCAGCCACCCIGITGIGIGICAGGGGGAAAAGAGGCTCTCTGCTGCAGG 66
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Tel: 3018699056
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Vertebrata: Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl qov) for further information Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillaria Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S. Hillaria, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Kucaba, T., Laoy, M., Le.N., Lennon, G., Marra, M., Martin, T., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Warsh, C., Wylie, T., Warsh, March, Fer project, 1997.
                                                                                    70 acycagottocaggcacctutntttttutntotocaggggaaaagaccaccctotocigoagg 129
                                                                                                                                                                     130 deceagicadadititadeageageiaetiaetiageeiggiaeeageagaaeeeiggeeaggei 189
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                                               Saps
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                                           0; Mismatches 25; Indels 4:
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    Length 277:
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/sex="Female"
    Score 135; DB 24;
Pred N= 7 19e-218.
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Washu-Merck EST Project
Washington University School of Medicine
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82 c 60 q
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Query Match • 42.9%,
Best Local Similarity 96.1%,
Matches 180: Conservative
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Admis M. C. J. Lee. N. H. Kirkness, E. F. Weinstock, K. G. Gocayno. J. D. Lee. N. H. Kirkness, E. F. Weinstock, K. G. Gocayno. J. D. Lee. N. H. Kirkness, E. F. Weinstock, K. G. Gocayno. J. D. Glayton, R. A. Cline, T. P. Octron. M. P. Falle-Hughes J., Finc. L. D. Fitzgarald, I. M. Fizzhugh W. M. Fritchman, J. L., Geodhaden, N. S. Glodek, A. Ghehm, C. Liu, L. -T. Marmaros, S. M. Merrick, J. M. Moreno-Palanques, R. F. McDonald, I. A. Nguyen, D. T. Pelligrino, S. M. Phillips, C. A. Pyder, S. E. Scott, J. L. Saudek, E. M. Shirley, K. Bednarik, D. P. Cao, L. Cepeda, M. A. Coleman, J. F. Liv, L. M. Bednarik, D. P. Cao, L. Cepeda, M. A. Coleman, J. M. Shirley, K. Bednarik, D. P. Cao, L. Cepeda, M. A. Coleman, J. M. Shirley, K. Kozak, D. L. Wulk, H. J. S. Grone, J. M. Gruber, C. Hastings, G. A. Kazak, E. L. Wulk, Kim, A. K. Dillkon, P. J. Panneyun, J. Li H. Meisener, P. S. Olsee, H. Priser, C. M. and Venfer, J. C. M. Ansentine, W. A. Fields, C. M. Erser, C. M. and Venfer, J. C. M. Frieds, C. M. Erser, C. M. and Venfer, J. C. M. Erser, C. M. Fields, C. M. Erser, C. M. Erser, C. M. Fields, C. M. Erser, C. M
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Vertebrata, Mammalia: Eutheria: Primates: Catarrhini: Hominidae;
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Ecoki: Site_2: Xhoi"
/clone_lib="Colon I"
/close_tage="adult"
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Score 130, PR 86; Length 244;
Pred. No. 1.45e-207;
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Nature 377 (6547 Suppl), 3-174 (1995)
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Statistics: Mean 9.921; Variance 1.934; scale 5.129

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                           Butheria; Archonta; Primates; Catarrhini; Hominidae; Homo
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Tel: 314 286 1800
Fax: 314 286 1810
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Eucaryotae, Metazoa, Chordata, Vertebrata, Gnathostomata, Mammalia,
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EST69430 Homo sapiens cDNA 5' end similar to immunoqlobulin light
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Deuterostomia: Chordata; Vertebrata; Gnathostomata; Osteichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stops: 296 Source: IMAGE Consortium, LLNL Source: TASE Consortium, LLNL Contact the This clone is available royalty-free through LLNL contact the IMAGE Consortium (info@image ilnl.gov) for further information.
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11 (bases 1 to 451)

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hyman clone=1178]] library=Stratagene lung (#917210)
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larity 90.1%; Pred. No. 0.00e+00;
Conservative C; Mismatches 20
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Fax: 314 286 1810
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Fax 3018699423
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                                                             A GROWN TO REPLAYAGE A P. Fleischmann P.D. Fuldber P. A. Wirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J. Lee, N. Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J. Sutton G. Blake, J. A. Prandon P. C., Chiu, M. W. Clayton, R. A., Cline, R. T. Cotton, D. Elizcerald, L. M., Fitzhudh, W. M., Fritchman J. L., Geoghagen, N. S. Glodek, A., Ghehm, C.L., Hanna, M. C., Headhom, E. Hinke, D. P. S. Kelley, J. G., Liu, L. J. Marmaros, S. M. Merrick, J. M., Moreno-Palanques, P. F., McDonald, L. A., Nguyen, D. T., Pellegrinos, S. M., Phillips, G. A., Pyder, S. B., Cott, J. L. J. Marmaros, S. M., Weidman J. F., Li, Y. Pednarik, D. P., Cao, L., Cepada, M. A., Collans, E. Li, Y. Bednarik, D. P., Cao, C., Cepada, M. A., Collans, E. T., Dimke, D. Feng, D., Ferrie, A. Fischer, C., Hastings, S. A., Hew W. Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Ji, H., Li, H., Weister, P. S., Olsen, H., Raymond, L., Weilly, P., Pennon, M. P., Pesen, C. M., Haseltine, M.A., Fields, C., Fraser, C. M. and Venter J. C., Inpublished (1995).
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11ght chain, V region (GB:M27025) (HT:3778).
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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               Butheria: Archonta, Filmates, Catarrhill, Hominidae, Homol (bases 1 to 281)
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Pred. No. 2.18e-301;
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
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PS Adams, To S83)

Adams, M. D. Kerlavage, A. P. Fleischmann, P.D., Fuldner, R.A., Rult, C.J., Loe. N., Kirkness, F. F., Weinstock, K.G., Gocyme, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chuu, M.-W., Clayton, R. A., Cilne, F. T., Cotton, M. D., Earle Hughes, J. Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fitzchman, J. I., Geoghagen, N.S.M., Kilmek, K. M., Kelley, T.C., Liu, E. I., Marnaros, S.M., Merley, J.M., Kilmek, K. M., Kelley, T.C., Liu, E. I., Marnaros, S.M., Merlick, J.M., Moreno-Palanques, F. F. Scott., J. Nauyen, D. T., Pellegrino, S. M. Phillips, T. F., Rydar, S. F., Scott., Cepeda, M.A., Shirley, R., Small, K. V., Spridas, T.A., Utterback, T.R., Weidman, J.F., Li, Y. Bednarik, D., Collins, E. J., Engels, P., Ferric, A., Fischer, C., Hastings, G. A., He, W. W., Hu, T.S., Grevne, J.M., Gollins, E. J., Dimke, D., Feng, P., Grevne, J.M., Grich, F., Weisher, J., Hudsen, F., Kim, A., Kozak, D., Koren, J., Kim, A., Kozak, D., Kun, J., Kun
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For clone availability, additional sequence and expression
information related to this EST, please contact the IIGK Database
Eukaryokae, Metazoa, Eumetazoa, Bilateria, Guviomata:
Deuterostomia, Chordata, Vertetrata, Gnathostomata, Ostelichthyes;
Sarcopterygli; Choanata: Tetrapoda: Amniota: Mammalia: Theria:
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1 (bases 1 to 383)
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Best Local Similarity 81 6%; Pred No. 3 506-297;
Matches 257; Conservative 0; Mismatches 52;
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20078
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                                                                                                                                                                                                                                                                                                                       Eutheria; Archonia, Primates, Catarrhini, Hominidae, Homo.

Eutheria; Archonia, Primates, Catarrhini, Hominidae, Homo.

I (bases I to 332)

S Adams, M.D., Kerlavage, A.P. Fleischmann, P.D., Fuldner, R.A.,

Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

Khite, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M. W.,

Clayton, P.A., Cline, P.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzserald, L.M., Fitzstysh, W.M., M. Fritchman, J.L., Geoghagen, N.S. M.,

Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L. I., Marmaros, S.M.,

Merick, J.M., Moreno-Palanques, P.F., McPonald, L.A., Ngyyen, D.T.,

Pellegrino, S.M., Philips, C.A., Fyder, S.E., Scott, J.L.,

Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., "Itterback, T.R.,

Weidman, J.F., Li, Y., Bednarik, D.P., Gao, L., Cepeda, M.A.,

Coleman, T.A., Y., Bednarik, D.P., Gao, L., Cepeda, M.A.,

Coleman, T.A., Y., Bednarik, D.P., Gao, L., Cepeda, M.A.,

Eischer, C., Hastings, A., He, W.W., Hu, T.S., Greene, J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Faymond, L., Wei, Y. -F., Wing, J., Xu, C., Yu, G.-L., Puken, S.M., Dillon, P.J., Fannon, M.R., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J. C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
T29342 332 bp mRNA EST 06-SEP-1995
EST77181 Homo sapiens CDNA 5' end similar to immunoglobulin kappa
                                                                                                                                                                                                                                                                     Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database
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0; Mismatches 32; Indels
                                                                                                                                                                                human primer=M13 Reverse library=Human Pancreas.
                                                        light chain, V region (GR:M29469) (HT:3066).
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Best Local Similarity 86.2%; Prod No. 4.436-295;
Matches 212; Conservativo 0; Mismatches 32;
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Location/Qualifiers
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Contact: Venter, JC
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                                                                                                                                                                                                                   Homo sapiens
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Gruber, J. Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yi, G.L., Puhen, S.M., Dillon, P.J., Fannon M. R., Resen, C.A., A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C., Initial Assessment of Human Gene Diversity and Expression Patherns Based Upon 52 Million Pasepairs of CNNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
                             end similar to immunoglobulin kappa
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            06-SFP-1995
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                                                                                                                                                     human primer=M13 Reverse library=Human Lung.
DEFINITION ESTIGOTO Home Sapiens CDNA 5' end similar to light chain V region (GB:X06763) (HT:3087).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
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    Location/Qualifiers
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Other_ESTs: THC24452
Contact: Venter, JC
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                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deuterostomia: Chordata, Vertekrata, Gnathostomata, Osteichthyes, Sarcopteryni, Choanata, Tetrapoda, Anniota, Mammaia: Theria. Butheria: Archonta, Frimates, Catarthini, Hominidae, Home Lasses: Lo 361)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hutman, M., Rocaba, T., Le, M., Lennon, G., Marra, M., Parsons, T., Hiffing, T., Soares, M., Tan F., Treyaskis, E., Materston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stops: 308
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                               DST 18-MAY-1995
yj7lb97 rl Home sapiens cDNA clone 154155 5' similar to
PE-MI2740_cd81 is KAEPA CHAIN PERCIESSER VIII FESICH (HUMAN):
PS1922
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Pred No. 2.54e-220;
0: Mismatches 29; Indels 8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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Charmacia) with a modified polylinker host-thibe (ampicillin resistant) primer-M13PP1 Fisitel-Not I Reitel-Eco R( Adu)! temale. Ist strand CDNA was primed with a Not 1 - oligo(df) primer (5 temale.) TGTTACAATCTGAAGGGGGCGCTTITITITITITITITITI 3), double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI stees of a modified piTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Pento Soares and M.Fatima Bonaldo.
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similar 'o ql:X06764
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Hilliar,L. Clark, N. Duhuque,T., Elliston,K. Hawkins,M., Holman,M., Hultman,M., Kuraba,T., Le,M. Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8591, St. Louis, MC 63108
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Fax: 314 286 1810
331 agtetattattgt 343
                                                                   246 AGITIATITCIGI 258
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Eucaryotae; Metazoa; Chordata, Vertebrata, Gnathostomata, Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IG KAPPA CHAIN PPECURSOR V-III PESION (HUMAN):
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                           333 ttgcagtgtattactgttcagcgatattgatgggctcancccttttnggccctgggacc 392
                                                                  74 etecaggeaccetgtetttgtetecaggggaaagagecacceteteetgeagggecagte 133
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Pitkin,L., Philling,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,P., Williamson,A., Wohldmann,P. and
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Pred. No. 5.78e-220;
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Local Similarity 84.4%;
es 259; Conservative
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human clone=146041 library=Soares placenta Nb2HP vertor=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13P91 Psite1=Not i Psite2=Erc PI Female placenta obtained at birth (full term). Ist strand cDNA was primed with a Not I - oligo(dT) primer [5'
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                                                                                                       70 etgaegeag-etceagecaccetgtetgtgtetceaggggaaagagteacceteteetge 128
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254 tgggtotgggggacagatttcactcttcaccattcagcagactgggagcctgaagattttt 313
                  314 gcagtgtatttactgttcagcagtattggtagctcaccgttcacttttcgggcggaggga 373
                                                                                                                                                                                                                                                                                         R79907 360 bp mPNA EST 09-JUN-1995 yi85f01.rl Homo sapiens cDNA clone 146041 5' similar to gb-M12740_cds1 IG KAPPA CHAIN PPECUPSOP V-III PECION (HUMAN);
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Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata: Deuterostomia; Chordata; Vertebrata; Gnathostomata: Osteiof Sarcopterygii; Choanala; Telrapoda; Amijota; Mammalia, Ther Euthelia; Archouta; Primates; Catarrhiti; Hominidae, Homon (bases 1 to 360)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 7.88e-216;
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100 c 86 q 98
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WashU-Merck EST Project
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Deujerostomia, Chordata, Vertekrata, Grathostomata, Ostejohthyes,
Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalia, Iheria,
Eutheria: Archorta, Primates, Catarrhini, Hominidae, Homo.
1 (bases i to 359)
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64 AGGGCAGICAGAGIGIGIGIGATAACAATIIAGCIIIGGIATCAGGAGAAAGCTGG-CCAGGC 122
                                               189 teceaggetecteatetatgatgeatecaceagggeestagtgtegeogeogeegeteeag 248
                                                                                               123 ICCCAGGCICCTCAIIIAI3SIGGAAACACCAGAGGGAGTGGIACCCCAGACAGAGAG 182
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Pred. No. 9.17e-214;
0; Mismatches 40; Indels 6; Gaps
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444 Forest Park Parkway, Box 8501, St L
Tel: 314 286 1810
Fax: 314 286 1810
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DeviceStomia, Chordata, Vertebrata, Gnathostometa, Ostolchthyes; Sarcopterygii; Chomanta, Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 232)
Hillier, L. Clark, N. Dubnque, T. Filiston, K. Hawkins, M. Hollman, M. Hultman, M. Kucaba, T. Le, M. Lonnor, G. Warra M. Parsons, J. Rifkini, I. Rohlfing, T. Scares, M. Tan, F. Treyaskis, E., Materston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 getgaegeaateteeagaeaeeetgtetetgteageaggggaaagageetegetetetg 103
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                                                                 267 gatotgggacagacttttagtotcaccatnoagtagactggageoctgaagattttnoag 326
                                                                                         : Ouis, MO 64108
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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/organism="Homo sapiens"
/clone="160031"
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High quality sequence stops: 1
Squrge: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and M.Fatima Ronaldo.
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Fax: 314 286 1810
                                                                                                                                                             327 tatattactqtc 338
                                                                                                                                                                                                            248 ITTATITCIGIC 259
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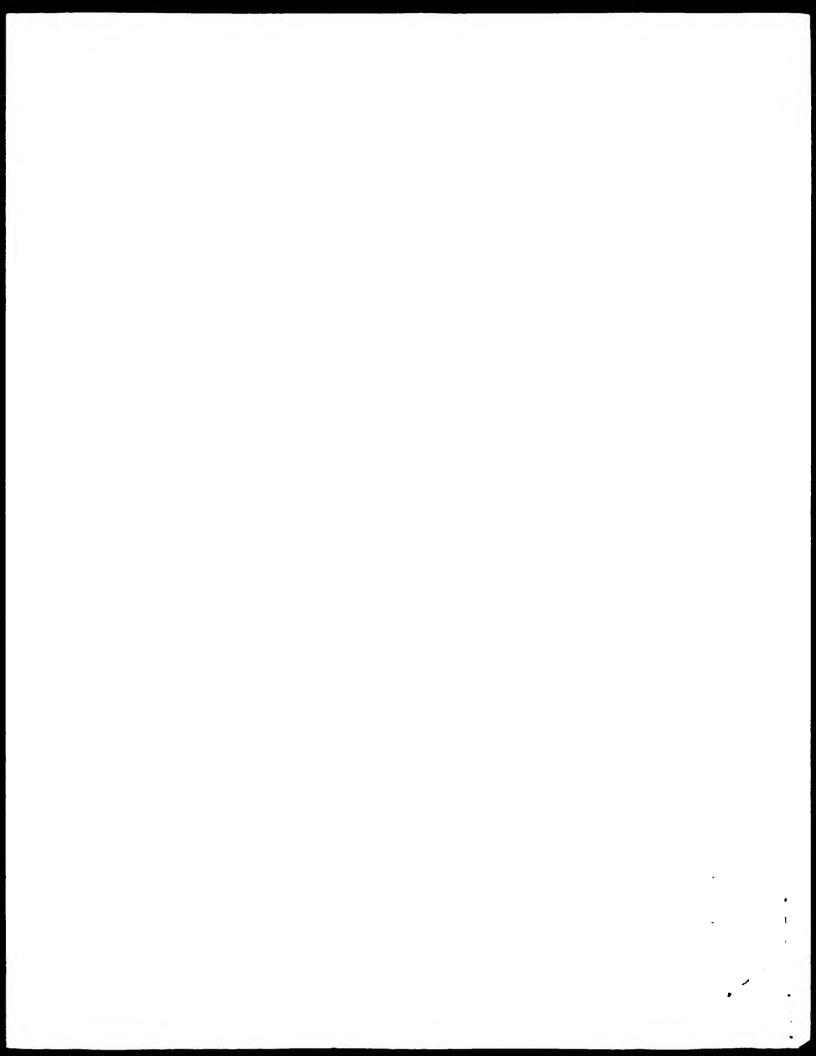
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double-stranded CDNA was ligated to ECO F1 adaptors (Pharmacia), digested with Not I and cloned into the Not I and ECO R1 sites of a modified pT713 vector (Pharmacia). Library went through one round of normalization to a Cot - 20. Library constructed by Bento Soares and M.Fatima Bonaldo.
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Deuterostomia, Chordata; Vertebrata, Gnathostomata, Osteichthyes;
Sarcopterygii, Choanata; Tetrapoda, Amniota, Mammalia, Theria;
                                                                                                                                                                                                                                                                                                                        yp24a10.rl Homo sapiens cDNA clone 188346 5' similar to gb:x06764
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63 CAGGGCCAGTCAGAGTGTCGGTAACAATTTAGCTTGGTATCAGCAGAAACCTGGCCAGGC 122
                                                 164 tececegaetectnatttatngegegtecaecaggnneaetgatateceagaeagatteae 223
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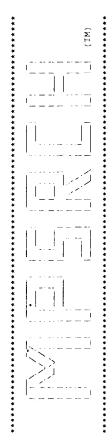
(bases 1 to 399)
Hillier, Clark, Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Hullman, M., Pullman, M., Lennon, G., Marra, M. Parsons, J., Pifkin, L., Pohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Tel: 314 286 1800
Fax: 314 286 1810
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Fred. No. 1.23e-209;
0; Mismatches 34;
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/clone="188346"
112 c 104 q 91
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High quality sequence stops: 289
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                     mRNA
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WashU-Merck EST Project
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| Similarity | 83.5%;
| 218: | Conservative
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HZ6475 385 bp mPNA EST 10-JUL-1995 y151g05.rl Homo sapiens GDNA clone 161816 5' similar to qb:M63438 GRAPPA CHAIN PRECUPSOR V-III PEGION (HUMAN);.
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                                        gtgacagtgggtetgggacagaetttcaetetcaccattcagcagaetgggageetgaag 309
                                                                                                                                                                                                                                                                                                                                                                       human clone=161616 library=Scares breast 3NbHBst vector=pI7T3U
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123 TCCCAGGCTCCTCATTTATGSTGSAAACACCASAGCCACTGSTAC-CCCAGACAGTICA 181
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Prod No 2 140-201,
0; Mismatches 50; Indels 4; Gaps
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Source: IMAGE Consortium, LLNL
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117 c 8
                                                                                                                          310 atttttgcagtgtattactgt 330
                                                                                                                                                                 239 ACTIT-GCAGITIAITICIGI 258
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78.58,
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Adms. M. Kerlavage A.R., Fleischmann, B.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, S., Blake, J.A., Brandon, R.C., Chiu, W.W., Cline, P. I. Cotton, M.D., Farle-Hughes, J. Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., FitzHugh, W.M., FitzHugh, W.M., FitzHugh, W.M., FitzHugh, S.J., Geoghagen, N.S.M., Kelley, J.M., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, P.F., McDonald, L.A., Nguyen, D.F., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hastings, G.A., Hw. Hu, J. S., Greene, J.M., Fischer, C., Hastings, G.A., Hw. W. W., Hu, J. S., Greene, J.M., Fischer, C., Hastings, G.A., He, W. W., Hu, J. S., Greene, J.M., Fischer, C., Hastings, G.A., He, W. W., Hu, J. S., Greene, J.M., Fischer, C., Hastings, G.A., He, W. W., Hu, J. S., Greene, J.M., Fischer, C., Mastings, G.A., He, W. W., Hu, J. S., Greene, J.M., Hu, J., S., Greene, J.M., 
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Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
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Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osteichthyes;
Saroopteryqii: Choanata: Tetrapoda, Amniota, Mammalia. Theria:
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Contact: Venter, JC
The Institute for Genomic Research
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Release I 1D John F Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by intelligenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Tup Feb 24 14 18 48 1998, MasPar time 19 79 Seconds 732 198 Million cell updates/sec Pun on.

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>US-08-844-215-18 (1-315) from US08844215.seq Description: Perfect Score

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TAPLE default Gap 5 Scoring table:

Dbase 0; Query 0 Nmatch SID 87531 seqs, 22996021 bases x 2 Searched.

Minimum Match 0% Listing first 45 summaries Post-processing:

Mean 7.559; Variance 4 251; scale 1 804 Statistics:

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query	Query Match Length	DB	ID	Description	Pred No.
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10	162	51.4		٠. ا	v-iasü-LJd	Sequence 158, Applicat	2.410-100
c 11	152	51.4	729	٢	-912-bu-Sii	168, Appl:	2,416-100
12	162	51.4	13254	۲-	US-08-276-	156,	2.41e-100
13	162	51.4	13254	13	PCT-US95-0	156, Appl:	2.41e-100
c 14	162	51.4	13254	13	0-565H-LJd	170	2.410-100
c 15	162	51 4	13254	1	US-08-276-	170	2.410-100
15	139	44.1	387	9	US-08-217-	Sequence 1, Applicatio	3.55e-83
17	136	43.2	4238	,-	5453363-1		6.040-81
18	132	41 9	318	12	PCT-#894-1	Sequence 2, Applicatio	5. 61p-7R
1.3	132	41.9	318	-	0-8550-10d	Segmence 3 Application	5 610-7R

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OHER ARRIGOR SERVICE	201444444 2040

ALIGNMENTS

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E: Townsend and Townsend Khourie and Grew One Market Plaza, Stenart Tower, Suite 200
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IRM PG Compatible
OPERATING SYSTEM: PG-DOS/MS-DOS
SOFTWARE PATENTIN PRODS/MS-DOS
.T 1
US-08-053-131-178 STANDARD; DNA; UNC: 812 BP.
                                                                                                                                                                                                                26-APF-1993
                                                                                                                                                                                                                                                                                                                                                      PEGISTRAITÓN NOMBER: 30,223
PEFERENCE/POCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   APPLIANCE ATE 15 DEC. 2012
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/810, 279
TEXT DATE: 17-DEC-1991
                                                                                                                                                                                                                                                                                                 FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-WAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  CLASSIFICATION DATA:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
                                                                                                                                                                                                                                                                                                                                              NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                    CUPPENT APPLICATION DATA: APPLICATION NUMBER US,
                                                                                                                                         San Francisco
California
                                                                                                                                                                                                                                      FILING DATE: 26
CLASSIFICATION:
                                                                                                                                                          USA
                                                                                                                                                                  94105
                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                         502 GCCASTCASASTSTIAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCC 561
                                                                                                                                                                                                                                                                562 AGGCICCTCATCTAIGAIGCATCCAACAGGGCCACIGGCATCCCCAGCCAGCTTCAGIGGC 621
                                                                                                                                                                                                                                                                                                       622. AGTGGGTGTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA 681
                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                        Score 204; DB 7; Length 812;
Pred. No. 5.73e-132;
                                                                                                                                                              0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : One Market Plaza, Steuart Tower, Suite 200
San Francisco
California
X: USA
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                                                                                                           LOCATION: join(199 246, 418 714)
Sequence 812 BP; 201 A; 225 C; 187 G; 199 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE PATENTIN Release #1 0, Version #1 25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               682 GITIAITACIGICAGCAGCGIAGCAACIGGCCICCCAC 719
                                                                                                                                                                                                                                                                                                                                                          247 GITIATITCIGICAACACTATAGIACCIGGCGGGICAC 284
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-053-131-180 STANDARD; DNA; UNC; 900 RP
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16-DEC-1992
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25-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM SEMBLUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 180, Application US/08053131 Sequence 180, Application US/08053131 Patent No 5651016 SERVERL INFORMATION:
      INFORMATION FOR SEC 10 NO. 178.
SEQUENCE CHARACTERISTICS:
ILENGTH 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                           MOLECULE TYPE: DNA (genomic)
FEATURE:
415-326-2400
                                                                                                                                         / Match 64.8%;
Local Similarity 86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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FILING DATE: 16-DEC
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 TELEPHONE:
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                                                                                                   NAME/KEY.
                                                                      TOPOLOGY:
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421 ACACAGTCTCCAGCCACCCTCTTTGTCTTCGAGGGGAAAGAGCCACCCTCTCCTGCAGG 480
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. $661016-Human Animals for IIILE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 900;
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Sequence 900 BP; 225 A; 244 C; 204 G; 227 T; 0 other:
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COMPUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MG-DOS
SOPTWAPE: PatentIn Pelease #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 63.5%; Score 200; DB 7; L Local Similarity R6 0%; Pred. No. 6.05e-129; les 239; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       661 CITIATIACIGICAGCAGCGIAGCAACIGGCAICCCAC 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 GITTATITGIGAAGAGTATAAGTAGGTGGGGGGGGA 284
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                                                                                                                                                                                   14643-9-3
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-WAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 182, Application US/08053131.
Sequence 182, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
                                                                                                                                                           30,223
                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 180: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                NAME: Smith, William M
PEGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                 : 415-326-2400
415-326-2422
                                                                                                                                                                                                                                                                                                                                    LENGTH: 900 base pairs
TYPE nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            San Francisco
California
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: ALLEPGEN-SPECIFIC 19A MONOCLONAL ANTIBODIES AND TITLE OF INVENTION: PELATED PRODUCTS FOR ALLERGY THEATMENT NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555 GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTI 614
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                                                                                                                                                                                                                                                                                                                                                                                        375 ACGCASICICCAGGCACCCIGICIIISICICCAGGGGAAAGAGCGCGCGTCICCTGCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                  435 GCCASICAGAGIGITAGCAGCAGCIACITAGCCIGGIACCAGCAGAAACCIGGCCAGGCI 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GCCNSTCAGAGIGICGGIAACAA-I--ITAGGIIGGIAICAGCAGAAACCIGGGCAGGCI 123
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                            Ouery Match 61.0%; Score 192; DB 7; Length 900; Best Lucal Similarity 86.6%; Pred. No. 6.646-123. Matches 244; Conservative 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                               LOCATION: Join(116.163, 351..650)
Sequence 900 RP: 220 A: 241 G: 201 G: 208 T: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                615 GCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCTCCCAC 655
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PCT-US93-12501-1 STANDARD; DNA; UNC; 325 BP
                                                                              APPLICATION NUMBER US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR PAPLICATION DATA: 17-DEC-1991
APPLICATION NUMBER US 07/853,408
FILING DATE: 18-MAP-1992
ATORNEY AGENT INFORMATION NAME: SMILM, WILLIAM M.
REGISTRATION NUMBER: 30.223
PEFERENCE/DOCKET NUMBER: 14641-9-3
       JMBER: US/08/053,131
26-APR-1993
                                                  UMBER: US 07/990,860
16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Tanox Biosystems, Inc. STREET: 10301 Stella Link Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence I. Application PC/TUS9312501.
Sequence I. Application PC/TUS9312501
GENEPAL INFORMATION:
APPLICANT: Chang, ISE Wen
                                                                                                                                                                                                                INFORMALION FOR SECTIONS: 1820
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                                                                                                                                                                                            415-326-2400
415-326-2422
                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       900 base pairs
                                     PRIOR APPLICATION DATA.
APPLICATION NUMBER: US
FILIND DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           single
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      APPLICATION NUMBER:
FILING DATE: 26-APR
CLASSIFICATION: 800
                                                                                                                                                                                                                                                 nucleic acid
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01-JAN-1900
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METHOUS FOR PRODUCING ANTIBODY LIBRARIES USING UNIVERSAL OF PANDOMIZED IMMUNOGLOBYLIN LISH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
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Local Similarity 92.3%; Prod No 2 22e-118;
les 255; Conservative 0; Mismatches 52; Indols
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Sequence 325 BP: 79 A: 93 G: 79 G: 74 T: 0 other:
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PPCT-US94-01258-2 STANDARD; DNA; UNC; 646 BP.
                                                                                                                                     3.5" Hi Density Diskette
                                                                                                                                                                                                                                 1908, Version ← 30
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PUT/US93/12501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mirabel, Eric P.
PEGISTPATION NUMBER: 31,211
PEGISTPATION NUMBER: 71x92-3
TELECOMMUNICATION INFORMATION.
TELEPHONE: 713-554,2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9401258. Sequence 2, Application PC/TUS9401258 GENERAL INFORMATION:
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EDNESS: double stranded
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFHONE: 712.654.2288
TELEFAX: 713.664.8914
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
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                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Hi
                                                                                                                                                                    COMPUTER IBM PS/2
OPERATING SYSTEM: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 GTTGAAATCAA 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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Sequence 2, Application PC/INS9511235
Sequence 2, Application PC/TUS9511235
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: METHORS FOR PROGUCINS ANTIBODY LIBRARIES
TITLE OF INVENTION: USING UNIVERSAL OF PANDOMIZED IMMUNOSLOBULN LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                181 ICCAGIGGCAGIGGGICIGGGACAGACIICACICICACCAICAGCAGACIGGAGCCIGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IGCASSGCCASTCA/ASTSTTA/SCA/SA/CTACTTA/SCTG/STA/CCA/SCA/GAAAA/CCT/A// 120
                                                                                                                                                                                                                                                                                                                                                            1 GASCTCACGCASTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC 60
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                                                                                                                                                                                                                                                                                                                   Indels 3;
                                                                                                                                                                                                                                                                                          Length 646
           SOFTWARE: Patentin Pelease #1.0, Version #1.25 (EPO) CUPRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   ANTI-SENSE: NO Sequence 646 BP; 162 A; 187 G; 170 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: TRM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 GACTITICAGITIATITICIGECACACIATAGIACCIGGCCG 279
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ADDRESSEE: The Scripps Research Institute
STREET: 10666 North Torrey Pines Poad, TPCR
                                                                                                                                                                                                                                                                                       Score 185, DB 12, L
Pred. No. 1.26e-117;
0; Mismatches 38;
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PCT-US95-11235-2 STANDAPD: DNA; UNC; 646 BP
                                    APPLICATION NUMBEP - PCT/US94/01258
FILING DATE: 02-FER-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/11235
                                                                           APPLICATION NUMBER: HS 08/012,566
                                                                                         FILING DATE: 02-FEB-1993
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 08/174,674
PC-DOS/MS-DOS
                                                                                                                            FILING DATE: 28-DEC-1993
INFOPMATION FOR SEQ ID NO. 2-
SEQUENCE CHARACTERISTICS:
                                                                                      02-FEB-1993
                                                                                                                                                                      LENGIH: 646 base pairs
TYPE: nucleic acid
STPANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 70
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Local Similarity 85.5%;
hes 241; Conservative
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                                                                                                                                                                                                                       MOLECULE TYPE: CDNA HYPOTHETICAL: NO
OPERATING SYSTEM:
                                                                                                                                                                                                               linear
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Richard A
METHODS FOR PRODUCING ANTIBODY LIBRARIES
USING UNIVERSAL OF PANDOMITED IMMUNOSIORULIN LIGHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
Sequence 646 BP; 162 A; 187 C; 170 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 SAITITGGASTGIACTACTGTGACACIAIGGIGGGTGAGGG 282
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                                                                                                                                                                                                                                                                 UMBER: IIS 07/826,623
27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                           US 07/954,148
                                                                                                                                                                                                                                                                                                                                                                                                                                               115 OB/012,566
                                                                                                                                                                             TIS 08/174,674
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Sequence 2, Application US/UB300386A
Patent No. 5667988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: FILLING, Thomas
PRGISTRATION NUMBER: 34,163
PEFEBENCE/COCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dennis R
                                                                                                            FILING DATE: 02-SEP-1994
PPIOP APPLICATION DATA
APPLICATION WIMBER: US 08
FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 11S OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-FEB-1993 ATTORNEY/AGENT INFORMATION:
FILING DATE: 01-SEP-1995
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619-554-6312
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INFORMATION FOR SEG ID NO
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                         FILING DATE: 28-DEC-1
PPIOP APPLICATION DATA:
APPLICATION NUMBEP: I
                                                       PRIOR APPLICATION DATA:
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                                                                                      APPLICATION NUMBER:
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APPLICANT: Barbas, C
APPLICANT: Burton, D
APPLICANT: Lerner, R
TITLE OF INVENTION:
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                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                FILING DATE:
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
         NUMBER OF SECUENCES: 70
CORRESPONDENCE ADDRESS: ASSENTCH INSTITUTE
ADDRESSEE: ASSENTED SECTIONS STREET: 10666 NO. 5467988th Torroy Pincs Hoad, 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 185; DB 7; Length 646;
Pred. No. 1.26e-117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
Sequence 646 RP: 152 A: 187 C: 170 G: 127 I: 0 other:
                                                                                                  MEDIUM IYPE: Floppy disk
COMPUTER: IRW PC COMPUTED:
CERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1 0, Version #1 25
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                                                                                                                                                                                         APPLICATION NUMBER: US 08/174,674
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 07/825,523
FILING DATE: 27-7AN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TSPI 409.1
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
TELEBAX: 619-554-6312
                                                                                                                                     US 08/012,566
                                                                                                                                                                                                                                                                                                                   NAME: Fitting, Thomas
PEGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30 SEP-1992
PPIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 02-FER-1993
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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Local Similarity 85.5%;
                                                                                                                                                                     CLASSIFICATION 435
PPIOR APPLICATION DATA:
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                                                                                       COMPUTER READABLE FORM: MEDIUM IYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241; Conservative
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                               Abba.
STREET: Lour
TTTY: La Jolla
                                                                     AS:
                                                                             92037
                                                                     COUNTRY
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78 CTCACGCAGICICCAGGCACCIGICICIGICICCAGGGGAAAAAGCCACCIISICCIGI 327
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                                                                                                                                                                                                                                                                                            APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
IIILE OF INVENTION: HUMAN NEUTRALIZING WONCLIONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERCIENCY VIRUS
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEF. Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8 CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 63; Indels
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Sequence 729 BF: 173 A: 208 C: 192 G: 156 I: 0 other:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-NOS/MS-NOS
SOFTWARE: patentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 2.41e-100;
US-08-276-852-152 STANDARD; DNA; UNC; 729 BP
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30-SEP-1993
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FILING DAIE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                              Sequence 152, Application 08/08275855. Sequence 152, Application 08/08276852 Patent No. 555218 GENERAL INFORMATION:
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REGISTRATION NUMBERS: 34.163
PEPERECE/COCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
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TELEFRAX: 619-554-6312
INFORMATION FOR SEC ID NO: 1
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: double
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78.58;
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PPIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 30-SEP-)
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Best Local Similarity
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01-JAN-1900
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301 AAGGTCGAG 309

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181 AGIGGCAGTGGGTCTGGGAAAAATTGACTCTGAGAATTAAGTGTGGAGGTGGAGGAGGG 240
                                                                318 ITTGCACTGTACTACTGCGGTCTATGGTGCTCCTCGTCGTACATTTGGCCAGGGGACC 377
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Prod No. 2 410-100;
0; Mismatches 63; Indels 3; Gaps
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COMPUTER PEADABLE FORM:
MEDIUM TYPE: Flogby disk
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Sequence 729 BP, 173 A, 208 C, 192 G, 156 T, 0 other,
                                                                                                                                                                                                                        PCT-US95-08743-152 STANDAPD; DNA; UNC; 729 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUPPERT APPLICATION DATA
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-UUL-1995
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 08/276,852
                                                                                                                                                                                                                                                                      Sequence 152, Application PC/TUS9508743 Sequence 152, Application PC/TUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Local Similarity 78 6%;
hes 243; Conservative
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TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TO PC-POS/MS-POS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 51.4%; Score 162; DB 13; Length 729;
Local Similarity 78 6%; Pred No 2 41e-100;
Nes 243; Conservative 0; Mismatches 63; Indels 3
                                                                                                                                                                                                                       SOFTWAPE: Patentin Felease #1 0, Version #1 25 (EFO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
Sequence 729 PP: 156 A: 192 C: 208 G: 173 T: 0 other:
JI 10
PCT-US95-08743-168 STANDARD: DNA; UNC: 729 BD.
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                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/11S95/08743 FILLING DATE: 11-70L-1995
                                                         Sequence 168, Application PC/TUS9508743. Sequence 168, Application PC/TUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/276,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 168, Application US/08276852.
Sequence 168, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 729 base pairs
TYPE: nucleic acid
TYPE: nucleic double
TOPOLOGY. linear
MOLECULE TYPE: DNA (genomia
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Carlos
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO.
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Barbas, (
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APPLICANT:
                                           01-JAN-1900
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404 CASISCAAASICIICAS VIISTACIOTSAIGSISASASISAASICISICCCASACO: 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 ACTGCCACTGAACTTSTCTSGGGTACCAGTGGCTCTGGTGTTTCCACCATAAATGAGGAG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Indels 3; Gaps
APPLICANT: Lerner, Richard A FITTE OF INVESTIGATE ANTIRCHES FITTE OF INVENTION: RUMAN NEUTPALIZING MENOTIONAL ANTIRCHES FITTE OF EXPENTIONS: 179 HOWAN IMMUNIDEFICIENCY VIPUS NUMBER OF SEQUENCES: 179
                                                         JORRESPONDENTE ACTREESS:
ADDRESSEE: The Stripps Husharth Institute offlice of
ADDRESSEE: The Stripps Husharth Institute offlice of
STREET: 10666 NO. 5652129th Torrey Pines Road Suite 220,
STREET: Mail Drop IPC8
STREET: A Jolia
STATE. CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1627 DB 7; Length 729,
Pred No 2.41e-100;
O: Mismatches 63; Indels
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Polease #1 P, Version #1 25
CUPPENT APPLICATION FAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
Sequence 729 BF. 156 A, 192 C, 208 S, 173 T, 0 other.
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER 198 077954,148 FILING DATE: 30-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER 115708/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCP1452P
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fitting, Ihomas
REGISTRATION NUMBER: 34,163
PEFFPRENCE/POCKET NUMBEP: SCP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 168: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     729 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 78 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                   COMPUTER REALABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243; Conservative
                                                                                                                                                                         USA
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                                                                                                                                                                       COUNTRY: U(
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12728 GOTTOGAAGGGTSGTGATAGATGGTGTTTGGAATAGGGGGTGTGTGGGATGTGAAA GAGGTGG TAGGTTG GAATAGGGGGG
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TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIRODIES
TITLE OF INVENTION: TO HUMAN IMMONOBEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPPESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 1655 No. Ff52138th Torrey Pines Foad, Suite 229, STREET: Mail Drop 1908
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91 4%: Score 182: 194 7: Longth 13284:
Best Local Similarity 78:6%: Pred: No. 2:41e-100;
Matches 243, Conservative 6: Mismatches 63: Indexis *
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Sequence 13254 BF: 3296 A: 3559 C; 3251 G; 3238 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Pelease #1.0, Version #1.25 CURPENT APPLICATION DATA:
J 12
48-00-274-052-154 STANDARD, DNA, UNC. 13254 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-JUL-1994

CLASSIFICATION: 514
PPIO APPLICATION DATA:
APPLICATION NUMBER: US 09/178,302
FILING DATE: 30-SEP-1993
PRICH PAPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/276,852 FILING DATE: 18-JUL-1994 CLASSIFICATION: 514
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                                                                                                                                               Sequence 155, Application US/08276852. Sequence 155, Application US/05276852 Patent No. 5552138 GENERAL INPOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
(PEPATIN) SYSTEM: PC-EWS/MS-DOS
SOFTWARE: Patentin Poles
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REPPRENCE/DOCKET NUMBER: SCR
TELECOMMINICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-6212
INFORMATION FOR SEQ ID NO: 156:
                                                                                                                                                                                                                                                                                              Burton, Dennis R
Barbas, Carlos F
Lerner, Richard A
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EDNESS: double
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                                                                                                                01-JAN-1900
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           RESULT
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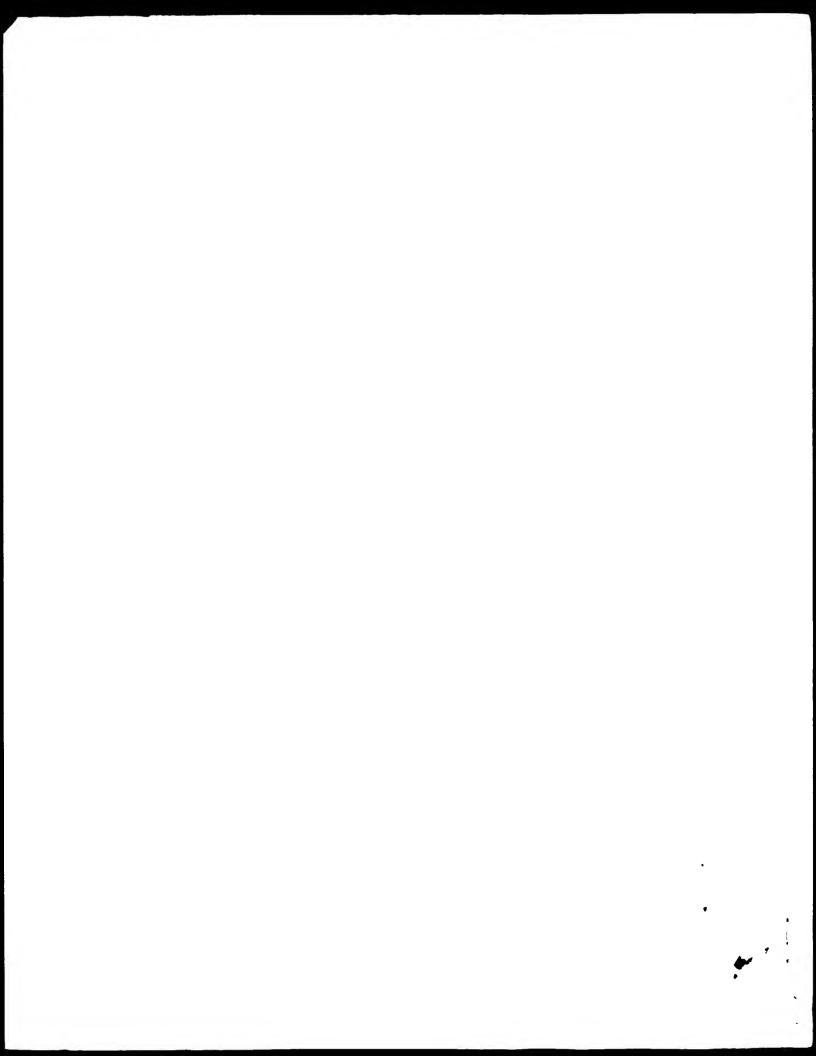
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12606 CTCACGCAGICICCAGGCACCCTGICICIGICICCCAGGGGAAAGAGCCACCTICICCIGI 12665
12846 TITGCACTGTACTACTGTCAGGTCTATGGTGCCTCGTCGTACACTTTTGGCCAGGGGACC 12905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AGIGGCAGTGGGTGTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGTCTGAGGAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TIGCAGITIATITICIGICAACACIATAGIACCIGGCGCGCTCACTITICGGCGGGGGGCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 AGGGCCAGTCAGAGTGT-CG--GTAACAATTTAGCTTGGTATCAGCAGAAACCTGGCCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 63; Indels 3; Gaps
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS COMPUTER PEADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 13254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: DNA (9*nomic)
Sequence 13.254 BF; 3.206 A; 3.559 C; 3.251 G; 3.238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: PCT/US95/08743 FILING DATE: 11-JUL-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 162; DB 13;
Pred. No. 2 41e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
ID PCT-3S95-08743-170 STANDARD; DNA; UNC; 13254 BP.
                                                                                                                                                                PCT-US95-08743-156 STANDARD; DNA; UNC; 13254 BP
                                                                                                                                                                                                               Sequence 156, Application PC/TUS9508743. Sequence 156, Application PC/TUS9508743 GENERAL INFOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-40L-1994
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   SUG-SW/SUG-DOS
                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13254 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
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249 AACTSCAAAGTCCTCAGACTSCAGGCTGGTGATGAGAGAGAGATTCTGTCCCAGACCC 190
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                                                                                                                                                                                                                                                                                                                                                                                                    3; Gars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521 CCTTGGAGCCTGGGCAGGTTTGTGCTGGTACCAGGCTACGCGGCGGCGGCTGCGAATGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Barbas, Carlos r
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTPALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBFICIENCY VIRUS
                                                                  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIPUS
170
                                                                                                                                                                                                                                                                                                                                                                          Length 13254;
                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
Sequence 13254 BP; 3238 A; 3251 C; 3559 G; 3206 T; 0 other;
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                       / Match 51.4%; Score 162; DB 13; I
Local Similarity 78.6%; Pred. No. 2.41e-100;
ies 243; Conservative C; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .7 15
US-08-276-852-170 STANDARD; DNA; UNC; 13254 BP.
                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/08743
             Sequence 170, Application PC/TUS9508743. Sequence 170, Application PC/TUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/274,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08276852. Application US/08276852.
                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                       FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dennis R
Carlos F
                                                                                                                                                                                                   FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          double
                                                                                            NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                         circular
                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                              OPERATING SYSTEM:
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Barbas,
                                                                  TITLE OF INVENTION:
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APPLICANT. Burton,
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Sequence 170, Appli
Patent No. 5552138
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                                                                                                                      MEDIUM TYPE:
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                                                                                                                                    COMPUTER:
                                                       APPLICANT:
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01-JAN-1900
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ADDRESSEE: Faired Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 120,
STREET: *Mail Drop IPC8
CITY: La Jolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 51.4%; Score 162; DB 7; Length 13254; Local Similarity 79 6%; Pred No. 2 41e-100; es 243; Conservative 0: Mismatches 63; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
Sequence 13254 BP; 3238 A; 3251 C; 3559 G; 3206 T; 0 other;
                                                                                  MEDIUM IYPE: Floppy disk
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18 JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION WUMBER:
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/954,148
FILING DATE: 30-SEP-192
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        SCP1452P
                                                                                                                                                                                                                                                                                               NAME: Fitting, Thomas
REGISTRAITON NUMBER: 34,163
PEREPENCE/FOCKET NUMBEP: SCP1
IELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO. 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDFURES: double
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                                                               USA
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Search completed: Tue Feb 24 14:19:44 1998 Job time: 56 secs.



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Release 2.1D John F. Cellins, Biocomputing Pesearch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U Distribution rights by Intelligenatics, Inc.

- n.a. database search,

ח.מ.

MPsrch_nn

using Smith-Waterman algorithm

Tun Enb 24 08-18-55 1999; Maspar time 49-58 Seconds 731.747 Million cell updates/sec Run on:

Tabular output not generated.

(1-315) from US08844215.seq 315 >US-08-844-215-18 Description Perfect Score: N.A. Sequence:

GGACCAAGTUGAGITGAAG 315 GGTGGTTGCAGGTCAAGTTG CTCCASTOCCTCAGAGGTCG 1 GANGTONGORGANTOTONION

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 SID Nmatch

159651 seqs, 57698962 bases x 2 Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

Database:

n-geneseg30 lipart1 2.part2 3.part3 4 part4 5.part5 6.part6 7 part7 8.part8 9.part9 10.part10 11.part11 12.part12 13.part13 14.part14 15.part15 16.part16 17.part17 18.part13 19.part19 20.part20 21.part21 22.part22 23.part23 24.part24 25.part25 26.part26 27.part27 28.part28 23.part24 30.part30 31.part31 32.part32 33.part33

Mean 8.057; Variance 4.906; scale 1.642 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	* Query Match Length DB	DB	01	Description	Pred. No.
-	C4 C4	r i.L	924	. c.	271972	Sequence coding human	4 750-120
C	204	54 P	815	5	T37190	DNA fragment vk65 3,	9 278-119
٣.	204	54 R	812	(4	278852	Human Vikappa gene vk	9.27e-119
4	\$0C	54.8	C4	٢	244222	Muman DNA fragment wk	9.276-119
L €	503	54.4	C. C.	S	179922	Immunoqlobulin r101-2	4.51e-118
ç	200	53.5	300	C1	278853	Human V-kappa gene vk	5.19e-116
Ļ	000	63.5	300	۲-	044223	Human DNA fragment vk	5.19e-116
ου (200	53.5	000	7.7	T37181	DNA fragment vk65.5,	5.19e-116
5	000	(1) (4)	1204	.4	C11879	igG light chain varia	5.19e-116
10	000	63.5	1242	C 1	011878	1B1 1qG aberrant ligh	5.19e-116
11	196	52.2	387	۲.	049155	F105 rearranged varia	2.89e-113
C	192	C) - 1	000	L-	042707	F105VK-F1053K	1.600.110
۲.	192	C) #39	000	۲-	244224	Human DNA fragment vk	1 60e-110
14	192	61.0	006	12	078854	Human V-kappa gene vk	1.60e-110
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k325-1k2. enc for Ly region o locative colitis-a comba extression se	ression vector, ht chain of Amb	Inerative colitis-a C3AP313 anti-tetanu nti:tetanus toxoud	ti-pseudomonas a ti-p aeruginosa	9 E 6	ucleotide sequenc EA-specific antib	Ab L chain V g sequence for VL coding sec	DNA contg an ORF nti-cancer monoclo	Anti-cancer monociona DNA encoding light ch Buman anti-HBS light	48RLC VL región nized 1308E VL	08 VL en 48RLA VL n anti-t
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16 17 18	1911	000 640	27	2 C1 W	33	ሠ መ ም መ ዳ ሊያ	37	υ κ. Δ Ο Φ. Ο:	41 42	6 4 4 4 4 4

ALIGNMENTS

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France mast cells by allergen stimulation, useful for release from mast cells by allergen stimulation, useful for preventing allergies.

Claim 4, Page 17: 21pp; English.

971872 encodes the light chain of a human type antilize peptide monoclaim and the base of the light chain of a human type antilize peptide the release of chemical mediator from mast cells and basophils stimulated with allergen. The antibody can be used for the
CT 1 (77872 standard; cDNA; 924 BP. (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (77872) (7
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07-07-1994.
07-07-1992. 3P-29806.
(SNOW ) SNOW BRAND MILK PROD O LTD
GCto M. Kobayashi F. Mizunc A. Morinaga T.
Yoshida T:
Preshed T:
P-PSDB: R52951.
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/note= "Human monoclonal anti-1qE antibody
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/note- "C or G, illegible sequence."
misc feature 908..910
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/note- "N is an unidentified base"
misc feature 71..394
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/note= "L-chain variable region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 aggetecteatetatggtgegtecaceagggecactggtateceggecaggtteagtgge 262
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                                                                                                                                                                                                                                                                                                                                                                                  143 gccagtcagagtgttagcaacaacatagcctggtaccagcagaaacctgcccaggctccc 202
                                                                                                                                                                                                                                                                                                                                                                                                                                               67 GCCAGTCAGAGTGTCGGTAACAATTTAGCTTGGTATCAGCAGAAACCTGGCCAGGCTCCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AGGCTCCTCATTTATGGTGGAAACACCAGAGCCACTGGTACCCCAGACAGGTTCAGTGGC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 agtgggtetgggacagaettcaeteteaecatcageageetacagtetgaagattttgca 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 atttattactgtcagcaatatagtagctggcctcggacgttcggccaagggaccaaggtg 382
                                                                                                                                                                                                                                                                                                                7 ACGCAGICICCAGCCACCCIGICIGIGICICCAGGGGAAAGAGCCICCCTCICCIGCAGGG 66
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The present sequence is the variable kappa chain gene segment.

Octobating human DNA fragment, vk65.3, which was co-injected along with the human DNA tragments vk65.5, vk65.8 and vk65.15 into half day mouse embryo pronuclei, to generate an unrearranged light chain minitorus transgene. The resulting transgenic mice can be used for the production of heterologous (i.e. human) antibodies against specific antigens, this comprises immunishing a mouse with a preselected antigen and collecting antigen binding heterologous
                                                                                                                                                                              Gaps
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DNA fragment vk55.3, containing variable kappa chain gene.
Variable; kappa chain; gene segment; human; DNA fragment; vk65.3;
unrearranged; light chain; minilcous, transque, transqueic, mouse, production; heterologous; antibody; gamma; immunoglobulin; ss.
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                                       216 6;
                                                                                                     Score 232; DB 10;
Fred. No. 4.76e-138;
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prophylaxis and the therapy of allergy. Sequence 924 BP; 230 A, 277 C,
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                                                                                                     Query Match
Best Local Similarity 87.7%;
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419..717
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23-JUN-1992; US-904068.
16-DEC-1992; US-990860.
(GENP-) GENPHARM INT INC
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29-AUG-1990; US-574748.
31-AUG-1990; US-575962.
17-DEC-1991; US-810279.
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                                                                                                                       561
                                                                                                                                                                                                                                                              442 acaeagteteeageeaeeetytetttgteteeegggggaaagageeaeeeteteetgeagg 501
                                                                                                                                                   67 GCCAGTCAGAGTGTCGGTAACAAITIAGCTTGGTALCAGCAGAAAGTTGGGTAGGTTGCT 126
                                                                                                                                                                                                               127 AGGCTOCTCATTTATGGTGGAAACACCAGAAGCACTGGTACCCCAAAAAAATTTAGTAGC 186
                                                                                                                                                                                                                                              agigggictgggacagacticacteteaceateageageetagaggeetgaagattitgea 681
                                                                                         7 ACGCASTOTOCAGOCACOCTGIOTOTOTOTOCAGAGAAAAGAGOOTOCOCTOTOCTGOTAGAGAGAG
                              0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig. 41, 296pp, English.

Why and Pragments vk65 3, vk65 R and vk65.15 (given in Q7885-Q78855, respectively) each contain a V-kappa gene segment that can be used to form a complete human light chain minilocus transgene for expression in a nonhuman transgenic animal for betarologus antihody production. The deduced amino acid sequences of the V-kappa coding regions are given in RPG-92R-983 Sequence 812 BP; 2.2.8.; 187 5; 199 T;
                                                                                                                                                                                     aggetecteatetatgatgeatecaacagggeeactggeateceageeaggtteagtgge
                                                                                                                       502 gecagteagagtgttageagetaettageetggtaeeaacagaaacetggecaggeteee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic non-human animals producing heterologous or chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for binding a pre-determined human antigen with
                                                                                                                                                                                                                                                                                                                                                                                                                            77-JUN-1995 (first entry)
Human V-kappa gene vk65.3.
Transgenic mouse, transgenic animal; antibody engineering; variable region; light chain; minilocus transgene; chimeric antibody; ss.
 Length 912:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 812;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 204; DB 12; E
Pred N. 9 27e-119;
0; Mismatches 37;
Score 204; DB 27; I
Pred No. 9 276-119;
                              Mismatches 37;
                                                                                                                                                                                                                                                                                                           682 gtttattactgtcagcagcgtagcaactggcctcccac 719
                                                                                                                                                                                                                                                                                                                           247 GITIATITCIGICAACACTATAGIACCIGGCGGICAC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                    Q78852 standard; DNA; 812 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombination_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.9%;
Logal Similarity 86.7%,
es 241; Conservati
 Query Match
Best Local Similarity 86,78;
                              241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Splicing_signal
misc_signal 736..744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-PEC-1993; US-165699
09-MAR-1994; US-209741
(GENP-) GENPHARM INT INC
KAY RM, Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   714..723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297..417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199..764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-053131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-096762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U04580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             increased affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94-358263/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; P62928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9425585-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0-NOV-1994
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Rest Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
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                              Matches
                                                                                                                                                                                   295
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561
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                                                                                                                                            621
                                                                                                                                                                            127 AGGCTCCTCATITATGGTGGAAACACCAGAGCCACTGGTACCCCAGACAGGTTCAGTGGC 186
                                                                                                                                                                                                                                   The V-Kappa specific oligonalisatile usois was used to prote a human placental genomic DNA library cloned into lambdaEMBL3/SP6/T7. BNA fraqments containing V-kappa segments from positive phage clones were subcloned into plasmid vectors. Variable gene segments from the resulting clones were sequenced and functional clones were selected on the basis of open reading frames, intact donor and acceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were lessinated from four different plasmid clones were assumed from four different plasmid clones were
442 acacaqtqtorageracectqtetttgtetecaqqqqqaaaqaqeeeceteteetgeagg
                                                                     502 accaaticagagitatiagicauctaetiagicitggiaecaacagaaaceiggecagaeteee
                                                                                                                                            562 aggetecteatetatgatgeatecaacagggecaetggeateceaggeeagtteagtgge
                                                                                                                                                                                                                  522 agigggictgggacagacticactcicacoatcagcagcciagagcctgaagaittigca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic non-human animals contq. immunoglobulin heavy chain
trans gene - used to produce useful antibodies by isotype
                                                                                                                                                                                                                                                                                                                                                                                                                       10.NVV-1993 (first entry)
Human DNA fragment vk65.3 containing V-kappa gene segment.
Humanoblobulin; light chain variable region; minilocus;
isotype switching; unrearranged functional Vk gene segment;
human light chain transgene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= d
/note= "splicing and recombination signal sequences"
                                                                                                                                                                                                                                                                                   582 offitaltactoficadeagegiageaactogeeteeeae 719
                                                                                                                                                                                                                                                                                                                     247 GITTATITCIGICAACACIATAGIACCIGGCCGCTCAC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        initiation codon, i.e. the start of the ORF; the precise start point of the exon is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number= 2
/noin= "OPF not terminated by a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number- 1
/note- "nucleotides 199-201 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 199..247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 21; Fig 41; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           044222 standard; DNA; 812 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENP-) GENPHARM INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248..418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
23-JUN-1992; US-904068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1993.
17-DEC-1992; U10983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lonberg N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .214169/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R38548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respectively).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= a
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claim 4; Page 12; 1889; Japanese.
T79919-T7992 represent the immunoslobulin heavy and light chain variable regions isolated from peripheral blood lymphocyte strains. These sequences were isolated from the B687 and 10.7 strains of peripheral blood lymphocytes of a Basedow's disease patient. These sequences are pelaced, deleted or inserted into an antibody, to create the antibodies of the invention. The antibodies of the invention activity, and act by combining with thyrotropin receptor. The stimulating activity and act by combining with thyrotropin receptor. The thyroid function stimulating activity and locativity and activity and activity and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-ocr-1997 (first entry)
Immunoglobulin r101-2 light chain variable region coding sequence.
Immunoglobulin, variable region, heavy chain, thyrotropin receptor:
thyroid stimulating activity: light chain: Basedow's disease; antibody:
peripheral blood lymphocyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       [111] HELLELLE I TELLET HELLE TELLET HELLET HELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 622 agtgggtetgggacagaetteaeteteaceateageaeetagageetgaagattttgea 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 GCCAGICAGAGIGICGGIAACAA-I--ITAGCIIGGIAICAGCAGAAACCIGGACAGGCI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 AGIGGGICIGGGACAGAAIICACIGIGACGAICAACAGCAGCTGGAAIGTGAGGACIIIIGGA 246
                                                                                                                                                                                                                                            442 acacagtetecsagecaceetgtetttgtetecsaggggaaagagecaeeeteteetgeagg 5/1)
                                                                                                                                                                                                                                                                                                                                                                                                  502 gecaqteagagtgitageagetacitageciggiaceaacagaaacitggeeaqqeinee 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C: Caps
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Local Similarity 86.3%; Pred. No. 4.51e-118;
Nos 259; Conservativo D: Mismatches 38; Indels ?; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 gocagteagagtgttagcaacagctacttagcctggcaccagcagagarctggccagac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody containing immunoglobulin heavy chain mutation - with thyroid function stimulating activity
                                                                          Query Match
    64.8%; Score 204; DB 7; Length 812;
Best Local Similarity 86 7%; Pred, No. 9.27e-119;
                                                                                                                                                         0; Mismatches 37: Indels
187 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682 gittaitacigicagcagcgiagcaaciggceiccae 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 GITTATITICIGLOACACIAIASTASCISGCSGSISAC 284
225 C;
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T79922 standard; DNA; 372 BP
201 A;
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22-NCV-1905: JP-328235.
22-NOV-1995: JP-328235.
(EFKE) EIKEN KAGAKU KK.
WPI: 97-344899/32.
                                                                                                                                                         241; Conservative
912 BF;
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    Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T79922;
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                                                                                                                                                             Matches
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541 aggeteetgatetatgatgeateeaacagggeeactggeateecageeaggtteagtgge 600
253 ggcagtgggtctgggacagacttcactctcaccatcagcagactggagcctggagatttt 312
                           184 GGCAGTGGGTCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGTCTGAGGACTTT 243
                                                         313 gcagigiatiacigicagcagiatggiaccicaccgiacactitiggccaggggaccaag 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 acacagtotocagocaccetgtetttgtotocaggggaaagagccacceteteetgcagg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48l gecagteagggtgttageagetaettageetggtarragragaaaertggreaggetere 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure: Fig. 42, 296pp, English.

Human DNA fragments vv65 3, vv65 5, vv65 8 and vv65 15 (given in 40852-078855, respectively) each contain a V-kappa gene segment that can be used to form a complete human light chain minilocus transgene for expression in a nonhuman transgenic animal for heterologous antibody production. The deduced amino acid requences of the V-kappa coding regions are given in PAP202P-P62931 Sequence 900 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic non-human animals producing heterologous or chimeric antibodies - for binding a pre-determined human antigen with
                                                                                                                                                                          77-307.1995 (first entry)
Human V-kappa gene vk65.5.
Hransgenic mouse; transgenic animal; antibody engineering; variable region; light chain; minilocus transgene; chimeric antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 200; DB 12; I
Pred. No. 5.19e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 39,
                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                  Q78853 standard; DNA; 900 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                         /label- Recombination_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 63.5%;
Local Similarity 86.0%;
Nes 239, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENP-) GENPHARM INT INC. Kay RM, Lonberg N;
                                                                                                                                                                                                                                                                                                                   227..396
                                                                                                                                                                                                                                                                                      180..693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-053131.
US-096762.
US-155301
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US-165699.
                                                                                                                                                                                                                                                                                                                                                                             /label= Splicing_signal
misc_signal 715.72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-209741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94-358262/44.
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18-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-1993;
09-MAR-1994;
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                 misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                         W09425585-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                  078853;
                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                     /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
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421 acacagicticcagecacectgiettigietecaggggaaaagagecaceeteteetgeaqg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from the resulting clones were sequenced and functional clones were selected on the basis of open reading frames, intact donor and acceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were designated p65 3, p65.5, p65.8 and p65.15 (see Q44222:244225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 21, Fig 42, 196pp, English.

The V-kappa specific oligonucleotide Q50327 was used to probe a human placental genomic UnA library cloued into lambdaEMELS/SPP.T7.

DNA fragments containing V-kappa segments from positive phage clones were subcloned into plasmid vectors. Variable gene segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iransgenic non-human animais contg. immunoglobulin heavy chain
trans gene - used to preduce useful antibodies by isotype
                                                                                                                  10.NOV-1993 (first entry)
Human DNA fragment vk65.5 containing V-kappa gene segment.
Immunoglobulin: light chain variable region; minilogus;
isotype switching; unrearranged functional Vk gene segment:
human light chain transgene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 200; DB 7; Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                      /note= "splicing and recombination signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.19e-116;
661 gtitattantginagnagngiagdaantggnathnnan 698
                         247 SITIATITCISICAACACIATASIACCISSCSSICAC 284
                                                                                                                                                                                                                                             /*tag= a
/note= "splicing and recombination signal ?"
                                                                                                                                                                                                                                                                                                                                                              finitiation codon, i e the start of the OPF; the precise start point of the opp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not terminated by a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 ##C
                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 A;
                                                                                      Q44223 standard; DNA; 900 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1992; US-904068.
(GENP-) GENPHARM INT INC.
                                                                                                                                                                                                                             119..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1992; U10983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        900 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 93-214169/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; R38649
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                          misc_recomb
                                                                                                                                                                                                                               misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "OPF
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                                                                                                                                                                                                                                                                                                                                                    /number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number= 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                intron
                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
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67 GCCARTRAGAGREROSSIAAGAAIIIAGGIIGGIATCAGCAGAAACGIGGCQAGGCICCC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 adigagectgggaesagaetteacteteaeceateagesgesgestagageetgaagattttgea 660
                                                                  127 AGGCTGGTGATITATGGTGSAAAGAGGAGGAGTSGTAGTGGAGASAGASGTTCAGTGGC 186
                                                                                                                                    601 agigggocigggagacticactotococatoagocagociagagocigaagatttigoa 660
                                                                                                                                                                                                          187 ASTGGSTCTGGGACAGAAIICACICICACCAICAGCAGCIGCAGICTGAGGACIIIGGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 acacagicinnagnnacentgieitiginienaggggaaagagecaneeisterierigeagg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 gornagicagggigitattaciacitagociggiacocagocagasasociggocaggsisse 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 AGTSOGTGTGGSAGASAATIGAGTGTGAGGATGASGAGGTTGGAGGAGTTTTGGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 39: Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1997 (first entry)

DNA fragment vk65.5, containing variable kappa chain gene.

Bustiable: kappa chain: gene segment; human: DNA fragment; vk65.5;

unrearranged; light chain: minilocus; transgene; transgenic; mouse;

production; heterologous; antibody; gamma; inmunoglobulin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the variable kappa chain gene segment containing human DNA fragment, vk65 5. Which was co-injected along with the human DNA fragments vk65.3, vk65.8 and vk65.15 into half day mouse embryo promutel, to generate an unrearranged light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      minilocus transgene. The resulting transgenic mice can be used for the production of heterologous (i.e., human) antibodies against specific antigens, this comprises immunising a mouse with a preselected antigen and collecting antigen binding heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of heterolegeus human immunoglobulin(s) - by immunising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.5%; Score 200: DB 27: Length 900: Best Local Similarity 86.0%; Pred. No. 5.19e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                 661 atttattactgtcaqnaqqgtagqaaqtggcalcccar 698
                                                                                                                                                                                                                                                                                                                                               0 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 21; Fig 42; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . ·
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Sequence 900 BF, 200 A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T37181 standard: DNA; 900 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENP-) GENPHARM INT INC
Kay RM, Lonberg N;
WPI: 96-383736/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180..228
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US-853408.
US-904068.
US-990860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W03947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30- Arts - 1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000
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US5545806-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag- a
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WPI: 96-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE COURT SAN COURT SAN
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811 aggeocoteatetatgatgatgeateeaaeagggeoattattatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  751 gecagteagagtyttygeagetaettageetygtaecaaeagaaaeetygeeagusteee M10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ADGIZASTOTOGASCOACOUTSTCTGTGTGTGTASSSSAAAGAGGTGCCLCTGTGTGTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C) Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 43; Fig 17: 104pp; English.
The leader peptide and the LV region are encoded in different reading frames. The LV region corresponds to the last three amine acids of the leader peptide and the rearranged V2 gene. Close two such LV regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligometic immunoalobulin(s) with high avidity for antiden(s) -
formed by duplicating esp. Variable region of light their of 196
                                                                                                                                                                                                                                                         01-Aug-1991 (first entry)
19G light chain variable region clone.
immunoglobulin G: light chain; variable region; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 IgG aberrant light chain clone 489/Vk15.
immuncglobulin G: Light chain: variable region: duplication:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 A; 283 C; 290 G; 302 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match (52.5%) Score 2007 DB 2: Length 1204:
Best Local Similarity 88.8%: Pred. No. 5.19e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- L'V region
/note- "translates from different reading frame
661 gtttattactgtcagcagcgtagcaactggcatcccac 598
                                                            247 GITTATTICIGICAACACIATAGIAGCIGGCGGCICAC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C: Mismatches
                                                                                                                                                                                                                                                                                                                                                                    passive immunity; group B streptococci; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
450..498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIR
Shuford WW, Harris LJ, Raff HV,
WPI: 91-183947/22
F-PSDE, R12129, P12130, F12131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mis78 standard; cDNA; 1242 BP
                                                                                                                                                                                                Q11879 standard; DNA; 1204 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     931 gittatiaciqicaacac 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 STITATITCTGTCACAC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668..1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-1990; U06426.
07-NOV-1989; US-432700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c.f. leader peptide"
W09105305-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1204 BF;
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
mat_peptide
                                                                                                                                                                                                                                                                01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligomeric
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                                                                                                                                                                                                                            011879;
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Claim 42; Fig 16: 104pp; English.

This sequence encodes an aberrant light chain containing two L'V regions. Antibody molecules of the invention can include one or two such aberrant light chains to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The clone is not complete; it starts with the G of the ATG initiator codon.

See also 011879 and 011880.

Sequence 1242 BF; 231 A; 383 C, 302 G, 266 T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 acacagicticcagiccaccitititititiciticaggggaaagagcaccititiciticaggg 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 gecagticagagigtitggcagniactiageciiggiaceaacagaaaceiggneaggeinnn 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 aqtgggtetgggacagaettcaetetcaceatcagcagectagageetgaagattttgea 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ACGCASTCTCCAGCCACCCTGTCTGTCTCTCAGGGGAAAGAGCCTCCCTGTCTGCAGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 0; daps
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F105.rearranged variable region light chain.
Monocleaal antibody: MAb: envelope: glycoprotein; gpl20; HIV; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of 19{\rm G}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 200; DB 2; Length 1242;
Pred. No 5 19e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                          /note* "encodes last 3 amino acids of leader and
the rearranged VJ gene"
                                                                                                                                                                                                                                                                                                                                                                                                  %-tag- c //label- L/v 2 //label- encodes last 3 amino acids of leader and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
passive immunity; group B streptococci; ss.
                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIR
Shuford WW, Harris LJ, Raff HV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   049155 standard; cDNA; 387 BP. 049155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 gtttattactgtcaacac 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 88 8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   728..1044
                                                                                                                                                                                                                                                                                                                                                            389..726
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/note= "constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the rearranged VJ gene"
                                                                                                                                                                                                 50..388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1989; US-432700.
                                                                                                1..49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 91-163947/22.
                                                                                                                                                                                                                                                                                                                             the rearranged VJ
                                                                                                                                      /*tag= a
/note= "leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R12128
                                                                                                                                                                                                                                /*tag= b
/label= L'V l
                                     Homo sapiens.
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                                                                                                sig_peptide
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                                                                                                                                                                                                 misc RNA
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F105VK-F105JK.
Monoclonal antibody: MAb: envelope: glycoprotein: gp120: HIV: AIDS:
CD4: receptor: hybridoma: polymerase chain reaction: PCK: heavy: light:
2D4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 ggcagtgggtctgggacagacttcactctcaccatcagcagagtggagcctgaagatttt 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 gecagtcagagtgttagcagcaggtacttagcetggtaccagcagaaaectggccaggct 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193. decaggantdettattettattggtganafonagnagggandantggnathnonaganaggffnagff 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 GGCARTGGGTCTGGGACAGAATTCACTCTCACCATCAGGAGGTGTGAGTTTGAGGACTTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 goagigiatiaoigicagcaataigataaciccgitigiacitiiqgccaggggaccaag 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 acgcagictccaggcacccigictitgicigcaggggaaagagccaccictccigcagg 132
                                                                                                                                                                                                                                                                                                                                                        parts of the heavy or light chains and having restriction sites to permit cloning. The extension prods. were isolated and sequenced. The recombinant human monoclonal antibody (MAb) binds to a discontinuous epitope on the HIV gpl20 envelope glycoprotein, blocks the binding of gpl20 to the CD4 receptor, and neutralises a broad range of HIV isolates. The MAB may be used to treat immune deficiency, esp. at doses of 0.1-10 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 47; Indels 3; Gaps
                                                                                                                                                                                                                                                                           DNA segments encoding monoclonal antibody - which binds to gp120 and neutralises HIV, for treating AlDS, and for diagnosing and monitoring HIV infection and claim 1; Page 79; 109pp; English.

mRNA from the known hybridoma F105 was converted to cDNA and this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 387;
                                                                                                                                                                                                                               Sodroski 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 62.2%; Score 196; DB 7; Lv
Similarity 83 9%; Pred No 2.89e-113;
                                                                                                                                                                                          (DAME) DAMA FARBER CANCER INST INC
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                Marasco WA, Posner MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain; epitope; immune deficiency; ss.
              immune deficiency; ss.
                                               Location/Qualifiers
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Q42707 standard, DNA, 390 BP.
Q42707;
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                                                                                                58..387
                                                                                                                                                                                 US-804652
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                                                                 1..57
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                                                                                                                                                            10-DEC-1992; U10928
10-DEC-1991; US-804
                                                                                                                                                                                                                               Haseltine WA, Mara
WPI; 93-214174/26
                 epitope;
                                                                                                                                                                                                                                                              P-PSDB; R41286
                                 Homo sapiens.
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                                                                                                                              W09312232-A.
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                                                                                              mat_peptide
                                                                                                                                                24-JUN-1993
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              chain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 godantoagaytyttujengenggtacttageetggtaceageaetgagaeebggeeaggee 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 CCCAGGCICCICATTIAIGGIGGAAAAAACAGGAGAGTGATAGIGGGAGAGAGTTGAGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HILLITHILITHILITY FULL TO THE TOTAL ASSOCIATION OF THE PROPERTY ACCOUNTS TO THE PROPERTY OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 40; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA segments encoding monoclosal antibody - which binds to gpl2n and neutralises HIV. for treating AIDS, and for diagnosing and monicoring HIV infection infection infection and pisclosure: Page 73-74, 109pp; English.

Pisclosure: Page 73-74, 109pp; English.

Pisclosure: Page 73-74, 109pp; English.

Compared Mich sequence of FIDS VK (042707) - sequence differs from other FIDS VK sequence elsewhere in the specification) was compared With germline yeare Humwills (042706), showing 37-78 similarity. By nucleotide sequence analysis, FIDS appears to be derived from a member of the VK III subgroup gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NoV-1997 (first entry)
Manao DAA fragment v85.8 containing V-Kappa gene segment.
Immunoglobulin: lidht chain variable region: minilocus:
ISV-1900 SA-11051ins, unreastanged functional VK gene segment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 390,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marasco WA, Posner MR, Sodroski JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 Match 51.0%, Score 192, DB 7; De Local Similarity 85.4%; Pred. No. 1.50e-110; PS 258, Conservative 0. Mismatches 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1991; US-804652,
(DAND ) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q44224 Standard: DNA; 900 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       328..354
                                                                                                                                                         352..390
                                                                                                                                                                                                                                                     130..165
                                                                                                                                                                                                                                                                                                                                                        211..231
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10-DEC-1991; US-8046
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WPT: 93-214174/26
                                               misc_RNA
/*tag= c
/label= F105Vk
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/label= F105Jk
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P-PSDB; R38672
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/label= CDR1
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mat_protein
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375 acgeagletecaggeacoetglettlgletecaggggaaggaageececeteloetgeagg 434
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The V-kappa specific eligonalestide 25927 was used to probe a human placental genomic ENA library closed into lambdagment (Sp6/77).

DNA fragments containing V-kappa segments from positive phase clones were subcloned into plasmid vectors. Variable gene segments from the resulting rances were sequenced and functional clones were selected on the hasis of open reading frames, intest donor and acceptor splice sites and intest recombination sequences. The sequences obtained from four different plasmid clones were designated from four different plasmid clones were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4, Cape
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trans gene - used to produce useful antihodies by isotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= e
/note= "splicing and recombination signal sequence"
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                                                                                                                                                                                                                                                                 /note "splicing and recombination signal ?" exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             initiation codon, i.e. the start of the ORF:
the precise start point of the exon is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **tag= d
'note= "ORF not terminated by a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /number= 1
/note= "nucleotides 116-118 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
53..60
human light chain transgene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 A,
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17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
23-770-1992; US-974-68.
(GENP-) GENPHARM INT INC.
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WPI; 93-214169/26.
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                                                         Homo sapiens.
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375 acgeagtetecaggeaccetgtetttgtetecaggggaaagagecaccetetectgeagg 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 3, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig. 43, 296pp, English.

Human DNA fragments vk65.3, vk65.8 and vk65.15 (given in V8852-Q78855, respectively) each contain a V-kappa gene segment that can be used to form a complete human light chain minilocus transgene for expression in a nonhuman transgenic animal for heterologous antibody production. The deduced amino acid sequences of the V-kappa coding regions are given in RF928731 Sequence 900 BP; 220 A; 241 C; 201 G; 238 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic non-human animals producing heterologous or chimeric antibodies - for binding a pre-determined human antigen with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 900;
                                           Human V-kappa gene vk65.8.
Transgenic mouse: transgenic animal; antibody engineering;
variable region: light chain; minilocus transgene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 615 gcagtgtattactgtcagcagtatggtagctcacctcccac 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .Match 61.0%; Score 192; DB 12; L
Local Similarity 86 8%; Pred No 1 60e-110;
es 244, Conservative 0, Mismatches 34.
                                                                                                                                Location/Qualifiers
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[137]82 standard; DNA; 900 BP.
Q78854 standard; DNA; 900 BP
Q78854;
                                                                                                                                                                                                                                                                                                 /label- Recombination_signal
                                 07-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T37142;
14-APR-1997 (first entry)
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                                                                                                                                                                                                                  653..659
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misc_signal 672.680
                                                                                                                                                                                                                                                                                                                                                                                                                  US-161739.
                                                                                                                                                                                                                                                                                                                                                                 US-053131
                                                                                                                                                                                                                                                                                                                                                                                                US-155301
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09-MAR-1994; US-209741,
                                                                                                                                                                                                                                                                                                                                                                                 13-006762
                                                                                                   chimeric antibody; ss.
                                                                                                                                                                                                                                                                                                                                                 25-APR-1994; U04580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increased affinity
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                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                   26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                 22 - IUI - 1993;
                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1993;
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gocagtcagaagtgttagcagcagctacttagcctggta-ccagaagaaaactggcaggct 494
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Example 21: Fig 43: 94pp; English.

The present sequence is the variable kappa chain gene segment ontaining human DNA fragment, vk65:8, which was co-injected along with the human DNA fragments vk65:3, vk65:5 and vk65:15 into half day mouse embryo pronuclei, to generate an unrearranged light chain minitocus transgene. The resulting transgenic mice can be used for the production of heterologous (i e human) antibodies against specific antigens, this comprises immunising a mouse with a preselected antigen and collecting antigen binding heterologous human gamma immunoglobulins.
DNA fragment vk65.8, containing variable kappa chain gene. variable; kappa Châin, gene segment; human: DNA fragment; vk65.8; unrearranged; light châin; minilocus; transgene; transgenic; mouse: production; heterologous, antibody, gamma, immunoglobulin; ss.
                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of heterologous human immunoglobulin(s) - by immunising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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86 8%; Pred. No. 1 60+110;
vative 0, Mismatches 34;
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                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 A;
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                                                                                                 116..164
                                                                                                                                     352..650
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23-JUN-1992; US-904068.
16-DEC-1992; US-990860.
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wes 244, Conserv
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WPI; 96-383736/38.
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                                                                   Homo sapiens
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US5545806-A.
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Release 2 10 John F Collins, Ricromputing Pescarch Unit Copyright (c) 1993, 1994, 1995 university of Edinburgh, U K Distribution rights by IntelliGenetics, Inc

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Tue Feb 24 (08:05:51 1998: MasPar time 120:07 Seconds 668.183 Million cell updates/sec not generated Tabular output Run on:

(1-318) from US08844215.seq >US-08-844-215-17 318 Description: Perfect Score: N.A. Sequence: Sedausto.

GONGCAAGTIGGAAATGAAA 318 GONGGIIGAAGGIGAAGIIT 1 GAGGTGAGGGAGTGTGGAGG CICGAGIGGSICAGAGGIGG

TABLE default Gap 6 Scoring table:

333433 seqs, 126143548 bases x 2 Searched:

Dbase 9: Query 9

Nmatch STD

Minimum Match Ow Listing first 45 summaries Post-processing:

Database:

1:STS1 2.STS2 3:STS3 4.STS4 5.STS5 6.CTS6 7.STS7 9.STS9 9:STS9 10.STS10.1:STS1 12.STS12 13.STS13 14.9TS71 15.STS12 15.STS13 14.9TS71 15.STS12 15.STS12 15.STS12 15.STS13 15.ST

Mean 9.849; Variance 1.939; scale 5.079 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	00.4000.0
Score Match Length DR ID Description	CGAF_L
ID	100 60 HS1244859
Query Match Length DB ID	41.4
Query Match 1	255 83 5 237 74 5
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ALIGNMENTS

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07-50N-1997 (Release Wary turb: NEBCI Home sapiens cina clude 70541
57 similar to gh:x06764 iG KAPPA CHAIN PHECURSOR V-III PEGION (HUMAN):
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Contact: Wilson RK WashJ-Merck BST Project Washington University School of Medicine 4444 Forest Park Parkway. Box 8501. St. Louis. MO 63108 Tel. 314 286 1810. Email: MO 63108 Tel. 314 286 1810. Email: estimation wasti.edu This cleur is available republiyetre illungh ILNL, contact the INAGE Consortium (infolimage:lini.gov) for
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Eukaryotae: mitochondrial eukaryotes. Metazoa. Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae: Homo.
    standard; RNA; EST; 400 BP
HS1244850
AA456778;
92177199
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nacleuses ald bp mRNA EST 14-JUL-1997 ng69c07.s1 NCI CGAP Lip2 Homo sapiens cDNA clone 940044 similar to gab.MS4438 IC KAPPA CHAIN PPECTRSOP V-III PEGION (HUMAN);.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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further information. Trace considered overall poor quality Seq
primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 400;
                                                                                                                                                                                                                                                                           /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                 /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                     Sequence 400 BP; 90 A; 120 C; 106 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     Score 266; DB 60;
Pred. No. 0.00e+00;
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Email: Robert_Strausberg@nih.gov
                             Location/Qualifiers
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/clone="770541"
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Local Similarity 93.3%;
Nes 292; Conservative
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cDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                             /note*"Vector: pAMP10; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarcose gel, average insert size 600 bp. Peference: Krizman et al. (1996) Cancer Pescarch
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A-JUL-1997 (Rel. 52, Last updated, Version 2)
ngGG-O7 s1 NCT_GGAP Lip2 Home sapiens CDNA clone 940044 similar to
gb-M63478 IG KAPPA CHAIN PPECTIPSOP V-III PEGION (HUMAN);.
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Eukaryotae; mitochondrial eukaryotes, Metazoa; Chordata,
Vertebrata; Mammalia, Eutheria, Primates, Catarrhini, Hominidae;
  Jeffrey Medeiros, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 418;
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                                                                                                                      Consortium/LLNL at:
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/tissue_type="liposarcoma"
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Pred. No. 0.00e+00:
0: Mismatches 34: Indels 1: Gaps
                                                     Contact: Poper Strausberg Ph D Tel: (301) 404-1550 Email: Contact: Poper Strausberganh, gov Tissue Procurement: L. Jeffrey Medeiros, M.D. Michael P Fomer-Fluck M.D. D ChNA Library Properation: David P. Krizman. Ph D. ChNA Library Arrayad by: Greg Lennon. Ph.D. David P. Krizman. Ph D. ChNA Library Arrayad by: Greg Lennon. Ph.D. David P. Krizman. Ph.D. Green Emperation of Contact of Strausberghy Green Sequencing Center Clone distribution: NGL-GSAP clone distribution information can be found through the I M.A.G. B. Consortium/LNL at: Length: 1070 Std Www.bio.linl.gov/bbrp/image/image.html Insert Length: 1070 Std Sequence stop: 413.
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23-JUN-1997 (Rel. 52, Last updated, Version 1)
2035D05:r1 Soures ovary tumor NEHOT Homo sapiens CENA clone 739953
5' similar to gb:x06764 IG KAPPA CHAIN PPECHPSOH V-III PEGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapions (human)
Eukaryotae: mitochondrial eukaryotes: Metazoa: Chordata:
Vortebrata: Eutheria: Primates: Catarrhini: Hominidae: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="940044"
/clone_lib="NGI_3GAF_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Homo sapiens"
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AA479857;
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Local Similarity 98.8%:
Nos 277: Conservative
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Fumor Sene Index";
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LOCUS AA479857 242 kp mena EST 19-3BN-1997 DEFINITION ZU35b05.rl Soares ovary tumor NbHOT Homo sapiens chua elone 739953 5' similar to gh:X06764 IG KAPPA CHAIN PPECURSOP V-111 PEGION
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy.M., Le,N., Lennon,G., Marra.M.,
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Vertebrata, Mammalia: Eutheria, Primates, Catarrhin: Hominidae:
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                                                                                                                                     Contact: Wilson PK Washington University School of Medicine 4444
Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 285
B00, Fax. 314 286 1810 Email: estawatson wusti adu his clone is available royalty-free through LLNL: contact the IMASE Consortium (info@image.ilnl gov) for further information. Seq primer: -28ml3
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F5 4%; Score 211: PR 54; Longth 242;
Best Local Similarity 94:6%; Pred, No. 0.00e-00;
Matches 229; Conservative 0; Mismatches 12: Indole 1:
Krizman D., Kucaba T., Lary M., Lo N., Lennon G., Murra M.,
Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,
Theising H., White P., Wylle T., Waterston P., Wilson R.:
"WashU-NGI human EST Project".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="ovarian tumor"
/lab_host="DH10R (ampicillin resistant)"
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/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/clone="739953"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNE; contact the
IMAGE Consortium (info@image.ilnl.gov) for turther information.
Seq primer: -26ml3 rev2 ET from Amersham.
Location/Qualifiers
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01-JUN-1997 (Pel. 52, Last updated, Version 1)
01-JUN-1997 (Pel. 52, Last updated, Version 1)
5. similar to gb-z11R94 IG KAPPA CHAIN PPECHRSOP V-III PEGION (HUMAN);
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, E., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
                                                                                                                                                                                               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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<1..>242
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                                                                                                                                                                           Washington University School of Medicine
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Pred. No. 0.00e+00.
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HS1236090 standard; RNA; EST; 269 BP.
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94.68,
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                                                                                          Unpublished (1997)
                                                                                                                                              Contact: Wilson RK
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AA476303 171 bp mPNA EST 19-TUN-1997
2w29d09.s1 Soares ovary tumor NbHOT Homo sapiens CDNA clone 770705
3' similar to gb:x06764 IG KAPPA CHAIN PPPCHESOR V-III PFGION
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Hillier, L. Allen, M. Rowles, L., Dubuque, T., Geisel, G., Tost, S., Krizmen, D., Kurcabe, T., Lary, M., Le. N., Lennen, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                            Contact: Wilson RK Washt-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Mn 63108 Tel·314-286 1800 Fax: 314-286 1810 Enail: Gest-Wastson wustl.edu This cione is available royalty-free through LLNL; contact the IMAGE Consortium (info@image llnl gov) for further information. Seq primer: -28m13 rev2 ET from Amersham. Rey
                                                                 Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wilson R.; Theising B., Washu-Merck EST Project 1997";
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae:
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/sex="Female"
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Unpublished (1997)
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                                                                                                                            This clone is available royalty-free through LLNL : contact the IMAGE Consortium (infolimate.llnl.gov) for further information. Seq primer. 41ml3 fwd. ET from Amersham. Location/uslifiers
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23-JUN-1997 (Rel. 52, Last updated, Version 1)
28-JUN-1997 (Rel. 52, Last updated, Version 1)
28-JUN-1997 (Rel. 50-20)
37 similar to qb-X06764 iq KAPPA CHAIN PRECIDED V-III PEGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S. Kriman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Thisling B., White Y., Wylle T., Waterston R., Wilson P., Unpublished.
                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501. St. Louis, MO 63108
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/lab_host="HHOB (ampicillin resistant)"
complement(<1..>171)
/dh_xref="GDB-5980579"
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Eukaryotae, mitochondrial eukaryotes; Metazoa: Chordata;
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/sex="Female"
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Rest Local Similarity 96.5%: Pred. No. 1.42e-255:
Matches 165: Conservative 6: Mismatches 5:
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AA476303;
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                                                                                                             Email: est@watson.wustl.edu
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                   Contact: Wilson PK
                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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/noted-normovary: Vector: p1713D (Pharmacia) with a modified polylinker; Site_1 Not_1: Site_2. Eco RI. 1st strand coDA was primed with a Not_1: Site_2. Eco RI. 1st strand coDA was primed with a Not_1 - oligo(df) primer [5'] double-stranded cDNAwas size selected. ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not_1 and cloned into (Pharmacia). Library constructed by Bento Soares and
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5' similar to gb:M12742_cds1 IG KAPPA CHAIN PFECURSOR V-11' FFCTOR
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Hillier, L. Allen, M., Enwiehl, Cubuque, T., Telst, B., Str.S.,
Kuraba, T., Tary, M., Le. N., Lennon G., Marra, M., Marrin, J.,
Monre, B., Schellenberg, K., Steptoe M., Tan, F., Theising, H.,
White, Y., Wylle, T., Waterston, K. and Wilson, R.,
WashJ-Merck ESI Project 1997
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Fax: 314 286 1810
Examil: est@watson.wustl.edu
This clone is available royalty-free through LINL : contart the IMAGE Consortium (info-winnage iln gov) for further information. Song primor. "PREL" from Amersham
High quality sequence stop. 161.
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae:
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available royalty-free through LLNL ; contact the IMAGE Consortium (info@image llnl gov) for further information Seg primer: -4lml3
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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//isex femas.
/lab_host-"DH10B (ampicillin resistant)"
complement(<1...)771)
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Sequence 171 BF: 36 A; 58 C; 45 G; 32 T; 0 other:
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Pred. No. 1.42e-255;
0: Mismatches 5;
                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                           Location/Qualifiers
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/clone="770705"
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WashU-Merck EST Project
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Local Similarity 96.5%;
Nes 165; Conservative
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AA464224
g2189108
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Gaps 3;
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13-JUN-1997 (Rel. 52, Last updated, Version 1)
18-JUN-1997 (Rel. 52, Last updated, Version 1)
18-JUN-1997 (Rel. 52, Last updated)
18-JUN-1997 (Rel. 52, Last updated)
18-JUN-1997 (Rel. 52, Clast updated)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 324;
                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                            /clone="810346"
/clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 148; DB 16; L
Pred. No. 3.49e-243;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                         /tissue_type="ovarian tumor"
                                      /organism="Homo sapiens"
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Location/Qualifiers
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Matches 192; Conservative
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                               Length 324;
                                                                                                                                                                                                                                                                                                                           0; Mismatches 14; Indels
                                                                                                                                                                                                               /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                      /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                Sequence 324 BF; 68 A; 102 C; 82 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                          Score 148; DB 63; I
Pred No 3.49e-243;
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             /organism="Homo sapiens"
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Email: Robert_Strausberg@nih.gov
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                     /sex="Female'
                                                                                                                                                                                                                                                                                               46.58;
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               //cinnise="Netor aspines"
/note="Vector: pample: mRNA made from liposarcoma, cDNA
made by oligo-dr priming wan directionally cloned
Size-selected on agarcse gel, average insert size 600 bp
Reference: Krizman et al. (1995) Cancer Pesearch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ACCOMMENTATION STANDARD THE THE CONTRACT AND ACCOMMENTATION OF THE CONTRACT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberginih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D. Ph.D. GDN Library Preparation: David B. Krizman Ph.D. Town Library Arrayed by Greg Lennon. DNA Sequencing by. Washington University Senome Sequencing Center Clone distribution: NGI-GSAP clone distribution information can be waw-bio.lini.gov/bbrp/image/finage.html Insert Length: 922 Std Error: 0.00 Seq primer: -40ml3 fwd ET from Amersham
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LOCAL-1997 (Fw. 52. Last updated, Version 2)
ng61b01 si NCI-CRAP_LIP2 Home sapiens CDNA clone 939241 similar to qb:XO6754 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN):.
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Vertebrata; Mammalia; Būtheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                  Length 217;
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/clone=10:9241"
//clone=10:9241"
//issup=1ypd="liposarroma"
//ab_host="DH108"
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/tissue_type="iiposarcoma"
/lab_host="DH10p"
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HS1284569 standard: RNA; EST; 217 BP.
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adaptors, 5 cycles of PCR applied to the chNA with an adaptor specific primer, and the resultion PCR product subcloned into pAMP10 by the UDS-cloning method (Life Technologies). Average insert, Size is 600 kg.N.TE. Not directionally cloned. This library was constructed by Davidirectionally cloned.
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62-VUL-1997 (Rel. 52, Last updated, Version 5)
62-VUL-1997 (SAP FIL Homo sapiens CDNA close 1009353 similar to gb-211894 IG KAPPA CHRIN PPETUPSOP V-III PEGION (HUMAN):.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Emai...
M.D., Robert_Strausberg*anh.gov Tissue Procurement: W. Marston ilnehan.
M.D., Podrigo Chuaqui. M. D. Michael Emmert-Buck. M.D., Ph.D. cDNA
Library Proparation: David B. Kritman, Ph.D. cDNA Library Arrayed
Washington Systems Inc., Gred Lennon, Ph.D. DNA Sequencing to Washington University Genome Sequencing Center Clone distribution.
NCI-CGAP clone distribution information can be found through the
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Error: 0.00 Seg primer: -4lml3 fwd. ET from Amersham High quality
sequence stop: 250.
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Tumor Gene Index":
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini: Homimidae;
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                                                                                               Length 217;
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                              57 5 48 1, C other;
                                                                                         Score 143, DB 67, 1
Pred, No. 6.95e+233;
0: Mismatches 14;
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/sex="Male"
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/lab_host="DH10B"
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HS1145z81 standard: PNA; EST: 250 BP.
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44 A. 75 C.
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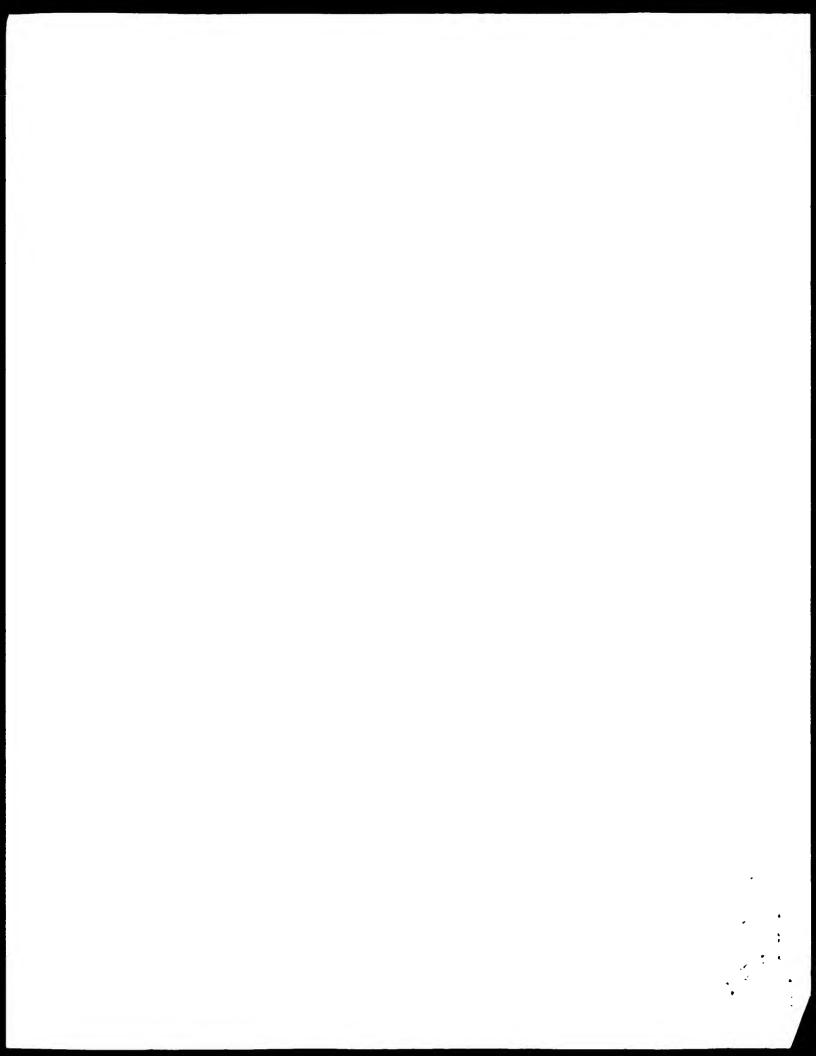
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCT-CSAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Ahlchael Emmert, Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Fh.D. CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS AA225858 250 kp mPNA EST 20-JUN-1997 DEFINITION nc27d05.sl NCI_CGAP_PrI Homo sapiens cDNA clone 3490 similar to gb-211894 iG KAPPA CHAIN PRECURSOR V-III PEGION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata, Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
                                                                                                                                                                      90 cgcagnetecaggcaccetgtetttgtetecaggggaaggaggecacceteteetgcaggg 149
                                                                                                                                                                                                                                                                  150 ccagtcagagtgtcagcagcagatacttagccctggtaccaacaaaaacctggccaggct 209
                                                                                                                                                                                                                                                                                                                 68 CCAGTCAGAGTGTTAGGAGCAACTAGTTAGGG-TGGTAGGAAGAAAAAAAAGGTGAGGGT 126
                                                                     Score 135; DB 49; Length 260;
Prod No 1.850-216;
0, Mismatches 13; Indels 1; Gaps
                                                                                                                                                                                                                    8 CGCAGICICCAAGGCACCTGICITIGICIACCAAGGGGAAAAAAACACCACCCTGCIGCTGCGGGGG 67
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 260 RP; 57 A; 84 C; 66 G; 49 T; 4 other;
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Location/Qualifiers
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//lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                     Ouery Match
Best Local Similarity 91 6%;
Matches 153, Conservative
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Unpublished (1997)
  >260
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CDNA Library Fregaration: David B. Krizman, Ph.D.
CDNA Library Arrayed by Greg Lennon. Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NoT-CGAP clone distribution information can be
found through the I M A G B Consortium/LLNL at:
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//organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Homo color: Theorems of the colored c
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Vertebrata, Mammalla, Eutheria, Frimates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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          Length 250;
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Score 135; DB 27; I
Pred No. 1.85e-216;
O. Mismatches 13.
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/lab_host="DH10B"
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Emmert-Buck, M.D , Ph D
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     Query Match 42.5%;
Rest Local Similarity 91.6%;
Matches 153; Conservative
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Best Local Similarity
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Releas Copyri	e 2.1D John F. Collins, Biocomputing Research Unit. oht (c) 1993, 1994, 1995 "riversity of Edinburgh, " x Distribution rights by IntelliGenetics, inc.
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
Run on:	Tue Feb 24 08:09:15 1998; MasPar time 411 0A Seconds 1088 498 Million rell indates/sec
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Title: Description:	>US-08-844-215-18 (1-315) from US08844215.seq
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Scoring table:	TABLE default Gap £
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Searched:	430251 seqs, 710217276 bases x 2
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Database:	DEW7 BCT 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG3 7:HTG HTM2 10:HTM3 11:HNV1 12:HNV2 13:GPG 14:MAM
Database:	DECKELL 17 FROIT 19: FROIT
Database:	11 116:VRL2 117:VRL3 118:VRL4 119:VPL5 120
Database:	21.VPL. 122:VPL8 123:VPL9 124:VRL10 125:VRL11 bank-new7 26:8CT 127:CEN 128:HTG1 129:HTG2 130:INV 121:MAM
Database:	77 137 PHG 134 PLB1 135 PLB2 136 FEXT 13 20 139-SYN 140-11NA 141-VPL 1201 143:part2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

Mean 10 014: Variance 4 688; scale 2,136

Statistics:

and is derived by analysis of the total score distribution.

ription Pred. No	sapions mPNA for ro 9.976-19 man immunoglobullo 4.336-19 sapiens mRNA for im 2.026-18 sapiens mPNA for ka 7.456-18	sepiecs (BR1) re 7.45e-18 sepiecs (BR1) re 7.51e-18 anti mables vir 1.28e-17 lens mRNA for im 1.28e-17 anti-sables vir 1.9e-17 anti-sables vir 1.9e-17	Sapiens (clone p 5.980-17 hepatitis R sur 1.980-17 sapiens MNAA fra 5.980-17 sopiens (clone im 4.640-17 iens mRNA for im 4.640-17 gormline [qr. % 2.150-17 sapiens (clone im 1.670-18 anti-ssDNA anti [1.670-18	recell receptor V 1878-18 sapiens greatline in 1296-16 kappa 198 monoc 1296-18 sapiens (cell in 1296-18 germine V(kapp 1296-18 ig rearranged) 1296-16	itens Iq acemiline 129 quermiline 19K ch 129 piens mkNA for 12 773 imens for 12 773 imensoqlobulin 7.73 ifa rearranged a 7.73 ifa rearranged a 7.73 ifa rearranged bit if rearranged a 7.73 ifa rearranged bit ifa rearranged a 7.73 ifa rearranged bit ifa rearrang	piens makk for to 1,460-16 piens makk for in 5,980-16 sapiens (8190, 1 4,50-16 sapiens (6100, 1 4,50-16 sapiens (6100, 1 4,50-16 for immunosibility (20-16 for immunosibility (20-16 for immunosibility (20-16
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DEFINITION	ed Ig kappa light chain
	(III.41).
ACCESSION	X-12472
CIN	9441412
KEYWORDS	immunoglobulin; J-seqment; kappa light chain; V-region.
SOURCE	human.
OPGANISM	HOW OWN
	Eukaryotae, mitochondrial eukaryotes, Motazoa, Chordata:
	Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 352)
AUTHORS	Zachau, H.G.
TITLE	Direct Submission
JOURNAL	Submitted (26-APR-1993) H.G. Zachau. Institut fuer Physiologische
	Chemie, der Universitaet Muenchen, Schillerstr 44, 8700 Muenchen z.
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/translation-LiuMLpDTTGETVMTQSPATLSVSPGEBATLSCPASQSVSSNLA
WYQQKPGQAPPLLIYGASTPATGIPAPFSGSSSSTEFTLTISSLGSEDFAVYYCGQYN
2 (bases 1 to 352)
Klein,P., Jaenichen,P and Zachau,H G
Kressed human immunoglobulin Kappa genes and their hypermutation
Eur. J. Immunol. 23 (12), 3248-3252 (1993)
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Submitted (18-FER-1997) Division of Molecular Immunology,
Department of Pathology, Cornell University Medical College, 1300
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1 (bases 1 to 324)
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Human immunoglobulin light chain mRNA, partial cds.
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/clone_lib="lambda zap II phage library"
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Pred No 8 970-192;
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                                                                                                                              /organism="Homo sapiens"
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RLLIYGASTRATGIPARFTGSGSGTEFTLTISSLGSEDFAVYYCQQYNKWPLAFAGT
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2200 Copenhagen N. DENMARK
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Vertebrata, Eutheria, Frimates, Catarihini, Hominidae, Homo.
1 (bases 1 to 388)
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York Avenue, New York, NY 10021, USA
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                                                                                                                                                                                                                                                                                                 /map="2p"
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1 (bases 1 to 322)
Mariettee, X., Tsapis, A and Brouet, J C
Nucleotidic Sequence Analysis of The Variable Domains Of Four Human Monoclonal IqW With An Antibody Activity To Myelin-Associated
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Immunopathologie, Hopital, Saint-Louis, 1, avenue Claude Vellefaux,
Paris, 75010, France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 aqtqgqtctqqqahaqaqtthoactctnahoatcagoagnaqnntqcagthtqaagattttqca 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 AGIGGICIGGGAÇASAAIICAÇICICACICICAGGAGGIGGAGICIGAGGACTITGCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 dittailaniginagoacialaalaliiggnogotonoggaggaggaacgaggtg 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 anghagtetneagneacetgtetgtetgtetetgaggggaaaggggeaegeetetentgeagg 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 grossprospagitisgosgescitsgovigaecettsgovigatsecagesgaecetggocaggetoec 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GCCASTCASASIGICGSIAACAATITAGTTIGGTATCAGCAGAAACCTGGCCAGGCTCCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 AGGCTGCTGATTTATGGTGGAAAGACGAGAGGGAGTGGTAGGAGGAGGAGAGAGGGTGAGIGGG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sake
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria, Primates, Catarrhini, Hominidae; Homo.
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H.sapiens mRNA for immunoglobulin V-region of Kappa chain.
218330
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Pred. No. 2.02e-186;
0; Mismatches 31; Indels
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                                                                                                    /cell_type="mononuclear cells"
/chromosome="2"
/map="pil-12"
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/tissue_type="blood"
                              /isolate="individual La"/tissue_type="blood"
/organism~"Homo sapiens"
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117 c 103 q
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Local Similarity 89.9%;
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/cell_line="Epstein-Barr transformed lymphoblastoid cell

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The progeny of a single virgin B cell predominates the human recall B-cell response to the capsular polysaccharide of Haemophilus influenzae type b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION H.Sapiens mRNA for kappa immunoglobulin light chain (V-J-C region) clone HSSIM002).
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                                                                                                                                                                                                                                                               Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata:
Vortebrata: Eutheria: Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 345)
Barington,T., Hougs,L., Juul,L., Madsen,H.C., Ryder,L.P.,
Heilmann,C. and Svejgaard,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constant region; immunoglobulin; immunoglobulin kappa chain;
Immunoglobulin light chain; joining region; variable region.
                                                                                                                                                     vuery Match 76.8%; Score 242; DB 91: Length 322;
Best Local Similarity 89.3%; Pred. No. 7.45e-183;
Matches 275; Conservative n. ...
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/cell_type="B lymphocyte"
/clone="SIM002"
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                                                        /note="VK iIIa family" /product="kappa chain"
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Barington, T.
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Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 agigggicigggacagagitcacicicaccaicagcagccigcagictgaagaittigca 252
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 384)
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                                                                                                                                                                                                                                                                                                                                                           Score 242, DB 93, Length 345, Pred. No. 7.45e-183, 0; Mismatches 33; Indels (
/note="variable region and joining region"
/product="immunoglobulin kappa light chain"
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/clone_lib~"lambda cap II phage library"
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/product="Ig kappa light chain (VJ)"
/db_xref="PID:q441375"
                                                                                                           /gene="V-kappa-L2 and J-kappa-1"
325..>345
/note="constant region"
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Best Local Similarity 89.3%;
Matches 275; Conservative
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/evidence=experimental
/label=V_region
/product="immunoglobulin light chain"
/db_xref="PID:g306985"
/translation="ETVMTGSPATVSVSPGFFATLSGPASGSVTTNLAWYDGKPGOAF
/translation="MEAPAQLFLLLLWLPDTTGEIVMTQSPATLSVSPGERATLSOR
ASQSVSSNLAWYQQKPGQAPTVLIYGASTRATGIPARPSGSGSGTEFTLTISSLQSED
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Vertebrata; Butheria; Primates; Catarrhini; Hominidae: Homo.
1. (bases 1 to 322)
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                                                                                                                                                                 /product="Ig kappa light chain (VJ)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 242; DR 91:
Pred No 7.45e-183;
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                                                                                FAVYYCQQYNNWPYTFGQGTKLEIKR"
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/cell_type="B-cell"
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115 c 97 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 89 3%;
Matches 275; Conservative
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346..384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 qaqatcaa 380
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/clone="mAb50"
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Matches 273; Conservative
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chain: joining region: variabie region
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/isolate-"PBMC pooled from ten healthy adults"
/tissue_type-"blood"
                                                                                    Length 322;
                                                                                    Sidre 239; DB 99; J
Pred No 3 51e-180;
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/chromosome="2"
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/translation="EIVMIGSPALLSVSPGERALLSCRASGSVSSNLAWYGUKFGUAP
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7631, Rigshospitalet, National University Hospital, Tagensvej 20,
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                                                                                                                                                                                                                                                                                                                193 agtgggtetgggacagagtteaeteteaecateageageetgeagtetgaagattttgea 252
                                                                                                                                                                                                                                                                                                                                       80 egcagtetecagecaceetgtetgtegtegteggagaaagagecaeeeteteetgeaggg 139
                                                                                                                                                           73 gccagtcagagtgttagcagcaacttagcctggtaccagcagaaacctggccaggctccc 132
                                                                          13 acgcagtctccagccacctgtctgtgtctccaggggaaagagccaccctcctgcagg 72
                                                                                                                 7 ACGCAGICITCCAGCCACCCIGICITGITGITCICAGGGGAAAGAGAGCTCCCICITCCIGCAGAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 393)
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                                                                                                                                                                                                                                                                                                                                                                                           253 gtttattactgtcagcagtataataactggcagatcaccttcggccaagggac 305
                                                                                                                                                                                                                                                                                                                                                                                                               247 GITTATITCIGICAACACIAIAGIACCIGGCGGCGCTCACIIICGGCGGGGGAC 299
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/isolate="PBMC pooled from ten healthy adults"
                                     Indels 0,
  Length 324;
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Score 235; DB 96; I
Pred. No. 1.28e-176;
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Pred No 1 28e-176;
                                   O, Mismatches 29;
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1 Similarity 90.1%;
264, Conservative
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Best Local Similarity 88 3%;
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/product="anti-ssDNA antibody light chain variable region"
/db_xref="PID:g1773057"
/translation="EIVWT@SPATLSVSPGERATLSCRAS@SFTSKLGWYQQKPGQAP
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Human anti-ssDNA antibody light chain variable region (Humkv328h5)
UR2258
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                  260 gigggictgggacagagitcactcicaccatcagcagccigcagiccgaagaittigcag 319
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 324)
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140 ccagtcagagtgttagcaacaccttagcctggtaccagcagagacctggccaggctccca
                                                                             200 ggetecteatetgatgettecaccagggecaetggtateccagecaggetatgtggea
                                                                                                                                                                                                   188 GTGGGTCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGTCTGAGGACTTTGCAG
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Submitted (14-DEC-1996) Immunology Pesearch Laboratory.
Hospital, 4400 Wornall Road, Kansas City, MO 64111, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suenaga, R. Molecular analysis of human anti-ssDNA antibody
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Best Local Similarity 88.0%; Pred. No. 9.93e-176;
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/qene="Humkv328h5"
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/db_xx=f-"pip-gi48204"
/trauslation="MAFLTQSPSTLSVSPSEBATLSCPASQSVSNNLAWYQQKSGQAP
RLLIYGASTRATSIPAFFSGSGSGTEFTLAISGLUSEDFAVYYOUHINNWPPSSFGGG
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Institute for Pesearch on Aging, University of California at San
Diego, La Jolla, CA 92093, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae, mitochondrial eukaryotes; Metazoa, Chordata, Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 321).
Sasano,M., Burton,D.P. and Silverman,G.J.
Molecular selection of human antibodies with an unconventional bacterial B cell antigen.
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                                                                                                           257 gittattactgitcagcagtataataataactggcottigacgitoggcoaagggaccaaggig 312
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                       12.1 AGGG1 GG1GAT11A1GG1GG1AAAAYAGG7AAAAGG1GAGAGGG1GAGAGAGAGAGTGGAGTGGG
                                                                   193 hgtjagfirtgjgacagagttiooctctcacicatcagcagictioatjiaatctgaagattttgion 252
                                                                                                                                                                                                 Human clone 0-16VL immunoglobulin light-chain mRNA V-J region, partial cds.
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Homo sapiens CDNA to mRNA
Homo sapiens
/product*"immunoglobulin light-chain V-J region"
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/tissue_lib="pcomb3-ITO (M13 phagemid vector)"
/clone="0-16VL"
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Pred. No. 9.93e-176:
0: Mismatches 22; Indels
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/dev_stage="adult"
/sex="male"
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Best Local Similarity 92.18;
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Silverman, G.J.
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Vertebrata: Eutheria: Primates: Gatarrhini: Hominidae: Homo. (bases 1 to 32)
Ohlin.M., Sundquist.V.A., Mach.M., Wahren.B. and Borrebaeck.C.A.
Fine specificity of the human immune response to the major neutralization epitopes expressed on cytomegalovirus qp54/215 (4H).
If Virol. 67 (2), 703-710 (1903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="this sequence has been corrected for primer equaded
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/translation="EIVLTGSPATLSLSPGERATLSCRASGSVSSYLAWYOUKPGOAP
RILIYDASNRATGIPARFSGSGSGTDFTITISSLEPPIPAVYYYOORSWPITFGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS HUMIKCVI 321 bp mRNA PRI 92-MAY-1995
DEFINITION Homo sapiens (clone pAG21B) 19 kappa chain mRNA, V-region, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin light chain; kappa-immunoglobulin; variable roqion.
Homo sapiens (clone: pAG21B) cDNA to mPNA.
Homo sapiens
                                                                                                                                                                                          187 agtggcagtgjatotgggaacagagttcactstogccatcagcajorigougi 1456 | 1466 | 1667 agtgroups | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868 | 1868
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Light chain shuffling of a high affinity antibody results in difft in epitope recognition
96174997
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Search completed: Tue Feb 24 08:18:36 1998 Job time : 561 secs.
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/translation="AELTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPR
LLIYDASNRATGIPARFSGSGSGTDFTLJISSLEPEDFAVYYCQQRSWMPPSFGGGTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody variable domain; hepatitis R surface antigen antibody
Homo sapiens (individual_isolate JM) (library: JM14) blood cDNA to
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Human hepatitis B surface antigen antibody variable domain mPNA,
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Sebedee, E., Barbas, C.F.III, Hom, Y.-L., Caothien, F., Graff, R., DeGraw, J., Pyati, J., LaPolla, F., Burton, D.F., Lerner, F. A. and Thornton, G.B.
                                                                                                                                                                                                                            193 agtgggtctggggacagacttcactctcaccatcagcagcctagagcctgaagattttgca 252
                                                                                                                                                                                       187 AGTGGGTCTSGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGTCTGAGGACTTTGCA 246
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/product*"hepatitis B surface antigen antibody"
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Pred. No. 5.98e-174;
0; Mismatches 41; Indels
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/tissue_lib="JM14"
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Homo sapiens (library: BMHIV) male adult bone marrow obna to mRNA
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Vertebrata: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 373)
Barbas, C.F.III., Callet, T.A., Poben, P., Rinley, T., Amberg, W., Hoekstra, D., Cababa, D., Jones, T.M., Williamson, R.A.N., Pilkington, G.R., Haigwood, N.L., Satterthwait, A., Sanz, I. and
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                                     181 AGIGGCAGIGGGICTGGGACAGAATICACICTCACCATCAGCAGCCIGCAGICTGGAGGAC 240
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/tissue_lib="PMHIV"
117 c 92 g 84 t
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/cell_type="B-cell"
/dev_stage="adult"
/sex="male"
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J. Mol. Biol. (1993) In press
Location/Qualifiers
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Homo sapiens mRNA fragment.
L09087
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MACH THE STATE OF	SUMMARIES Tength DB ID Description	5 400 116 AA456778 2427f11 11 Scores over 3 46 25 AA300582 ES113427 Testis tomest	3 349 59 AA379044 EST91999 Skin tumor 3 (1 403 73 AA345486 EST51505 Gall bladder (5 405 52 AA360223 EST69341 Lymph sode 1 0	1 326 24 AA290311 ESTING4:1 Faboreas to C	5 363 55 AA367405 EST78511 Pancreas ton (277 24 AA295377 EST190538 Pancreas tu	289 37 AA327218 EST30586 Colon I Homo (7 253 25 AA295941 EST101165 Thymas III (7 294 55 AA366461 EST77408 Pandreas tum 6	1 264 24 AA295154 ESTICO323 Fancreas to S	o 200 87 AA434001 DAZDIDLIT SOBRES OVA LIGAGLEDI o ook hom aansen aansen aansen aansen o	283 53 AA361678 EST70983 T-cell lymph 1.540-240	5 209 100 AA292499 zt30all.rl Soares ova 1.940-23	7 238 62 AA383914 EST97387 Thymas II Bo 3,160 292	5 260 71 AA225858 nc27d05.s1 NC1 CGAP P 9	D43 P3 AA422182 SWSTDOK T SOUTH	243 99 AAI84594 LILZAIL I SOSIES 113	244 86 AA430565 2022509 1 Soares one	4 255 99 AA284552 ztz4g03.ri Soares dva 4	4 345 39 AA335086 EST39457 ESCENDAGES to 4,29e-191	7 253 100 AA291691 at39610 tl Spares 678	4 255 100 AA292047 zt50al2.rl Scores ona 5.87e-18	413 27 AA301347 EST14279 Testis tumor	5 335 33 AA318377 EST20620 Spleen I Hom 7	d son 2/ AASCILOI ENITAIGI TOSCIS COMOT CO 240 79 AAACCI150 GOURGE CO 3	3 357 53 AA361497 EST71040 T-cell lymph	5 442 80 AA405415 zu55d02.rl Soares ova 1	3 382 25 AA295786 EST100987 Pancreas tu	AANTOLI BOLISBOATTI NOI COAF F. C.	363 26 AA300651 EST13764 Testis tumor 1	2 303 26 AA300789 EST13648 TWS*1: * 307 1	2 398 94 AA423447 ve80a93 rl Spares mou]	240 ol AA419046 HTT32-09 TJ Spares coa	A LAKE BE AAABOOARY DALOHILLING CODE OUG CODE ABOUT OF AAADOORS OF SAATISTEEN TOTAL OF THEORY OF	328 33 AA318620 EST20808 Spleen I Hom J	\$ 323 37 AA327357 ESTACTOR COLOR I HOMO		8 400 kp mPNA EST 06-10N-1497	irl Sobres evary tager NEHOT Hemi sapiens of Jarit, at XPESET is MARRA PHAIN REFITESIS VI		m o		,	piens tae, mitumbundrial eukaryotes: Metazwa, Chuidala:	ata, Mammalia, Eutheria, Primates, Catarrhini, H	es 1 to 400)	.L., Allen,M., Bowles,L., Dubuque,T., Geisel.G., T. Taco M. Lo N. Tonnon G. Marra M. Martin F	ochollophora K stantos Maria d Theising B	CONTRACTOR OF THE PROPERTY OF
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EST13427 Testis tumor Homo sapiens CDNA 5' end similar to
immunoglobulin kappa light chain, VJ regions
                                                         Washu-Merck EST Project
Washington University School of Medicine
4444 Forest tark Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 266; DB 116; Length 400;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 20;
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                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 g
                                                                                                                                                    Email est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone-"770541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex-"Female"
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Best Local Similarity 93.3%;
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   Unpublished (1997)
                                         Contact: Wilson PK
                                                                                                                                                                                                                                                                                      400
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Adams, M. D., Kerlavage, A.R., Fleischmann, P. D., Fuldner, R.A.,
Bult, C.J., Lee, M.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, D., Sutron, S., Blake, J. B., Krandon, P. C., Man Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M. D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A. Gnehm, C.L., Hanna, M.C., Hedblom, E. Hinkle P. S. Jr.
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Pyder, S.E., Scott, J.I., Saudek, D. M. Shirley, P.
Small, K.V., Spriggs, T.A. Interback, T.P., Weidman, J.F., Liy, Y.
Bednarik, D. P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Bednarik, D. P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Welly, F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Praser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initial assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                             Eukaryotae, mitochondrial eukaryotes, Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria, Primates; Gatarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: testis; Vector: pBluescript SK-: Site_1:
EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 tectnatetatggtgeatecageagggeeactggeateceagaeaggtteagtggeagtg 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research
9712 Medical Center Drive, Pockville, MP 20850 USA
Tel: 3018699056
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<1 .>346
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Contact: Kerlavage, AR
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nes 282; Conservative
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Homo sapiens
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AUTHORS
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8 Adams, M.D. Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A.,

8 Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A.,

8 Ruit, C.J., Leew, N.H., Kirkness, E.F., Wehnstock, K.G., Grayne, T.D.,

8 White, C.J., Leew, H.D., Brandon, F.C., Man-Wai, G.,

8 Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

8 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

9 Clayton, P.A., Cheby, C.L., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

8 Moreno-Palanques, P.F., McDonald, L.A., Mauyen, D.T., Pelligrino, S.M.,

8 Phillips, C.A., Meyer, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

8 Man, I.K., V., Spriggs, T.A., Urterback, T.P., Weidman, J.F., Liy, Y.,

8 Man, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, K.,

8 Kozak, D., Engy, P.F., Ming, J., Li, H., Meissner, P.S., Olsen, H.,

8 Raymond, L., Wail, Y.E., Wing, J., Li, H., Meissner, P.S., Olsen, H.,

8 Raymond, L., Wail, Y.E., Wing, J., Li, H., Meissner, P.S., Olsen, H.,

8 Fraser, C.M., and Venter, J.C.,

8 Initial assessment of human gene diversity and expression patterns
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Vertebrata, Mummalia, Eutheria, Primates, Catarrhini, Hominidae,
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                                                                                                                                                   end similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rockville, MD 20850 USA
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EST91999 Skin tumor I Homo sapiens CENA 5' +ση
immunoglobulin kappa light chain, VJ regions.
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91.7%: Pred. No. 0.00e+00:
vative 0: Mismatches 23
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/note="Organ: skin: Vector: |
EcoR: Site=2: xho!"
/clone=lib="Skin tumor I"
/dev_stage="adult"
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Tel: 3018699056
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Best Local Similarity
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334 aatcaaa 340
                                       312 GATCAAA 318
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                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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10 (bases 1 to 403)

11 (bases 1 to 403)

12 Adams.M D. Kerlavage,A P. Fleischmann.R.D., Fuldner.R.A.,

13 Rulf.C J. Lee,N H., Kirkness.E. F. Wenfastock of Gocayne.J.D.,

14 White. Sutton.G. Flake.J.A. Hrandon.P C., Marwal.C.,

15 Clayton,R.A., Cline.T.R., Cotton,M.D., Earle-Hudhes.J., Fine.L.D.,

16 Clayton,R.A., Cline.T.R., Cotton,M.D., Earle-Hudhes.J., Fine.L.D.,

17 Clayton,R.A., Cline.T.R., Cotton,M.D., Earle-Hudhes.J., Fine.L.D.,

18 Clayton,R.A., Glehm.C.L., Hanna.M.C., Hadblom.E., Hinkle,P.S.,Jr.,

18 Clayton,R.A., Glehm.C.L., Hanna.M.C., Hadblom.E., Hinkle,P.S.,Jr.,

18 Morriel.P., Spriggs.T.A., Morriel.A., Nguyen,D.T., Pelligrino.S.M.,

18 Cad.L., Spriggs.T.A., Utterback.T.R., Weidman.J.F.,L.Y.,

19 Bednarik.D.P., Cao.L., Cepeda.M.A., Follom. L.A., Collins.E.J.,

19 Ednarik.D.P., Greene.J.M., Gruber.J., Hudson.P., Kim.A.K.,

10 Kozak.D.L., Kunsch,C., Hungjun.J., Li,H., Meissner.P.S., Clsen.B.,

10 Raytondl.L., Well.Y.F., Wing.J., Xu,C., Yu,G.L., Ruber.S.M.,

10 Dillion,P.J., Fannon,M.R., Rosen.C.A., Haseltine.W.A., Fleids.C.,

10 Eraser.C.M. and Venter.J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA345486 403 bp mPNA EST 21-App-1947
ESTS1505 Gall bladder II Homo sapiens CDNA 5' end similar to
similar to immunoglobulin kappa light chain, V region (GF-X06764).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: arkerlavitign.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Homan Gene
lodex (http://www.ligr.org/tdb/hgl.html)
Seq primer: MI3 Reverse.
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Vertebrata, Mammalia, Eutheria, Primates, Catorrhini, Buminidue;
                                                                                                                                                                                                                                                                                                                                                                                                                                   127 COCASSCIDITICATOTATASTATASCAMANAMATASCATOCCAMACASTICAGI 186
                                                                                                                                                                                                                                  208 ggcagtgggtctgggacagacttcactctcacdatcaacagactugagrotuwamantit 247
                                                                                                                                                                                                                                                                                                            187 GRUAGITGGGIATOTGGGANASACTITGACTOTGACTATGAGGAGGGGGGGGGGGGGGGAAAGTTTI 246
                                                                                                                                                                                                                                                                                                                                                                                          268 gcagtatattactgtcaagcagtatggtagtttacccctcaantttcggccctggggaAc 327
/note="Organ: gall bladder: Vector: pBinescript.SK-:
Site_1: EcoRI: Site_2: XhOI"
/SIne_1: EcoRI: Site_2: XhOI"
/Sex="female"
                                                                              148 cccaqqctcctcatctatggtgcatocaycaqqqccactoqqcatccaqacagutcagu
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Nature 377 (6547 Suppl), 3-174 (1995)
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9712 Medical Center Drive, Pockville, MD 20450 USA
1711: 3018699056
Pax: 3018699423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 acagtggatatcaaa 342
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Other_ESTs · THC169106
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                                            FEATURES
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Adams, M D., Kerlavage, A R., Fleischmann, R.D., Fuldner, R.A.,

Adams, M D., Kerlavage, A R., Fleischmann, R.D., Godayne, J.D.,

White, D., Sutton, G., Rlake, J. A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.P., Cotton, M.D., Barle-Hughes, J., Fine, L.D.,

Flizgerald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoghapen, N.S.,

Glodek, A., Gnehm, C.L., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.E., McDonald, L.A., Nguyen, D.T., Perligitno, S.M.,

Phillips, C.A., Ryder, S.E., Scott, L.L., Saudek, D.M., Shirley, R.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J.,

Rozak, D., Keng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Rywond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.I., Puben, S.M.,

Plillon, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C., Socho, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: *arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this ESI, please check the TIGP Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST69341 Lymph node I Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region.
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Vertebrata; Mammalla; Eutheria, Frimatcs, Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                     97 GCCTGGTACCAGCAAAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGTATCCAGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                              222 accatcagcagactggagcctgaagattttgcagtgtattactgtcagcagtatggtgac 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 ACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC 276
                                                                                                                                                                              42 ccaggggaaagagccgccctctcctgcagggccagtcagcgtgttagcagcagtcactta 101
                                                                                                                                                                                                                                                                   102 geetggtateageagaaaeetggeeaggeteeeaggeteeteatetggtgegteeagg 161
                                                                                                                                                                                                     21-APR-1997
                                                                                                                                 Gaps
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                                                                                    Score 242; DB 73; Length 403;
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                       4 others
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 tcacctaggacgttcggccaagggaccaaggtggaaatcaaa 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 TCACCTCGGACTTTTGGCCAGGGGACCAAGTTGGAGATCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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                                                                                                            Pred. No. 0.00e+00;
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                  107 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 bp
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1 Similarity 92.9%;
262, Conservative
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1113 c
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                                                                                                              Best Local Similarity
                     86 a
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                                                                                         Query Match
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
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Home.

Badams, M.D., Kerlavage, A.R., Fleischmann, P.D., Fuldner, R.A.,

Ball, C.J., Lee, N.H., Kirkness, E.F., Wanistock, K.G., Sacayne, J.D.,

White, O., Sutton, G. Blake, T.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzerald, I.M. Flitzhigh, W.M. Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Liu, L.-T., Marmaros, S.M., Merrick, J.M.,

Moreno-Palangues, P.F., McDenald, A., Mouyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y.R.,

Bednarik, D.P., Peng, D.-F., Ferrich, A., Fischer, C., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.W., Gruber, J., Hudson, P. Kim, A.K.,

Kozak, D.L., Kunsch, C., Hungjun, T., Lill, M., Meisner, P. Kim, A.K.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G., Ruber, S.M.,

Paymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G., Ruber, S.M.,

Fraser, C.M. and Veneter, J.C.

Initial assessment of human gene diversity and expression patterns
                                                                                                                                                             /note="Organ: lymph node; Vector: pBluescript SK-; Site_l:
EcoRI; Site_1: XhoI"
/clone_lib="Lymph node I"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Mammalla, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST100471 Pancreas tumor I Homo sapiens CDNA 5' end similar to immunoglobulin kappa light chain, VJ regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 405;
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Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seg primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 237; DB 52;
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                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 attactgtcantggtatggtagctcaactc 361
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                                                                       Location/Qualifiers
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Matches 250; Conservative
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gycayne, J.D.,
White, D., Satton, G., Blake, J.A., Brandon, P.C., Man-Wall, C.,
Clayton, R.A., Cline, T.P., Porton, M.D., Erie-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Soehm, C.L., Hanna, M.C., Hellium, E., Hinkle, P. S.J.,
Kelley, J.M., Melley, J.C., Lin, L.I., Warmancos, S.M., Merrick, J.M.,
Moreno-Palanques, E.F., Monoald, L.A., Nguyen, D.T., Pelligino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Bednatik, V., Spriggs, T.A., Hitchack, T.P., Weidman, T.F., Li, Y.,
Bednatik, P., P., P., A., Hitchack, T.P., Weidman, T.F., Li, Y.,
Bednatik, P., P., P., Cheria, A., Fischer, C., Hastings, G.A.,
He, W. Hu, T.S., Greene, T.M., Grüber, C., Hastings, G.A.,
                                                                                                                                                         For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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//ordanism-"Homo sapiens"
//note-"Grain: pancreas: Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
//clone_lib-"Pancreas tumor I"
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Vertebrata: Mammalia; Euthoria; Primates; Catarrhini; Hominidae,
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                                                                 9712 Medical Center Drive, Pockville, MP 20850 USA
Tel: 3018699056
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                    Bioinformatics
The Institute for Genomic Research
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<1..>328
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                                                                                                                                       Email: arkerlavētigr.org
                                                                                                                                                                                                                                       Seq primer: M13 Reverse.
Contact: Kerlayage, AP
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Kczak D L. Kunsch, C. Hungjun, T. II.H. Meissner, P.S., Clsen, H., Waymond, L., Weil, Y.F., Wing, J., Xu, C., Yu, G.L., Ruhen, S.M., Uillion, P.J., Fannon, M. P., Rosen, C.A., Haseltine, M.A., Fields, C., Fraser C.M. and Venter, J.C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of enNa sequence. Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please check the TISR Human Seme Index (http://www.tigr.org/tdb/hgi/hgi.html)
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/note="Organ. pancreas. Vector. pBluescript SK.. Site_1:
Ecom. Site_2. MoI"
/clone_lib="Pancreas tumor !"
/dev_stage="adult"
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Adams, M.D., Kerlavage, A.P., Fleischmann, F.D., Fuldner, R.A.,
Bult, G.T., Lee, N.H., Kirkness, E.F., Weinstrock, K.G., Scrayne, J.D.,
White, C., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, F.A., Cline, T.F., Cotton, M.D., Earlo-Houbes, T.F., Flue, L.L.,
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Vertebrata: Mammalia: Eutheria: Primates: Caturrhini: Hominidae:
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Pred No. 0.00e+00;
0: Mismatches 26: Indels
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9712 Medical Center Drive, Pockville, MD 20950 USA
Tel: 3018699056
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Contact: Kerlavage, AR
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Best Local Similarity 88 8%:
Matches 231; Conservative
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Fitzgerald L.M., Fitzhugh, W.M., Fritchman, T.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.C., Liu, L.T., Marmarcs, S.M., Merrick, J.M., Moreno-Palaques, B.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S. Scott, J.L., Saudek, D.M., Shirley, R. Sanli, K.V., Spriggs, I.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kusch, C., Hungjun, J., Li, H., Maissner, P.S., Olsen, H. Paymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Puben, S.M., Dillion, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C. Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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EcoRI; Site_2: XhoI"
/clone_lib-"Pancreas tumor III"
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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<1 >363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 Reverse.
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Best Local Similarity 82.9%;
Matches 252; Conservative
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LUCUS AA29537 277 bp MRNA EST 18-APR-1997 DEFINITION EST100538 Pancreas tumor 1 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VJ regions.

AA295377

RESULT 9

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Ladams, M. D. Kerlavage, A. P. Fleischmann, P. D. Fuldner, R. A.,
Rult, C. J. Lee, N. H., Kirkness, E. F. Weinstock, K. G. Gorayne, J.D.,
White, C. Sutton, G. Blake, J. Brandon, P. C. Man-Wall, C.
Clayton, P. A. Cline, T. P. Cotton, M. D. Larle-Hughes, J. Fine, L. D.
Eltzgerald, L. M., Fitzhugh, W. M. Fritchman J. L. Geoghagen, N. S.
Glodek, A. Geneh, C. L. Lau, L. L. Marmaros, S. M. Merrick, J. M.
Kelley, J. M., Kelley, J. C. Liu, L. L. J., Marmaros, S. M. Merrick, J. M.
Moreno-Palanques, R. F. McDonald, L. A., Nguyen, D. T., Pelligrino, S. M.
Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shriey, R.,
Small, K. V., Spriggs, T. A., Utterback, T. P., Weldman, J. F. L., Y.
Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. P. L., Y.
Dimke, D. Feng, D. F., Ferrie, A. Fischer, C., Hastings, G. A.,
Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,
Raymond, L., Wel, Y. E., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
Fraser, C.M. and Venter, J. C.
Thillah assessment of fhuman gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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/organism="Homo sapiens"
/note="Graph: pancreas; Vector: pBluescript SK-: Site_1:
Ecoff: Site_2. XhoI"
/clone_lib=*Panoreas tumor I"
                                                                                                                                  Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Pred No 0 000+00
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Rest Local Similarity 93.8%
Matches 196; Conservative
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                      91947711
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Dases 1 to 289)

Relacy, M. P. Kerlavage, A. P. Fleischmann, P.D., Fuldner, P.A.,

Radams, M. D., Kerlavage, A. P. Fleischmann, P.D., Fuldner, P.A.,

Radams, M. D., Kerlavage, A. P. Handon, R. G., Man-Wai, C.,

Milte, G., Sutton, G., Hake, J. A., Hrandon, R. G., Man-Wai, C.,

Clayton, R.A., Cline, T.P., Cotton, M. D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhuch, W.M., Fitchman, J.L., Geoghaden, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S.,

Kelley, J. M. Kelloy, J. C., Liu, L. I. Marmaros, S. M., Merrick, T.M.,

Moreno-Palaques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Pyder, S. F., Scott, J.L., Saudek, D.M., Shiriey, P.,

Ramil, K. V., Spriggs, F. Scott, J.L., Saudek, D.M., Shiriey, P.,

Ramil, K. V., Spriggs, F. Scott, J.L., Saudek, D.M., Shiriey, P.,

Bednarik, D.P., Geole, Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Bednarik, D.P., Geole, C., Gepeda, M.A., Coleman, T.A., Collins, E.J.,

How, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Olsen, H.,

Raymond, L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Fannon, W. F., Presen, C. A., Haseltine, W.A., Fields, C.,

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                                         Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                       DEFINITION - BSINGSE DOLDS I Homo suppermental ST and STAIL to similar to immunoglobulin kappa light chain. VNI regions (GB:Z11894).
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0: Mismatches 18; Indels 1; Gaps
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/clone_lib="Colon !"
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9712 Medical Center Drive, Rockville, MD 20859 USA
Tel: 3018699056
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Rest Local Similarity 91.3%;
Matches 200: Consermed:
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                                                                                                                                                                                                     AA205941 253 bp mPNA FST 18-APR-1997
ESTIGI165 Thymus III Homo sapiens cONA 5' end similar to similar to
immunoglobulin kappa light chain, V region (GB:YQC(44)).
AA295941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae, mitochoodrial eukaryotes, Metazoa (hordata)
Vertebrata: Mammalia: Eutheria: Primates: Catarrhiri: Fominidae)
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EcoH: Site_2: XhoIT
/clone_lib="Thymus III"
/dev_stage="adult"
/1 .253
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The Institute for Genomic Research
9712 Medical Center Drive, Pockville, Mt 20859 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O 69
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AUTHORS
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Bull, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Googne, J.D.,
Bull, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Googne, J.D.,
Bull, C.J., Lee, N.H., Fland, M.D., Earle Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, T.L., Geoghagen, N.S.,
Gloddk, A., Ghehn, C.L., Hanna, M.C., Hedblom, E.H., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.G., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Fyder, S.E., Scott, J.L., Saudek, D.M., Shifey, P.,
Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J. F., Li, Y.
Bednarik, D.P., Cao, L., Cepeda, M.A., Foleman, T.A., Collins, E.J.,
Dimke, D., Fangy, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Well, Y.F., Windy, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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EcoR: Site_2: XhoI"
/clone_lib="Pancreas tumor III"
/dev.stage="adult"
<1..>294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata, Mammalia, Eutheria; Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                               AA366461 294 bp mRNA EST 21-APR-1997
EST77408 Pancreas tumor III Homo sapiens cDNA 5' end similar to
similar to immunoglobulin kappa light chain, V region.
AA366461
147 TGTATCCAGCAGGGCCACTGGCATCCCAGAGAGAGTTCAGTGGCAGTGGGTCTGGGACAGA 206
                                                          121 giticacteteaceateageageetgeagtetgaagatitineagitiattaetgieagea 180
                                                                                                                207 CTTCACTCTCACCATCAGCAGAGAGCGGAGAGATTTTGCAGTGTATTACTGTCAGCA 266
                                                                                                                                                                                                            181 gtataaaaactggccagagacgttcggccaagggaccaaggtggaaatcaaa 232
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Pred No. 6.67e-299,
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Best Local Similarity 92.29,
Matches, 189; Conservative
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
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85 acqcaatctccaqccaccctqtctqtgtctccaqgggaaaqaqccaccctctcctqcagg 144

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Adams, M.D., Kerlavage, A.B., Fleischmann, B.D., Fuldner, P.A.,
Bult, C.J. Lee, N.H., Kirkness, E.F., Weinstock, K.G., Groayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, P.A., Cline, T.B., Cotton, M.D., Earle-Hudhes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.I., Geoghagen, N.S.,
Glodek, A., Genhu, C.L., Hanna, M.C., Hedblom, F. Hinkler, P. S.J.,
Kelley, J.M., Kelley, T.C., Liu, L. J., Marmaros, S.M., Merrick, J.M.,
Morenc-Palanques, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, P.,
Small, K.V., Spriggs, T.S., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.W., Gruber, J., Hudson, P. Rim, A.K.,
Kozak, D.L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Raymond, I., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Fraser, C.M., and Vencer, J.C., Hugh, J., Roben, S.M.,
Fraser, C.M., and Vencer, J.C., Hugh, J., Roben, S.M.,
Fraser, C.M., and Vencer, J.C., Mashim, gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
/clone_lib="Pancreas tumor I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae, mitochondrial eukaryotes. Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                    205 cccaggctcctcatctatggtatctccaccagggccagtggtgtcccagccaagttcagt 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST100323 Pancreas tumor I Homo sapiens cDNA 5' end similar to
                                                                                                                                                                67 GCCAGTCAGAGTGTTAGGAGCAACTACTTAGCCTGGTACCAGCAAAAACCTGGCCAGGCT 126
                                                                                                                                                                                                                                                                                                    127 CCCAGGCTCCTCATCTATGGTGTATTCCAGCAGCACCACTGGCATCCAGACAGGTTCAGT 186
                        145 gecaginagagigitaggagaaactactiageetggiaecageagaaaeetggeeaggei
The Institute for Genomic Research
9712 Medical Center Drive, Mockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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.1.>264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other_ESTs: THC169106
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/note-"organ ovary; Vector: p17135 (Pharmacia) with a mondified polyliners; Site-1 Not 11. Site-2 For Br. 1st etrand cDNA was primed with a Not 1 - olio(dT) primer [5' ICTTACTAGTGAGGGGGGGGTHITTHITTHITTHITTHIT 3', adoble-stranded cDNA was site selected, lidated to Eco BI adaptors (Pharmacia), digested with Not 1 and cloned into the Not 1 and Eco PI sites of a modified p1713 vector M.Patima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata, Mammalia, Eutheria, Frimates, Catarrhini: Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 269)
Hillier.L., Allen.M., Bowles.L., Dubuque,T., Geisel,G., Jost,S. Kucaba,T., Lacy,M., Le.M., Lennon,G., Marra,M., Martin,J., Moore.R., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Walte,Y., Wylle,T. Waterston R and Wilson.R
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                                                                                                       Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108
Tel: 314 285 1800
Fax: 314 286 1810
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     Length 264;
Score 173: DB 24: Length 264
Pred. No. 8.330-297;
0: Mismatches 13: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-Merck EST Project
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     Query Match
Best Local Similarity 93.3%;
                                                                                                       181; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
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AUTHORS
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AA292250 209 kp mPNA EST 14-MAY-1997 2t29a12.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 723742 5' similar to gb:x06764 IG KAPPA CHAIN PRECURSOR V-III FESICN
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost.S., Kucaba,T., Lacy M., Le,N., Lennon,G., Marra,M., Marlin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,H., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae, mitochondrial eukaryotes, Metazoa; Chordata:
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini: Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL : contact the IMAGE Consortium (info@image llnl gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                     99 acgdagtetecaggdaecetgtetttgtetecaggggaaaggggdaeceeeeteteetgeadg 158
                                                                                                                                                                                                   159 gecagicadagiqitagcaqcaqciacticaqcotqqiaccagqaaaacotqqocaqqot 214
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                                                 5; Indels (), daps
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Fax: 314 286 1800
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Score 161, DB 87, I
Pred. No. 1.04e-271;
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/clone="723742"
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                                                                                                                                                                                                                           Release 2 10 John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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Statistics, Mean 9,870; Variance 1,923, scale 5,136

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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                                Leanaly outer, mentazod; bunmetazod; bilateria; Coelomata; Debutersotomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapodd; Amniota; Mammalia; Theria; Ettheria; Archonta; Primates, Catarrhini; Hominidae; Homo.

Ettheria; Archonta; Primates, Catarrhini; Hominidae; Homo.

1 (bases 1 to 381)

Radams,M D. Kerlavage,A R. Fleischmann,R.D., Fuldner,R.A.,

Bult,C.J., Lee,N., Kirkness,E.F., Wainstock,K.G., Gocayne,J.D.,

White,O., Sutton,G., Flake,J.A., Brandon,P.C., Chiu,M.-W.,

Clayton,R.A., Cline,P.T., Cotton,M.D., Farle-Hughes,J. Fine,L.D.,

FitzGerald,L.M., FitzHugh,W.M., Fritchman, T.L., Geoghagen,N.S.M.,

Glodek,A., Gnehm,C.L., Hanna,M.C., Hebblow,E., Hinkle,J.P.S.,

Kelley,J.M., Kline,F.R.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,

Meristck,J.M., Moreno Palanques,R.F., McDonald,L.A., Nguyen,D.T.,

Pellegrino,S.M., Phillips,C.A., Pyder,S.E., Scott,J.L.,

Saudek,D.M., Shirley,P., Sanall,K.V., Spriggs,T.A., Juterback,T.R.,

Kelley,J.M., Shirley,P., Sanall,K.V., Spriggs,T.A., Juterback,T.R.,

Kelley,J.M., Shirley,P., Sanall,K.V., Feng,P., Ferrie,A.,

Keldman,J.F., Li,Y., Rednarik,P.P., Cao, L., Capeda,M.A.,

Clumber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H.,

Meissner,P.S., Olsen,H., Paymond,L., Weily,Y.F.,

Mu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,

Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns

Based Upon S2 Million Basepairs of CINA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tdbinfo@tdb.tiqr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGP Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 ctccaggcaccetgtetttgtntccaggggatagagccacceteteetgcagggccagte 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 agagtgttagcagcaactacctagcctggtaccagcagaaacctggccaggctcccaggc 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 ggtctgggacagacttcactctcaccatcagcagacttggagcctgaagattttgcagtg 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .94 GGTCTGGGACAGACTTCACTCTCACCATCAGCAGACT-GGAGCCTGAAGATTTTGCAGTG 252
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932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 3018699423
     Homo sapiens
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Deuterostomia; Chordata, Vertebrata, Gnathostomata; Deuterostomia; Chordata, Vertebrata, Gnathostomata; Osteichthyes; Barcopterydii; Chordata, Vertebrata, Gnathostomata; Theria; Deuterostomia; Chordata, Vertebrata, Gnathostomata; Theria; Barcopterydii; Chordata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 383)

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For clone availability, additional sequence and expression
information related to this EST, please contact the IIGR Database
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human primer=M13 Reverse library~Human Pancreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 AAGTIGGAGATCAA 317
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318 gtattactgtcagcattatggtag 341

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Bukaryotae: Metazoa: Bumetazoa: Bilateria: Coelomata:

Bukaryotae: Metazoa: Bumetazoa: Bilateria: Coelomata:

Butaryotae: Thordata: Verrebrata: Gathopstomata: Osteichthyes:

Butheria: Archorta: Primates: Catarthin: Hominidae. Homo.

Eutheria: Archorta: Primates: Catarthin: Hominidae. Homo.

I (bases: I to 383)

8 Adam. M. D. Kerlavage. A. P. Fleischmann. P. D. Fuldher, P. A. Bult.C.D. Lee.N. Kirkness.E. F. Weinstock.K. G. Gorayna.T. D. Whiteo. S. Strings. A. M. Franca, M. D. Earle-Hughes: J. Fine.L.D. FitzGerald.L. M. Fitth.Jt.W. W. Frith.G. Liu.L. T. Gorayna.N. S. M. Kelley.J. M. Kilmek.K. M. Frith.G. Handelow.E. Hinkle Jr. P. S. M. Kelley.J. M. Kilmek.K. M. Frith.G. Hedblow.E. Hinkle Jr. P. S. M. Moreno-Palanques.P.F. McDonald.L.A. Nguyen.D.T. Pellegrino.S. M. Phillips G. A. Pyder S. E. Scht.J. I. Saudek.D. M. Shirley.F. Small: K. V. Springs. T. Coleman.A. Shirley.F. Small: K. V. Springs.T. A. Otteran. A. Coleman.T. A. Collins.E. T. Dimke.D. Feng. P. Ferris. A. Gruber.J. Hudson, P. Kim.A. Kozak.D. L. Kunsch.C. J. H. Li. H. Weisterner. Paymon.L. Paymon. M. P. Paren. B. M. Basettine.M. A. Fields.C. Fraser.C.M. and Venter.J. C. J. W. Hasettine.M. A. Fields.C. Fraser.C.M. and Venter.J. C. Dimbished Milling C. S. Million. P. J. Ramon.M. R. Poscan. A. Hasettine.M. A. Fields.C. Fraser.C.M. and Venter.J. C. Dimbished Milling C. Brancald. M. A. Kozak.D. M. A. Moreno. S. Million. P. J. Whom S. Million. P. J. Kozak.D. M. M. M. H. J. F. Mang.J. K. M. M. M. J. J. M. Hasettine.M. A. Fields.C. Fraser.C.M. and Venter.J. C. Dimbished Million. P. Million. P. M. M. M. M. Sequence
127870 383 bp mRNA EST 06-SEP-1995
BST19007 Homo sapiens CLNA 5' end similar to immunoglobulin kappa
light chain V region (GB:X05753) (HT:3087).
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Homo sapiens
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The Institute for Genomic Research
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Matches 245: Conservative
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double-stranded cDNA was ligated to Enn PI adaptors (Pharmania). digessed with Not I and cloned into the Not I and Fnn Bisites of modified prizia vector (Pharmacia). Library went through one round of normalization to a log - 13% (Ibrary possition of perto
                                                                                                      EST Similar to qb:XuA764
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Cases I to 570)
Hillier I Clark N Eubuque, I Filiston K Hawkins.M.,
Parsons, J. Piffin L., Parkins, Warra, M., Parsons, J., Palfin T., Sares, W., Tarevaskis, E., Waterston, P. Williamson, A. Wohldmann, P. Williamson, A. Wohldmann, P. Williamson, A. Wohldmann, P. and
                                                                                                                                                                                                                                                                 High quality sequence stops: 316
Source: IMAGE Consortium, LLN.
This clone is available royalty-tree through LLNL, curtart the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 205; DB 34; Length 570; Fred. No. 0.00e+00;
                                                                                                      LOCUS R70290 570 bp mRNA EST DEFINITION y)81408.rl Homo sapiens cond clone 155151 5' si 16 KAPPA CHAIN PRECURSOP V-III REGION (HUMAN):...
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252 STATTACTSTCASCASTATSSTAG 275
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140 c 141
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WashU-Merck EST Project
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Bost Local Similarity 84.8%;
Matches 258; Conservative
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
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Pred No 0 00e+00;
0; Mismatches 12; Indels 13; Caps 13;
                                                                                                                                                                                          yf3la06.rl Homo sapiens cDNA clone 128434 5' similar to gb:X06764
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333 itgcagtgtattactgttcagcgatattgatgggctcanccctttttnggccctgggacc 392
              245 TIGCAGISTATIACISI -CASCASIAIBSCICACCICGGACITIIGGSCCAGGGGACC 303
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                       IG KAPPA CHAIN PRECUPSOR V-III PEGION (HUMAN):
R10529
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Source: IMAGE Consortium, LLNL
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia), Library went through one round of normalization to a Cot = 20 Library constructed by Bento Soares
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Sarcopterygii, Choanata, Tetratoda; Amriota, Mammaiia. Theria:
                                                                                                                                                                                                                                                                                                                                            DEFINITION yp24a10.rl Homo sapiens cown clone 188346 5' similar to gb.x06764 IG KAPPA CHAIN PRECURSOR V-III RESION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                            192 HGGGTCTGGG-ACAGATTTGACTTT-7ACCAT-GAGGAGATGG-AGGTGGAAGATTTT-746
                                                                                                                 70 acgeagetneeaggeaecetgtetttgtetteeaggtgaaagageeaecetetetetgeagg 139
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Applan,M., Hultman,M. Kucheb,T. Le,M., Lennon,G., Marra,M.,
Parsons, J., Rifkin,L., Pohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,P., Williamson,A. Wohldmann,P. and
254 tagggtintggggadaggatitinacintinacnatinagnagantgggagnintgaaqattttt
                                                                                           314 gcagtgtatttactgttcagcagtattggtagctcaccgttcacttttcgggccqaaggga
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                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata,
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Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                             399 bp
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Hillier, L., Clark, N
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Fax: 314 286 1810
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RESULT LOCUS DEFINI ACCESS NID	RESULT 7 469532 463 bp mRL LOCUS PS 12 1 Homo Supiens CD REFINITION 9/82009.r1 Homo Supiens CD RACESSION R69532 4843049	p mRNA EST 01-JUN-1995 lens cDNA clone 155249 5' similar to gb:M63438 FFS.P V-111 PEGIEN (HUMAN):	RESULT LOCUS DEFINI ACCESS
SOUP	EXWORDS BY: SOUPCE (Pharmacia) with a resistant) primer=M. Ist strand cDNA was ISTIACCANICISANSISSIS double-stranded cDNA digested with Not modified pittle to to of normalization to	EST. burner clone-155249 library-Scares breast 2NbHBst vector-pT713B (Pharmacia) with a modified polylinker host-bH10B (ampicillin resistant) primer-M13PD Psyttel*Not I Psite2-Eop PI Adult female 1st strand cDNA was primed with a Not I - oligo(dT) primer {5' T51TACAARCICAAAST636A5735473507307111111111111111111111 5') double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Rento	NID KEYWOP SOUPCE OFGA REFERE AUTH
ō	SOGANISM BODATES AND METALINA SURARYOCAGE, METAZOA Deulerostomia: Chorr Sarcopterygli: Choar Surcopterygli: Choar	Honaido. - Eumetazoa: Bilatería: Coelomata: data: Vertebrata: Gnathostomata: Osteichthyes: nata: Tetrapoda: Amniota: Mammalía: Thería: Primates: Catarrhini: Hombidae, Homo.	
REF! At	REFFRENCE 1 (bases 1 to 463) AUTHORS Hillier, Clark,N Holman, M., Hultman, Parsons,J., Pifrin,I Parsons,J., Pifrin,I Milson	. Dubuque.T., Elliston.K., Hawkins,M., M., Kuraba,T., Le,M., Lennon.G., Marra,M., L., Rohlfing.T., Soares,M., Tan,F., ston.R., Williamson,A., Wohldmann.P. and	
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<u>=</u> 500		Contact: Wilson RK Washu-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Enax: 314 286 1810 Enax: 314 286 1810 Enax: 315 285 4810 Enax: 315 285 4810 Enax: 315 285 4810 Enax: 316 285 585 585 585 585 585 585 585 585 585	TITL JOUP COMMEN
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ōæ¥	Guery Match Best Local Similarity 89.9%: Matches 231; Conservative	Score 191: DB 34: Length 463; Pred. No. 0.00e-00: 0; Mismatches 23; Indels 3; Gaps 2;	BASE C ORIGIN
4 0	89 etecagecaecetatetgtetgt 	89 eticagocaenstgirigigiciscaggggaaagagcaenststotgeaggggaagt, 148 	Quer Rest Matc
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Deficiency Accordance (and accordance) and accordance (but and accordance). Sutton, G. Blake, J.A., Brandon, F.C., Chuu, M., White, C., Sutton, G., Blake, J.A., Brandon, F.C., Chuu, M., White, C., Blake, J.A., Brandon, F.C., Chuu, M., Willer, M., Flitchman, J.L., Geodhaden, N.S.M., Glodek, A., Gnehm, C.L., Hannah, M.C., Liu, L.I., Marmaros, S.M., Meristro, J.M., M., Krine, Palang, F.F., W.C., Liu, L.I., Marmaros, S.M., Meristro, S.M., M., Fritchman, M.C., Liu, L.I., Marmaros, S.M., Meristro, S.M., M., Fritchman, B. P., Cott, J.L., Soudek, D.M., M., Fritchman, M. P., Li, Y. Bedarik, D.P., Cao, L., Cepeda, M.A., Collen, J.M., M., Ha, M., Hu, T.S., Gropen, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Weister, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Weister, C.M., and Venter, J.C., Initial Assessment of Human Gene Diversity and Expression Pattherns and Chemister (1995)
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EST77181 Home sapiens ofnA 5' end similar to jenutrophotophin Kuppa
light chain. V region (GR:M29469) (HT:3066).
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Deuterostomia, Chordala, Vertebrata, Ghathostomia, Gribbithyes,
Sarcopterygii, Choanala, Tetrapoda, Amniota, Mammalia, Theria,
Eutheria, Archonta, Primates, Cacarrhini, Hominidae, Homo,
                                                         82 acadagteterageneaecetgtntttgtntecaggggaaaagageeeeenteteetgdagg 143
74 AGAGTGIIAGGAGGAAGJACIIAGGCIGGIAGGAGAAAAAACGIGGGCAGGJGGCGAGGG
                                                                                                                  266 ggtctgggacagagttctttctcaccateagcagcotgcagactgaagattttaca
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Pred No. 0.00e+00;
0; Mismatches 15; Indels 5;
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia) Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares
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y161g07.rl Homo sapiens cDNA clone 162780 5' similar to gb:X06764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
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Sarcopterygii: Choanata: Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta: Primates: Catarrhini: Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
259 ggcagtgggtctnggacagaetttcactcttnaccatcagcagcctagagcctgaagatt 318
                                                                                                 199 cccaggeteeteatetatgatgeatecaacagggeeaetggeateeeageeaggtteagt 258
                                                                                                                                            127 cccasscreercarctarssrearcasscrearssscaresscarecasacassreas 186
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Hillier,L., Clark,N., Dubyque,T., Elliston,K., Hawkins.M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Source: IMAGE Consortium, LLNL
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87 ct.ccagaraccetogecttgtetecaggggaaagagcaccactetoctgcaggtecagte 146

Indels 4: Gaps

Mismothes

23%, 'Ponsérvative

Matches

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vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13Rpl Rsitel=ECoRI Rsite2=XhoI Normal lung tissue from a 72
gar old male, Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Unil-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAG-1': 1' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eucaryotae, Metazoa, Chordata, Vertebrata, Gnathostomata; Mammalia; Eutheria, Frimates, Catarrhini, Hominidae, Homo.

1 (bases I to 451)

Hillior, L. (flark, N. Pubuque, T. Elliston, K., Hawkins, M., Holman, M., Hilthan, M., Kiraba, T., Le, M., Lennon G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Washersten, R., Williamson, A., Wehldmann, P. and Wilson, F., Uppublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image lln] gov) for further information.
                                                                                                                                                                                                                                            145 gocagtoagagtgttagcagcaact---tagcotggtaccagcagaaactggcraggct 201
                                                147 agaatattgacaacacccacttagcctggtaccagcagaaacctggccageeleeesgys 206
                                                                                            74 AGAGIGITAGGAGCAACTACTIAGCCTGGTACCAGCAAAACC1GGCCAGGCTGCCAGGC 133
                                                                                                                                               207 tecteatetateataateeaeeaggteaetggeateeeagaeagtteagtngeagin 266
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5' similar to
14 CICCAGGCACCIGICIIISICICCAASGSAAAAAAGACCACCICICIGGGGGGCCASIC 73
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION yel5d10 rl Homo sapiens cDNA clone 117811 5' similar
gb:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III PEGION
(HUMAN):contains Alu repetitive element;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human rinno=117811 library=Stratagene lung (#037210)
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0; Mismatches 18;
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Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
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WashU-Merck EST Project
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Best Local Similarity 90.1%;
Matches 219; Conservative
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yi22f09 rl Homo sapiens cDNA clone 140009-5' similar to gb:M63438
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN):.
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Deuterostomia: Chordata. Vertebrata. Giathostomiala. Ostelchthyes;
Sarcopterygli: Ocoanata: Tetrapoda: Amniota: Mammalia: Theria:
Eutheria: Acrhonia: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 43R)
Hiller.L., Clark.N. Dubuque, T. Filiston, K. Hawkins, M.,
Holman, M., Hutaman, M., Nucaba, T. (P.M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L. Pohlfina, T., Soares, M., Tan, F.,
Ireyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Source: IMAGE Consortium, DLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@lmade.lbd.gov, for further information,
Lonallon/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            human clone-140009 library-Soares placenta Nb2HP vector=pT7T3D

    caquacticalicicaccaticageauquectugagectgaaqattttgeagtgtattactgte

                                                                                                                                              67 GCCASTCAGAGISTIAGGAGGAGTACTIAGCCIGGIACCAGGAAAAACCIGGCCAGGCT 126
                                                                                                                           262 taacaatagaatetagaacaaaagtteaetttteaesatteagoagoetgeagtetgaagga 321
                                       202 occaaqotontoatnialigifanatonanonagagagosetaditainosagonagitinaa 261
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Washington University School of Medicine
4444 Forest Park Parkway, Box P501. St. Louis, MO 63108
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/clona="140009"
110 / 114 q 94
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Local Similarity 94.9%;
HS 167; Conservative
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double-stranded cDNA was ligated to Eco FI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco FI sites of a modified pI713 vector (Pharmacia). Library went through one round of normalization to a Cot \star 20. Library constructed by Benic Soares and M.Fatima Bonaldo.
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Y147106.II Home sapiens CDNA clone 161435 5' similar to qb:231894
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
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1 (bases 1 to 171)

Hiller L. Clark, N. Pubuque, T. Ellistom, K. Hawrins, M. Holman, M. Hultman, M. Kucaba; T. Lei M. Lennon, G. Marra, M. Parsons, J. Pifkin, L. Pobling, T. Scares, M., Tan, F. Treyaskis, E., Waterston, R., Williamson, A., Wohldman, F. Treyaskis, E., Waterston, R., Williamson, A., Wohldman, F. and
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Trace considered overall poor quality.
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                                                            1 ccaggeacectgietitigietecagggeaaaagaecaceteicetecigeauggeeathae 60^\circ
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4444 Förest Park Parkway, Pox 8501, St. Louis, MC 43108
Tel: 314-286-1800
Fax: 314-286-1810
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Washington University School of Medicine
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High quality sequence starts: :
High quality sequence stops: !
Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                             double-stranded CDNA was ligated to ECO RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo
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Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hellman, M., Hulfman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Trevaskis, E., Materston, R., Welling, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Welliamson, A., Wehldmann, P. and
                                                                                                       y151905.rl Homo sapiens cDNA clone 161816 5' similar to gb:M63438
IG RAPPA CHAIN PRECURSOR V-111 REGION (HUMAN);
                                                                                                                                                                                                                      This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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O; Mismatches 38; Indels 9, Caps
                                                                                         10-JUL-1995
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4444 Forest Park Parkway, Rox 8501, St. Louis, MO 63108
Tel: 314 286 1800
Eax: 314 286 1810
136 CTCATCTATGGTGTATCCAGCAGGGCCAGTGGCATCCCAGACAGGTTCAGT 186
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Best Local Similarity 82.7%;
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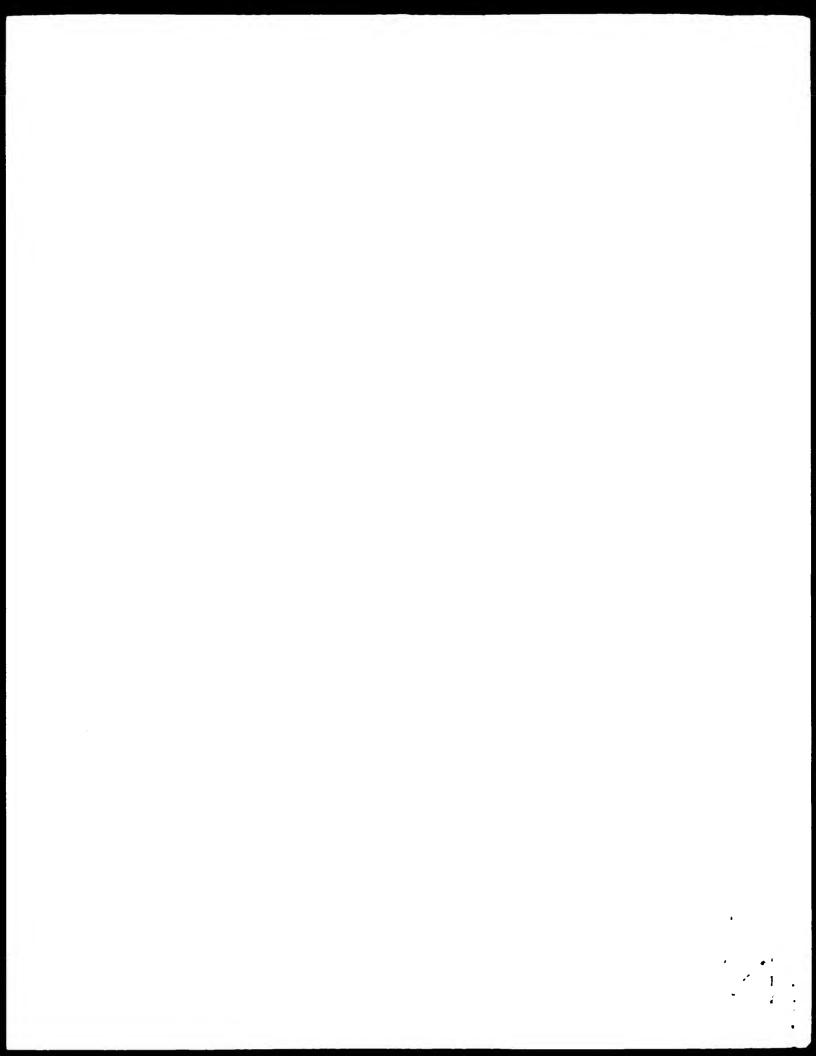
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yj66e01.rl Homo sapiens chWa clone 154720 5° similar to gb:X06764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image lln] grv) for further information.
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holhan, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osten,
Sarcopterygii, Choanata, Tetrapoda, Amriota, Mammalia, Th
Eutheria, Archonta, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MU 63108
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Best Local Similarity 90.68, Pred. No. 1.44e-222,
Best Local Similarity 90.68, Pred. No. 1.44e-222,
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/clone="153720"
114 c 110 q 110
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243 ITTIGCAGIGIATIACT-GICAGCAG 267
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                                                                                              421 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 285 1810
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Eukaryotae: Metazoa: Eumetazoa: Bilateria: Coelomata; Deukaryotae: Deuterostomia: Chordata: Vertehrata: Grathostomata: Osteichthyes: Sarcopterygli: Choanata: Tetrapoda: Amniota: Mammalia: Theria: Eutheria: Archonta: Primates: Catarrhini: Hominidae: Homo. 1 (bases i to 361)
Hillier.L., Clark.N., Dubuque,T., Elliston,K., Hawkins.M., Holfman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J., Pifkin,L., Pohlfing-T., Soares,M., Tan,E., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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yj71b07.rl Homo sapiens cDNA clone 154165 5' similar to
qb:M12740_cds1 IG KAPPA CHAIN PPECUPSOP V-III PEGION (HUMAN);
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Washington University School of Medicine
4444 Forest Park Parkway, Rox 8501, St. Louis. Mc 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 3.22e-212;
0: Mismatches 26, Indels 12,
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/clone="154165"
1 108 c 91 q 83
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Local Similarity 85.7%;
nes 229; Conservative
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Release 2 1D John F Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U Distribution rights by Intelligenetics, Inc.

 n.a. database search, using Smith-Waterman algorithm n.a.

Tue Feb 24 14:00-24 1998: Maspar time 19.72 Seconds 741.630 Million cell updates/sec Pun on:

Tabular output not generated.

>US-08-844-215-17 (1-31%) from "SO8844215 seq 318 Description: Perfect Score:

1 GAGCICAGGCAGICICCAGG. CICGAGIGCGICAGAGGICC. N.A. Sequence:

....GGACCAAGIIGGAGAICAAA 318GGIGGIICAAGCICIAGIII

TABLE default Sap 6 Scoring table:

87531 seqs, 22995621 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-issued | 1.back1 2:51 2:52 4:53 5:54 6:55 7:56 8.PCT90 9.PCT91 | 10.PCT92 11.PCT93 12:PCT94 13.PCT95 14:PCT96

Mean 7.525; Variance 4.259; scale 1.791 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.		Score	Ouery Match	Ouery Match Length	DB	ID	Description	Pred No
:		267	.0.48	006		18-04-063-	Sequence 192. Applicat	975-908
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		216	67.9	812	۲-	US-08-053-	118	4 176-140
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		141	44.3	350	ហ	US-08-026-	3, Ap	4
•		138	43.4	387	Ç	115-08-217-		6 670-82
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	61	131	41.2	339	Ξ	PCI-US93-0	Sequence 5, Applicatio	4 61b-77

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ALIGNMENTS

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APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
IIILE UF INVENTION: Iransyenic No. 5561016 Human Animais for
IIILE UF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
COPRESPONDENTE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: One Market Flada, Steuart Icwer, Saite 200
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COMPUTER 194103
APPLICATION NUMBER 1850
CLASSIFICATION 1840
PRIOR APPLICATION DATA:
APPLICATION NUMBER 1850
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Sequence 182, Application US/08053131.
Sequence 182, Application US/08053131
Patent No. 5651016
GENERAL INFORMATION:
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REEFERENCY FOOKET NUMBER: 144
TELECOMMUNICATION INFORMATION:
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CITY: San Francisco
STAIE: California
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IIILE OF INVENTION: ALLEPGEN-SPECIFIC 19A MONOCLONAL ANTIRODIES AND
IIILE OF INVENTION: RELATED PRODUCTS FOR ALLERSY TREATMENT
                                                                                                                                                                                       375 ACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGAAAGAGCCACCTCTCCTGCAGG 434
                                                                                                                                                                                                                                          187 GGCAGTGGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCTTGAAGATTTT 246
                                                                                                                                                                                                                                 435 GCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAAACCTGGCCAGGCT 494
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O
                                                                                                                                                 Length 900;
                                                                                                                                    Score 267; DB 7; Length 900;
Pred. No. 1.32e-178;
***matches 5; Indels
                                                                                                                LOCATION: join(115.163, 351..650)
Sequence 900 BP, 220 A, 241 C, 201 G, 238 T, 9 other:
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MEDIUM TYPE: 3.5" Hi Density Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US93-12501-1 STANDARD; DNA: UNC; 325 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS, Version 3.30 SOFTWARE: Wordperfect 5.1 CURPENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCI/US93/12501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNX92-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9312501. Sequence 1, Application PC/TUS9312501 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Tanox Blosycomes Grapher: 10301 Stella Link Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mirabel, Eric P. REGISTRATION NUMBER: 31,211
      TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO. 182-
SEQUENCE CHAPACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid.
                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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415-326-2400
                                                               single
                                                                                                                                                / Match
Local Similarity 98.2%;
nes 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                         CDS
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                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: .
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 TELEPHONE:
                                                                                                       NAME/KEY:
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GENERAL INFORMATION:
APPLICANT THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION METHODS FOR PROGNOUND ANTIBODY LIBRARIES
TITLE OF INVENTION OF USING UNIVERSAL OF PANDOMIZED IMMUNOCIORULIN LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 GCGAGGCTCCTCATGTATGCTACATCCATAAAATCATCTGGAATCGCAGAGAAATTCACT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 GCAGTGTATTACTGTCAGCAGTTTCGTAACTGAGAGAGGTTGGGGGGAAAGAGA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 GCACTGTATTACTGTCACCAGTATGGTAGCTCACCTCGGACTITTGGCCAGGGACCAAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 GCCAGTCAGACTGTTAGCAGCAACTACTTAGCCTGGTACCAGCACAAACCTGGCCAGGCT 132
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                                                                                                                                                                                                                                                                                                                                                                                                          127 CCCAGGCTCCTCATCTATGGTGTATCCAGCAGGGCCACTGGCATCCCAGACACAGTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 GGCAGTGGGGTCTGGGACAGACTTCACTCACCATCAGCAGACTGGAGCTGAAGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                      Length 325;
                                                                                                                                                                                                                                                                 Match 82.4%: Score 262; DB 11; Length 32; Local Similarity 92.0%; Pred No R 076-175; es 287; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CUPPENT APPLICATION DATA:
APPLICATION WIMBER: PCT/HS95/111206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: The Scripps Research Institute
STREET 10666 North Torrey Pines Road, TPC8
                                                                                                                                                                                                                 Sequence 325 BP; 79 A; 93 C; 79 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            л 3
PCT-US95-11235-2 STANDAPD; DNA; UNC; 646 BP.
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APPLICATION NIMBER: US 08/300,386
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 OB/174,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9511235 Sequence 2, Application PC/TUS9511235
                                                                                                                                                                         double stranded
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IBM PC compatible
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-664-2288
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                                                                                                                          LENGIH: 325 nucleotides
                        TELEPHONE: 713-644-228
TELEFAX: 713-664-8914
INFORMATION FOR SEQ ID NO:
                                            713-664-8914
                                                                                              SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                              nucleic acid
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                                                                                                                                                                                                Linear
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ADDRESSEE: The Scripps Pesearch Institute
STRFET: 10666 No. 564798th Torrey Pines Road, TPC8
                                                                                                                                                                                                                                             APPLICATION NUMBER 105 07/826.523
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 08/012,566
FILING DATE: 02-PEB-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                        CUCRENT APPLICATION DATA:
APPLICATION NUMBEP: US/08/300,386A
FILING DATE: 02-SEP-1994
                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA-
APPLICATION NUMBER: US 08/174,674
FILINS DATE: 28-DEC-1993
PRIOR APPLICATION NUMBER: US 07/826,523
APPLICATION NUMBER:
                                                                                                         COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-554-2937
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 646 hass -
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TELEPHONE: 619-554-2937
                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                    NAME: Fitting, Thomas
PEGISTPATION NUMBER: 34
PEFEPENCE/COCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 646 base pairs
nucleic acid
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                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                 STPFET· 10666 N
CITY: La Jolla
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HYPOTHETICAL: N
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                                                       COUNTRY
                                           STATE:
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USING UNIVERSAL OF PANDOMIZED IMMUNOSLOBULIN LIGHT
                                                                                                                                                                                                                                                                                                                                                                                              Indels 3; Gaps 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TGCASGGCCASTCACAGTGIIASGASGSGCIAGTIAGCTGGIAGGAGGAGGAAAAQCTGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CAGGCICCCAGGCICCICATCIAIGGIACAICCAGCAGGGCCACTGGCAIGCCAGACAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 IICASISGCASISSSICISSSACASACTICACITOTOACOATGASCAGACTSSACASOTISAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GATTTTGCAGTGTACTATTGTAGCAGTATGGTGGCTCACCGTGG···TTGGGCCAAGGG 297
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                                                                                                                                                                                                                                                                                                                                                                     Length 646;
                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO Sequence 646 BP: 162 A: 187 C: 170 G: 127 T: 0 other:
                                                                                                                                                                                                                                                                                                                                                                    Score 259; DB 13; L
Pred No 1 500-172;
0; Mismatches 19;
                                                                                                                                                       34,153
EP - TSPI 409.1 (PC)
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                         APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-7AN-1992
PRIOR APPLICATION DATE:
APPRICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08300386A Sequence 2, Application US/08300386A Patent US 5655988 GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.III APPLICANT: Burton, Dennis R APPLICANT: CARLON DENNIS R APPLICANT: CARLON DENNIS R APPLICANT: CARLON DENNIS R APPLICANT: CARLON DENNIS FOR PROTICE OF INVENTION: USING UNIVERSAL
                                                                                                                                                                                  IELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                         TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  FILING DATE: 28-DEC-1993
PPIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                              H. 646 base pairs
nucleic acid
DEDNESS: single
                                                                                                                                               NAME: Fitting, Thomas
PEGISTRAIION NUMBER: 34,
PEFFFRENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 93 1%-
Matches 296; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                         linear
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MOLECULE TYPE: CD!
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                                                                                                                                                                                                                                                  LENGTH
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                                                                                                                                                                                                                                                                 TYPE:
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61 IGCAGGCCAGTCACAGTGTIAGCAGGGCCTACTIAGCTGGIACCAGCAGAACCTGGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 646 BP; 162 A; 187 C; 170 G; 127 T; 0 other;
Patentin Release #1.0, Version #1.25
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NUMBER OF SEQUENCES:
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Patent No. 5652138
GENERAL INFORMATION:
                                                                                                                                                                           USA
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                                                                                                                                                                CA
                                                                                                                                                                STATE:
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                                                                                                     TITLE OF INVENTION: METHODS FOR PRODUCING ANTIROPY LIBRAPIES
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TCCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAGTGGAGCTGGAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CAGGCTCCCAGGCTCCTCATCTATGGTACATCCAGCAGGGCCACTGGCATCCCAGACAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGCTCAGGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGGCGACCCTCTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 19, Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 646;
                                                                                                                                                                                            SOFTWARE: Patentin Pelease #1 0, Version #1 25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER PCT/US94/01258
FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 646 BP; 162 A; 187 C; 170 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 259; DB 12; I
Pred. No. 1.50e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-276-852-153 STANDARD; DNA; UNC; 729 BP
         LT 5
PCT-US94-01258-2 STANDAPD; DNA: UNC; 646 RP
                                                                                                                                                                                                                                  FILING DAIR: .....
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 0.2-PEB-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,674
FILING DATE: 28-DEC-193
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 646 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                      Sequence 2, Application PC/TUS9401258. Sequence 2, Application PC/TUS9401258 GENEPAL INFORMATION:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
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Best Local Similarity 93.1%;
Matches 296; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                          APPLICANT:
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                                           01-JAN-1900
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138 AGGICCAGICACAGCAITCGCAGCCGCGGIAGCTTGGIACCAGCACAAACCTGGCAG 197
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TITLE OF INVENTION: HUMAN NEUTRALISING MONOCLONAL ANTIRODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: The Scripps Pescarch Institute, office of
ADDRESSE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 729;
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Pred. No. 7.20e-144;
0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 9.715
Sequence 729 BF; 173 A; 238 C; 192 G; 156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18 JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCR1452P
                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fitting, Thomas REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEFEPENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                               170
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS.
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Local Similarity 85.1%;
Les 268; Conservative
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  | 198 | 3017/2A/99/10310/A| ASTONOMIA | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987 | 1987
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4 CICACGGASTOTOCAGGGAGGGISTOTITGICICCAGGGGAAAGAGGGGGAGGGGIGIGGIGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green Caps
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN NEUTPALIZING MONOCLCNAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNOBERCIENCY VIRUS NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM IYPE: Eloppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWAPE: Patentin Polease #1 0, Vorsion #1 25 (PPO)
CURRENT APPLICATION DATA:
PPLICATION NUMBER: PCT/MSGS/08743
PILLING DATE: 11-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              • Match
Local Similarity 85.1%; Pred. No. 7 20e-144;
Res. 268; Conservative 0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L0CAIION: 9 715
Sequence 729 BP: 173 A: 208 G: 192 G: 156 I: G Other;
                                                                                                                                                                                   PCT-US95-08743-152 STANDARD; DNA; UNC; 729 BP
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(18-08-276-252-158 STANDARD: DNA: UNC: 729 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/276,852
FILLING DATE: 18-011-1994
INFORMATION FOR SED ID NO: 152:
SEDUENCE CHARACTERISIS:
LENGIH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                       Sequence 152, Application PC/TUS9508743. Sequence 152, Application PC/TUS9508743 GENEPAL INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLFGULF TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 AAACTGGAGAGGAAA 392
                                                379 AAACTGGAGAGGAAA 392
                                                                                            304 AAGIIGGAGAICAAA 318
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LOCATION: 9 7
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01-JAN-1900
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                                                                                                                                                             RESULT
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338 TIFOCICICICACTIIDGFOCCTGGGCAAAAGIGIACGAAGAGAGACACAIACAACGGGCAA 397
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                                                                                                            APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Leroer, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOPERIZIENCY VIRUS
CORRESPONDENCE: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 565138th Torrey Pines Foad, Suite 220, STREET: Mail Drop 1PC8 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Substraction 69.5% Score 121: DB 7: Lenath 719: Best Local Similarity 85:18: Pred. No. 7.20e-144: Marches 168: Cinsorvative 6: Mismarches 47: 1646:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLDGY: linear
MOLECULE TYPE: DNA (genomic)
Sequence 729 BF: 156 A: 192 G: 208 G: 173 I: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE Patentin Pelease #1.0, Version #1 25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTOPNEY/AGENT INFOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 9S 98/178,302
FILING DATE: 30-SEP-1993
                   Sequence 168. Application US/08275852. Sequence 169. Application US/08275952 Patent No. 5652138 GENERAL INPPRATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S: Floppy disk
IRM PC compatible
SYSTEM: PC-EOS/MS-FOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMME: TELLING, Thomas REGISTRATION NUMBER: 34,163 REFERENCE/TOWER UNBER: SOF IELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 168: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         729 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619-554-6312
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STRANDEDNESS: double
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APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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01-JAN-1900
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12906 AAACTGGAGAGGAAA 12920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 TITIGATCICCAACITIGGICCCCIGGCCAAAAGICCGAGGIGAGCIACCAIACIGCIGACA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 GIAGIACAGIGCAAAGICTICAGGCTCCACTCIGGIGATGGIGAGAGIGAAGICIGICC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 AGACCCACTGCCCTGAACCTGTCTGAGATGCCAGAGGCCCTATTGGAAACACACCTTAT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578 GCTGTGACTGGACCTACAGGAGAAGGTGGCTCTTTCCCCT+43AGACAGAGACAGGGTGCC--637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 ACTCTGACTGGCCCGGCASGASASSTSSCTGTTTGGCGTGGAAGAAAAAAAGGGTGGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 221; DB 13; Length 729;
Pred. No. 7.20e-144;
0; Mismatches 47; Indels 0; Gaps
                                                                                                                                                               TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNOBEFICIENCY VIRUS NUMBER OF SEQUENCES: 170
COMPUTEP PEADABLE FRM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
Sequence 729 RP, 1% A, 192 G, 208 G, 173 T, G other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID . US-08-276'852-156 STANDAPD; DNA; UNT; 13254 BF
                                                                             T 9
PCT-US95-08743-168 STANDARD; DNA; UNC; 729 BP.
                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA
APPLICATION NUMBER: PCI/US95/08743
FILIND ADTE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILIND ADTE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACIEPISTICS:
                                                                                                                       Sequence 168, Application PC/TUS950R743
Sequence 168, Application PC/TUS950B743
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DAS/MS-DAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 156, Application US/08276852.
Sequence 156, Application US/08276852
                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                             : 729 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 69.5%;
Local Similarity 85.1%;
nes 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                     double
                      538 IGGAGACTGUGTGAG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638 TGGAGACTGCGTGAG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                           18 TGGAGACTGCGTGAG 4
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                               01-JAN-1900
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                                                                                                                                                                                                                                                             APPLICANT: Lerner, Richard A TITLE OF INVENTION: HUMAN NEUTPALIZING MONOTIONAL ANTIRODIES TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Patent Counsel
STREET: 10666 No. 565138th Torrey Pincs Poad. Stite 220,
STREET: Mail Drop TPC8
CITY: La Joila
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85.1%; Pred. No. 7.20e-144;
ative o; Mismatches 47: Indels or
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MOLECULE TYPE: DNA (genomic)
Sequence 13254 BP; 3206 A; 3559 C; 3251 G; 3238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Polease #1.0. Version #1.25 CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
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FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
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                                                                                                                       APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
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INFORMATION FOR SEQ 1D NO-
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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nes 268; Conservative
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MEDIUM TYPE Floppy
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Patent No. 5652138
GENERAL INFORMATION:
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Verjonse 170, Application PC/TUS9T09743

Sequence 170 Application PC/TUS9T08743

GENERAL INFORMATION:

TITLE 'F INVENTION' HTMAN NEWFALIZING MONOTIONAL ANTIHOPIES
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCHONAL ANTEGDIES TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS NUMBER OF SEQUENCES: 170
COMPUTER PEADABLE FORM:
MEDIUM TYPE:
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Prod No 7,20e-144;
0; Mismatches 47; Indels 0;
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Sequence 13254 BF, 3299 A, 3259 C, 3251 G, 3238 T, 9 ither)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER IRM PC Compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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bot-1895-98743-170 STANDAPD: DNA; UNC: 13254 BP
                                                                                                                               LT 11
PCT-US95-U8743-155 STANUAPLY ENAY UNLY 13254 HP
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FILING DATE: 11-JUL-1995
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                                                                                                                                                                                                                                                                      Sequence 156 Application PT/TUS9508743 Sequence 156. Application PC/TUS9508743 GENERAL INFORMATION:
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TYPE: nucleic acid
STEANDEDNESS: double
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Local Similarity 85 1%;
nes 268; Conservative
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304 AAGITSGAGAICAAA 318
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MOLECULE IYPE:
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395 GIAGIACAGIGGAAAGICTICAGGCICCACICIGGIGAIGGICAGAGIGAGGCIGGCC 454 | HT | HT | HTH |
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OF AGENCY AND ACCOUNTY OF A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 69.5%: Score 221: DB 13; Length 13254; Best Local Similarity 85.1%; Prod. No. 7.20e-144; Matches 258, Conservative 0; Mismatches 47; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
Sequence 13254 PF: 3238 A: 2251 C; 3559 G: 2205 T; C other:
                                                                                                                                                                                                                                                                                                                                                                                                  SCHTWARE: Patentin Rejease #1.0, Version #1.25 (EPC)
TITLE OF INVENTION: TO HUMAN IMMUNOUSFICIENCY VIRUS NUMBER OF SEQUENCES: 170
COMPUTER PERDARLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r 13
05-08-276-852-170 STANDARD; DNA; UNC; 13254 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER - POTZMS95/08743
FILING DATE: 11-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/276,852
                                                                                                                                                                                                                                                                                                                                                                    PC-140S/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11-19-19-5 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UNRER: 18-19-19-4 INFORMATION FOR SEQ ID NO: 170: SEQUENCE CHARACTERISTICS: LENGTH: 13254 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-1058/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     635 TGGAGACTGCGTGAG 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455 AGACCCACTGCGGCTGAACCTGTCTGAGATGCCAGAGGCCCTATTGGAAACACCATGTAT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515 GACCAGCCTTGGAGCCTGGCCAGGTTTGTGCTGGTACCAGGCTACGCGGCGGCTGCGAAT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575 GCTGTGACTGGACCTACAGGAGAAGGTGGCTCTTTCCCCTGGAGACAGAGACAGGGTGCC 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
FITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tength 13254,
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
Sequence 13254 BP; 3238 A; 3251 C; 3559 G; 3266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 221; DB 7, Tength 132
Pred. No. 7.20e-144;
0; Mismatches 47; Indels
                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .r 14
US-08-053-131-178 STANDARD; DNA; UNC; 812 BP.
                                                                                                  APPLICATION NUMBER: US/08/276,852
FILING DATE: 18 -7UL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-6EP-1993
PRIOR APPLICATION DATA: US 07/954,148
                                                                                                                                                                                                            APPLICATION NUMBER: US 07/954,148 FILING DATE: 30-SEP-1992 ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                         NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENDE/FOCKET NUMBER: SCP1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 178, Application US/08053131.
Sequence 178, Application US/08053131
Patent No. 5641016
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
                                                                                                                                                                                                                                                                                                                                                                                   13254 base pairs
                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 59.5%;
Local Similarity 85.1%;
es 268; Conservative
            COMPUTER READARLE FORM-
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                  circular
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 92037
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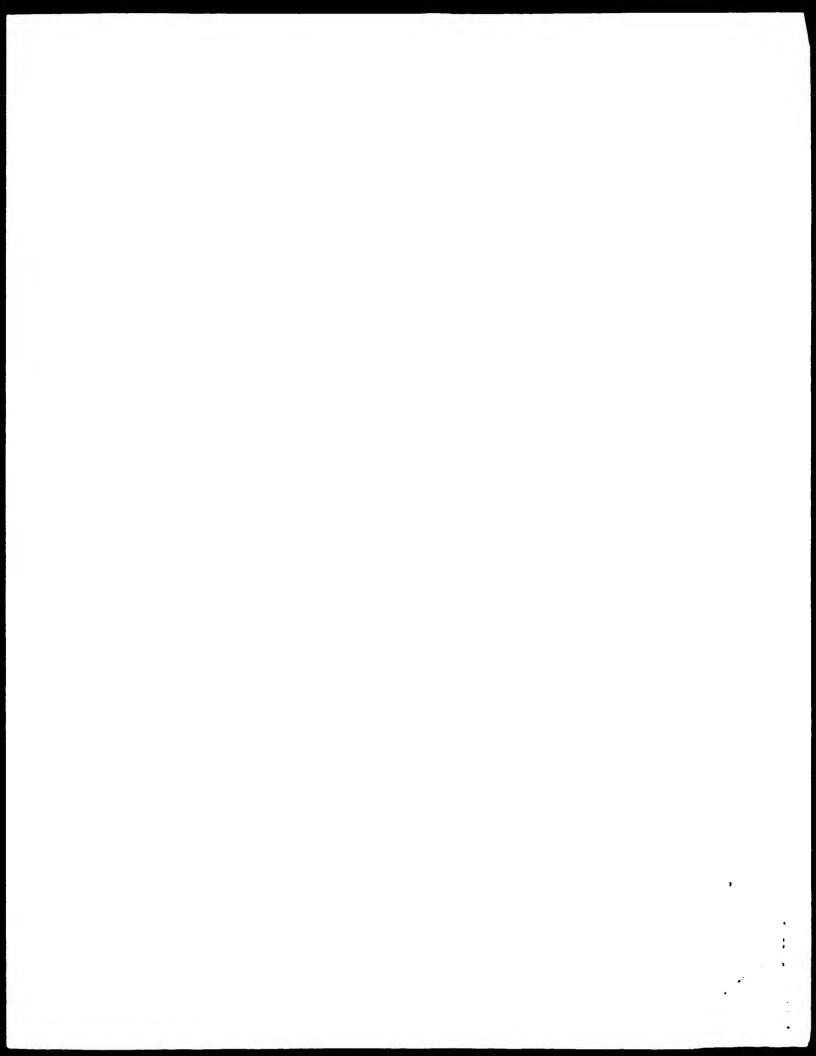
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619 GGCAGFGGGTGGGACACACATTCACTCTCACCATCAGAGCTTGGAGAGTTTT 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels
                                                  One Market Plaza, Stewart Tower, Suite 200
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
AndresSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOGATION: join(199, 246, 418,714)
Sequence 812 BF; 201 A; 225 C; 187 G; 199 T; 0 other;
                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRNT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 216; DB 7; L Pred No. 4.17e-140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 679 GCAGITIATTACICICAGCAGCGIAACAACIGGCCIC 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
It US-08-053-131-180 STANDARD; DNA; UNC; 900 BP.
AC XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
APPLICATION NUMBER: US 07/853,408
                                                                                                                                                                                     UMBER: US/08/053,131
26-APR-1993
N. ...
                                                                                                                                                                                                                                                                                                                                     APPLICATION NOTICE 1992
FILLING DATE: 18-MAR-1992
ATOENEY SAGENT INFORMATION:
MAME: SMILTH, WIlliam M.
                                                                                                                                                                                                                                                                                                                                                                                                     PEFERFNCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       812 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                    ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 91 7%;
nes 254; Conservative
                                                               CITY· San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                          USA
                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                          COUNTRY:
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421 ACACAGICICCAGOCACCIGICIIIGICIOCAGGGAAAAGAGCCACCICICCIGCAGG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 POPAGGIOCICATGIALGAIGCAIGCACAGGGGGAGIGGCAIGCCAGGCGAGGIICAGI 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 GCCASSCICCICAICIAIGGISIAIGCAGCAGGGGGGGGATGGCAGAGAGGIICAGI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 GGCAGIGGGCCIGGGAACAACIICACICICACOAICAGCAGCITAGAGCCIGAAGAITII 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Protert
ITILE OF INVENTION: Transgenic No. 5661016-Human Animals for
ITILE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 212; DB 7; Length 900; Pred. No. 4.25e-137; 0; Mismatches 14; Indels
                                                                                                                                                        SSEE: Townsend and Townsend Khourie and Crew: One Market Plaza, Steuart Tower. Suite 200 San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: join (180..227, 397..693)
Sequence 999 (F) 225 A: 344 G: 254 S: 227 I; 0 other)
                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990.860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-192
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/053,131
FILING DATE: 25-APR-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
            Sequence 130 Application US/08053131
Sequence 180. Application US/08053131
Patent No. 5551016
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14/
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEG ID NO: 180:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.5%;
                                                                                                                              NUMBER OF SEQUENCES: 19
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                              94105
                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                   STATE
01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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14; Indels 3; Gaps 1;
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658 GCAGITTATTACIGICAGCAS 678
                                                  247 GCAGIGIATIACIGICAGCAS 267
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Search completed: Tue Feb 24 14:09:25 1998 Job time : 60 secs.



GGACCAAGTTGGAGATCAAA 318 758.215 Million cell updates/sec CCTGGITCAACCTCIAGIFT >US-08-844-215-17 (1-319) from USOP944215.seq 318 1 GAGCTCACGCAGTCTCCAGG Tabular output not generated Description: Perfect Score: N.A. Sequence

Comp:

CICGAGISOSICAGAGATO

TABLE default Gap 6 Scoring table:

159651 segs, 57699962 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-geneseq30

| Spart | Spar

Mean 8.015; Variance 4.892; scale 1.538 Statistics:

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

					TOTAL STORY	5	
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Result No	ر م د د د د د د د د د د د د د د د د د د د	Query Match	Query Match Length	DB.	a :	Description	Pred. No.
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CI	276	6). Y.C.	990	٢	042707	オエランしゅ イクランじゅ	240-168
~	C1 C1	6.48	3.1	C	236625	Immunoalebalin x101.2	4.62e-164
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u'i	193	⊖ 60	<u>.</u> ن ن ق	C	237102	DNA fragment wkss 8,	010.165
۶	267	84.0	990	r	044224	Human DNA fragment vk	5.51e-162
۲-	254	93.0	7 (5	X.	134564	Anti-Iung tumour anti	6.550-160
œ	562	₹. (3)	325	Ξ	862335	Light chain of Amb al	486.150
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F *	251	다. 근 60	6166	16	092547	Expression vector, pP	7.786-158
12	522	0.1	646	4	115203	pd3AP313 anti-tetanus	1.880-155
13	255	91.4	546	_	Q70487	Anti-tetanus toxoid l	1.88e-156
14	257	30.8	324	u^	929766	Gene for Lv region of	4.53e-155
v -	C .	c F	E 7	Ċ	.00171	St. Statico Garage Tra	1790.151

7 0	1.216-142	27.6-14	.42e-13	1.0[4.	, ,	× 1 - 07	.276-3	3.5	.270-1	.630-12	.636-12	.636 att	.316-1	.330-12	6-015	.250-8	.266.8	9-060	8-96J.	8-060.	9-0-6	2-369	.050-7	480-7	11e-7	.116-7	.116.	.11e-7	66.7
	8001.001.00	A Lectificated 10	equence coding hu	id., fragmore on	encoding modi:	ectide sequenc	fragment vk6	DNA fragment	an Vikappa gene y	fragment wk65.5	an Vikappa gene v	uman DNA fragment v	chain va	Bl IgG aberrant lig	NA encoding kappa	indolponmun as	r L chain v	i-pseudomonas ser	nan antto nmour a	.pseudomonas aer	; abdambas bu	iludoiponmmi ni	conta, an OR	TGF beta-2 seF	i sednence t	To and took A see	odes V region of	es Vehi region	qht.
0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9	3)	u'.	160	160	313	C1	n d	ď.	0.0	4	0.7	187	334	344	** ***	163	C.	163	317	344	789	737	011	770	149	8094	005
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* * *	. 6	(1)	10.4	1.0	(∤	C 1	~~	+ 1	┛	П		-	c.	C.	3	5	и.	-7	- +	-7	マナ	4	4	**	⋖*	7	4	4	4
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ALIGNMENTS

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DNA segments encoding menoclonal antibody - which binds to apple and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV, for treating AIDS, and for diagnosing and monitoring HIV, for theating HIV, and for the AIDS and for the AIDS and for the AIDS and for the AIDS and AIDS an
                                                                                          Odernov.
Odernov.
P105 rearranged variable region light chain.
P105 rearranged variable region light chain.
Monoclonal antibody: MAD, envelope, glycoprotein, gp120; HIV: AIDS;
CD4; receptor: hybridoma: polymerase chain reaction: PCP; heavy: light:
chain; epitope; immune deficiency: ss
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10-DEC-19921 US-804652.

10-DAD D DNAM FREBER CANCER INST INC.

(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL COPP.

WASSELLING WA, MAIASCO WA, POSNER MR, SOGROSKI 163:

P-PSDB: R41286.
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
.r 1
Q49155 standard; cDNA; 387 BP.
Q49155;
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                                                                                                                                                                                                                                                                                          Homo sapiens.
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mat_peptide
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Query Match

87,4%! Score 278, DB 7; Length 387

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                                                                                                                                           67 GCCASTCAGAGTGTTAGGAGCAACTACTTAGCCTGGTACCAGCAAAAACCTGGCCAGGCT 126
                                                                                                                                                                            193 cccaggetecteatetatggtgeatecageagggeeaetggeateceagaeaggtteagt 252
                                                                                                                                                                                                                                      253 ggcagigggictgggacagacticactcicaccatcagcagagiggagccigaagaiitti 312
                                                                                                                                                                                                                                                                                                 gcagigitatiacigicagcaataigataaciccgittigiactitiggccaggggaccaag 372
                                                                                                                                                                                                                                                                                                                             247 GCAGTGTATTACTGTGAGGAGTATGGTAGGTGAGGTGGGAGTTTTTGGCCAGGGGAGCAAG 306
                                                                                7 ACCCAGICICCAGGCACCCIGICIIIGICICCAGGGGAAAGAGCCACCCICICCIGCGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody; MAb; envelope; glycoprotein; gpl20; HIV; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Paye 73-74; 109pp. English
The nucleotide sequence of F105 Vk (Q42707 - sequence differs from
other #105 Vk sequences given elsewhere in the specification) was
compared with germline gene Humvk325 (Q42706), showing 97.7%
                                                                                                               133 gocagteagagtgttageageaggtaettageetggtaeeageagaaaeetggeeagget
                                                                                                                                                                                                       127 CCCAGGOTOCTCATCTATGOTATCCAGGGGGGGGGGGGGATGCCAGGAGGTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA segments encoding monoclonal antibody - which binds to gpl20 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
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0
                   Indels
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                  Mismatches 17;
Best Local Similarity 94.6%; Pred. No. 1.34e-169; Matches 295; Conservative 0; Mismatches 17;
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(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain; epitope; immune deficiency; ss.
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Q42707 standard; DNA; 390 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4; receptor; hybridoma;
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WPI; 93-214174/26.
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/label- F105Vk
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/label= F105Jk
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/label= CDR1
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/label= CDR2
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thyroid function stimulatury course.

(alim 4, page 12, 18pp; Japanese.

T79919-179922 represent the immunoglobulin heavy and light chain variable regions isolated from peripheral blood lymphocyte strains. These sequences were isolated from the BBT and 101-2 strains of peripheral blood lymphocytes of a Basedow's disease patient. These sequences are replaced, deleted or inserted into an antibody, to create the antibodies of the invention have thyroid function stimulating activity, and act by combining with thyrotropin receptor. The antibody can be used in a method to detect autoantibodies which have thyroid function stimulating activity.

Sommence 372 BP; 81 A; 115 C; 95 G; 81 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-001-1997 (first entry) Inmunoglobulin riOl-2 light chain variable region coding sequence. Immunoglobulin, variable region, heavy chain, thyrotropia receptor; thyroid simulating activity; light chain; Basedow's disease; antibody; peripheral blood lymphocyte; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 acgoagtefocaggeacongtottigioteraggggaaagagcaconteroragag 132
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similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the V \kappa \ III subgroup gene family.
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0; Mismatches 15; Indels
                                                                                                                                                    86.8%; Score 276; DB 7; Length 390;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                            Pred. No. 3.24e-168;
                                                                                      102 G,
                                                                                                                                                                                                                                   Mismatches
                                                                              115 C,
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T79922 standard; DNA; 372 BP.
                                                                              86 A,
                                                                                                                                                                                                   96.2%;
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                                                                                                                                                                                                                                   303; Conservative
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WPI; 97-344899/32.
P-PSDB; W24539.
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22-NOV-1995; JP-3281
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es 285; Conser
                                                                                                                                                                                                Local Similarity
                                                                          390 BP,
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J09140386-A.
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                                                                                                                                                                                                                      25% ggcagigggicigggacagacticacticactoscatoagcagactggagcetggagatttt 312
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                                                                                                                                                                                                                                                                                                                                                                                                         375 acgeagtetonaggnaedettgtetttgtetoeaggggaaagagecaceetotoetgeagg 434
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67 GCCASTCASASIGIIAGSASCAACIASIIAASCASTASCAAAAAAAAAAAAGTGGGGAGGGT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig. 42: 295pp. English.

Human DNA fragments vk55.3, vk65.8 and vk65.15 (given in Human DNA fragments vk55.3, vk65.5, vk65.8 and vk65.15 (given in Human DNA fragments vk55.2) cospectively, each centain a V-kappa gene segment that can be used to form a complete human light chain minilocus transgene for expression in a nonhuman transgenic animal for sequence for expression in a nonhuman transgenic animal for sequences of the V-kappa coding regions are given in 869928-962931 Sequence 900 BP; 220 A; 241 C; 201 G; 238 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic non-human animals producing heterologous or chimeric antibodies \, \, for binding a pre-determined human antigen with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transqenic mouse; transqenic animal; antibody engineering; variable region: light chain; minilocus transqene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Human V-kappa gene vk65.8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label - Splicing_signal misc_signal 672..580
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US-096762.
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09-MAR-1994; US-209741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chimeric antibody; ss.
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22-THL-1993; U
18-NOV-1993; U
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                                                                                        187 GGCASTGGSICIGGGACACASACTICACICICACCAICAGCAGACIGGAGCCIGAASATITI 246
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Example 21; Fig 43; 94pp; English

The present sequence is the variable kappa chain gene segmen;

containing human DNA fragment; VK65 9, which was co-injectred along
with the human DNA fragments VK6 3, VK65 5 and VK65 15 into half
day mouse embryo pronuclei, to generate an unrearranged light chain
minilocus transgene. The resulting transgent mice can be used for
                                                                                                                                                                                                                                                                          14-APR-1997 (first entry)
May fragment wk6.8, containing variable kappa chain gene.
Variable: kappa chain, gene segment; human; DNA fragment; vk65.8:
unrearranged; light chain; minilocus; transgene; transgenic; monse.
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               127 CONTRACTOR TOTAL GG 161A LOCAGO A GG CONTRACTOR CANADA CONTRACT
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specific antigens, this comprises immunising a mouse with a preselected antigen and collecting antigen binding heterologous human gamma immunoglobulins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of heterologous human immunoglobulin(s) - by immunistua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the production of heterologous (i.e. human) antibodies against
                                                                                                                                                                                                                                                                                                                                                     production; heterologous; antibody; gamma; immunoglobulin; ss.
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Best Local Similarity 98.2%; Pred. No. 5.51e-162;
Matches 272; Conservative O: Mismatches 5; Indels /
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116..154
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I37182 standard; DNA; 900 BP.
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18-MAP-1992; US-853408.
23-JUN-1992; US-904068.
16-DEC-1992; US-990860.
(GENP-) GENPHARM INT INC.
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US-810279.
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P-PSDB; W03948.
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13-AUG-1996.
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P-PSDB; W11155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from the resulting clones were sequenced and functional clones were selected on the basis of open reading frames, intact donor and acceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q44225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The V-kappa specific oligonucleotide 050327 was used to probe a human placental genomic DNA library cloned into lambdaEMBL3/SPB/T7. DNA fragments containing V-kappa segments from positive phage clones were subcloned into plasmid vectors. Variable gene segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 decaggetenteatetatggtgeatecageaggagenactggeateceaganaggttnagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic non-human animals contg. immunoglobulin heavy chain trans gene - used to produce useful antibodies by isotype
                                                                                                                                                                       10.NOV-1993 (first entry)
Human DNA fragment vk65.8 containing V-kappa gene segment.
Immunoglobulin; light chain variable region; minilocus;
isotype switching; unrearranged functional Vk gene segment;
human light chain transgene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR 7; Length 900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "splicing and recombination signal sequence"
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84.0%; Score 267; DR 7; Us
Best Local Similarity 98.2%; Pred. No. 5.5le-162;
Matches 277; Conservative A. Minmatches
615 geagigatitacigicageagiatigitageicaceie 651
                                          247 GCAGISTATTACIGICAGCAGTATGGIAGCICACCIC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the precise start point of the GRF; indicated"
                                                                                                                                                                                                                                                                                                                                                                           /note= "splicing and recombination signal ?"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminated by a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note* "nucleotides 116-118 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 C;
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                                                                                                                               Q44224 standard; DNA; 900 BP.
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23-JUN-1992;
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555 ggcagtgggtntgggacaganttcantctcancatnagnagactggagnntgaagatttt 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 GCCASTCAGASTGIIAGGAGCAACIACTIAGCCIGGIACCAGCAAAAACTGGCCAGGCI 126
                                                                                                                                                  187 GGGAGTGGGGTCTGGGACAGACTTCACTCTCACCATCAGACTGGAGCTGGAGCTTAAGATTTT 246
127 CCCAGGCTCCTCATCTATGGTG1A1CCA3CA3G3CAACTGGCATCCCAGACAGTTCAGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ACGCAGTCTCCAGGCACCCTGTCTTTGTGTTCCAGGGGAAAAAAAGAGCAGATGTTGTTGTGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-ling turbour antigen monoclonal antibody TB2A36C3 - produced by Epstein-Barr virus transformation of human lung cancer patient B-cells, useful in conjunction with other agents for lysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 claim 12, Pages 24-25, 46pp; English chain from the monoclonal antibody (MAb) TB2A36C3, which has high specificity against lung tumour antigens and is produced by an Epstein-Barr virus (EBV) transformed TB945 human R cell line. The MAh can be used to screen serum or tissue samples for a carcinoma associated antigen, lyse tumours in anti-tumour therapy (optionally with other agents) and activate immune competent CD4 or CD8 cells in a patient's bload
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lung cancer) patient were cut into fine pieces and mashed. Fure B cells, isolated using CD19 coated immunomanetic beads, were immortalised by EBV transformation, and plated and assayed for activity. Clones which showed positive reactivity with autologous rumour cells from the patient and the SCLC cell line NC1H69, were subjected to limiting dilution to prepare the MAb. (Pevised entry submitted to correct cross-reference to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cumour draining lymph nodes obtained from a non-SCLC (small cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1997 (first entry)
Anti-lung tummour antigen monoclonal antibody light chain cDNA.
Light chain monoclonal; antibody; TB2A36C3; lung; tumour: EBV;
Epstein-Barr virus; TB945; human; B cell; screen; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : DB 28; Length 402;
6 55e-160:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 15: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 G;
                                                                                                                                                                                                                                615 gcagtgtattactgtcagcagtatggtagctcacctc 651
                                                                                                                                                                                                                                                                                                             247 GCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCTC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding protein record (Will55)).
Sequence 402 Br; 89 A; 117 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 254:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 83.0%, Score 264:
Local Similarity 94.3%; Pred No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                T33664 standard; cDNA; 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEDE/) MEDENICA R D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1996; U03661.
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Example: Page 27-29: 35pp: English.

Example: Page 27-29: 35pp: English.

Blood samples were collected from patients immunised with allergens including rapped (Ambrosia elator) extracts. The dominant allergen in short rapped (Ambrosia elator) extracts. The dominant allergen in short rapped (Ambrosia elator) extracts. The dominant allergen in short rapped and a protein A single cell such strand colores.

Then fused with mouse myloma cell line 653 and the resultant clones can be a single and a protein A single cell such strand colore Action and allergen in secreting was selected. Total RNA was propd from the AL 15-3.2 cells and first strand color was proped from the AL 16-5.2 cells and first strand color was the template, and the 5' and 3' kappa light chain primers (165540, 165541) were used in PCR and amplified band of the expected size was contact this amplified by a sequence are shown in 166538 and 185286. Comparison of the deduced to that the AL 165.2 L-chain is a member of the human VK III subpp.
                                                                                                                                                                                                   NECESTRATE AND CONTROLLED FOR THE CONTROLLED FOR THE STATE OF SOCIAL STATES AND CONTROLLED AND C
                                                                               187 GGCAGIGGG WIGGGACASACTICACTCCACCATCAGCAGATTGGAGCCTGAAGAITTI 246
                                                                                                                                                              67 GCCASICAGAGTGTIAGGAGCAACIAGTIAGGCIGGIACCAGCAAAAAACTGGCCAGGCI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 occasyneteeteatetatgetacatecataaggteatetggeateecagacaggtteaet 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 ggcadidagicidaggacagacticacticicacacatcagcadaciggagcotgaagatiti 252
253 ggcagigagiciqqacagacitcattctccccaccatcaqactgagcctgaagattt 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 gecagticagacigitageageaaciacitageeiggiaeceageacaaaacetggeeagget 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 acgraqiciccaqqoacceigicitiqiciccoaqqqqaaaqqecacceicciqcaqq 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsn. contq. allergen specific IgA for treating mucosal tissue and conjugates of allergen specific Ig with polymer, for treating IgE mediated allergies and for isolation of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain of Amb al-specific 1gG4 antibody.
Allergen-specific immuoglobulin A; 1qA; AL 15-5.2; light chain:
allergen Amb a 1; ragweed; Ambrosia elator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Longth 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sante 262; DR 11; Pred. No. 1.58e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 1..325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q66538 standard: cDNA: 325 BP.
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Chang IW:
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Best Local Similarity 92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287; Chrisbryalino
                                                                                                                                                                                                                                                                                                                        373 aagetggagateaaa 387
                                                                                                                                                                                                                                                                                                                                                                                                   304 AAGTIGGAGATCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1993; 012501
21-DEC-1992; 08-994126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09414475-A.
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Monoclonal antibody; MAD: envelope; glycoprotein; gp120; HTV: AIDS: CD4; receptor; hybridoma; polymerase chain reaction; PCR: heavy; light; chain; epitope; immune deficiency; ss.
73 acgeagieiecoaggeacecigieiiidieiigaeagagagaaaagaeceacecieieceigeagg 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 cecaggetecteatetatggtgeatecageagggeeactggeateceagaeaugtteagt 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ACGCAGTCTCCAGGCACCCTSIC11/S1C1/CCAGGGAAA3AGCGACCTCT/CTGCGGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA segments encoding monoclonal antibody - which binds to ap120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV, infection bisclosure, Page 73-74: 109pp; English.

Disclosure, Page 73-74: 109pp; English.

Disclosure, Page 73-74: 109pp; English.

Other PIOS Was sequence of FIGS VK 642707 - sequence differs from cother FIOS VK sequences quiven elsewhere in the specification) was compared with generalize group Humskalf (447705), showing 97.7% and lattice group Humskalf (447705), showing 97.7% similarity. By nucleotide sequence analysis, FIOS appears to be dequence 390 HP; 88 A: 115 C; 99 G; 88 F:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 gecaqteagagtgttageaqeaqetaettageetggtaeeaqeaqaaanetuqeeaqet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scare 262; DB 7; Length 390; Pred No. 1 58e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DAND ) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marasco WA. Posner MK.
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                 042706 standard; DNA; 390 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
Local Similarity 94 0%.
les 296: Conservative
                                                                                                                                                                               01-NOV-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           130..165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211..231
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                                                                                                                                                                                                                                                                                                                   51..390
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10-DEC-1991; US-804652.
                                                                                                                                                                                                                                                                                                                                                 1..351
                                                                                                                                                                                                                                                                                        9
                                                                                         307 TTGGAGATCAAA 318
                                                            313 gttgaaatcaaa 324
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WPI; 93-214174/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 93-214174/
P-PSDB; R38672.
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                                                                                                                                                                                                                                                           Homo sapiens.
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/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR3
                                                                                                                                                                                                                                                                                     sig_peptide
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                                                                                                                                                                                                                                                                                                                   mat_protein
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'label= Jk2
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2737 igcagggccagicacagigitagcagggcctactiagcciggiaccagcagaaacciggc 2796

QQ ά ď δ g ò Q à q ŏ

61 TGCGGGGCCAGTCAGAGTGTTAGGAGCAACTTAGTTAGTCTGGTAGCAGAAAAACCTGG

1 GAGCTCACGCAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGAAAGAGCACCCTCTCC 60

2797 caggeterraggeterteatetatggtacatecageagggeeaetggeateeeagg 2856

121 CAGGCTCCCAGGCTCCTCATCTATGGTATCCAGGAGGCCACTGGCATCCCAGGAGG 180

2857 ttcagtggcagtgggtctgggacagacttcactctcaccatcagcagactggagcctgaa 291%

181 TICAGIGGCAGIGGGIGIGGGAGAGAGIJGAGIGIJGAGGAIGAGCAGAGIGGAGGCIGAA 240

2917 gattttgcagtgtactactqtcagcagtatggtggctcaccgtgg

II-WAR-1996 (first entry)

Expression vector, pPho-TT.

Human, Fab, variable chain, heavy; light, region, VH; VL, HIV, qpl20;
3bl; 3b3; 3b4; 3b9, MT4; humanised; monoclonal antibody; MAb;

Immunoreaction, neutralisation, passive immunotherapy, tetanus toxin;
alkaline phosphatase; phoA; ss; cyclic.

.T 11 092547 standard; DNA; 6166 BP.

092547:

Lerner RA;

Burton DR,

Barbas CF,

(SCRI) SCRIPPS RES INST. 19-OCT-1994; U11907. 19-OCT-1993; US-139409. 26-APR-1994; US-233619. 19-SEP-1994; US-308841.

WÔ9511317-A1. 27-APR-1995. Synthetic

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HIV-induced disease

THY-induced disease

THY-induc
                                                                                247 GCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCTCGG---ACTTTTGGCCAGGGACC 303
253 ggcagtgggtctgggacagacttcactctcaccatcagcagagtggagcctgaagatttt 312
                                                                                                                                                           313 gcagtgtattactgtcagcaatatgataactccgtttgctacacttttggccaggggacc 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pcomb3 expression vector.

pcomb3; pagemid expression vector; bacteriophage; coat protein 3; Gene III; filamentous phage; minor phage coat protein; cpIII; cp3; bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120; combinatorial Fab lbbrary; cassette; Fd/cp3; lac2 promoter/operator; ribosome binding site; RBS; PelB leader; spacer; tether sequence; MT4; pMT4-3; antibody; ss; cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunodeficiency virus - used for diagnosis and immuno:therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1118 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic human neutralising monoclonal antibodies to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1232 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1171 C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies against gp120 of HIV.
Sequence 4691 BP 1170 A
                                                                                                                                                                                                                                                                                                                                                                                                                        092546 standard; DNA; 4691 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-1995.
19-OCT-1994; U11907.
19-OCT-1993; US-139409.
26-APR-1994; US-233619.
19-SEP-1994; US-30841.
(SCPI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                  373 aagctggagatcaaa 387
                                                                                                                                                                                                                                                                                                                    304 AAGTIGGAGAICAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burton DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-induced disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95-170235/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09511317-A1.
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consists of a DNA molecule having two cassettes to express two soluble proteins a heavy chain and a light chain. The vector comprises. operatively linked 5' to 3', a first cassette consisting of the phonorometer/operator sequences, an EcoRI restriction site, a ribosome binding site (RRS), an OmpA leader, a Stil restriction site, a spacer region, a cloning region bordered by 5' sacl and 3' Xbal restriction sites, an NcoI restriction site between the two cassettes, and a second cassette consisting of an expression control RBS, a PolB leader, a human consensus amino terminus spacer region comprising the sequence EVQLLE, a cloning region bordered by 5' XhoI and 3' SpeI restriction sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the expression vector, ppho-TI which is a modified version of the phagemid expression vector, promis given in Q92346. Pho-TI provides for the expression of soluble Fabs which are secreted into the periplasmic space which is regulated from the alkaline phosphatase (phoA) promoter. This plasmid was used within the scope of the invention to express various mutagenised human Fab's which comprise heavy and light variable regions which bind to HIV 99120. PPho-TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            followed by a Sfil site, expression control stop sequence EVOLLE, followed by a Sfil site, expression control stop sequences and a Notl restriction site. The pPho-TT expression vector contains a light chain stuffer that is 1200 bg in length and a Neary chain stuffer that is 300 bg in length. The nucleotide sequences of the heavy and light chain stuffers encode the heavy and light chain variable domains of a tetanus toxin-specific Fab.
                                                                                                                                                                                                                                                                                                                                                                                                                         immunodeficiency virus - used for diagnosis and immuno:therapy of
                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic human neutralising monoclonal antibodies to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV-induced disease
Example 2; Fage 193-197; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                       95-170235/22
Score 261; DB 16; Length 4691;
Pred. No. 7.78e-158;
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26N7 gagotinangnagtiticeaggnachitgtintttgtiticagggggaaagagmaniittin 2726

Mismatches

93.48;

Best Local Similarity

. . . .

Matches

ρp

Conservative

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4607 dagotoacgcagtotocaqqcachfqtotttgtctonagaggaaagagcahotin 4466
                                                                                                                                                       4567 tgcagggccagtcacagtgttagcagggcctacttagcctggtaccagcagaaacctggc 4726
                                                                                                                                                                                                                                              472] caggotocoagantoctoatotatagtacatocagoagggoootocagaoagg 4786
                                                                                                                                                                                                                                                                                                                                      4847 gattttgcagtgtactactgtcagcagtatggtggctcaccgtgg---ttcggccaaggg 4903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a human anti-teranus toxic invariant intermediate the moroded by a Poonba based expression vector. The heavy and light chain variable domains are used in an example to demonstrate the produ. Of antibodies for invention have sequences at their 3° and 3° onds both capable of binding different framework regions linked by a sequence 6 to 50 nucleotides long Different immunoglobulins produced using the primers may be used to produce antibody libraries having diverse movel immunospecificities and affinities. By using mutagenic ONs an extremely large produced the universal light chain increases the number of contacted and use of the universal light chain increases the number of contacted and use of the universal light chain increases the number of contacted and use of the universal light chain some statements. Sequence 645 BP: 152 A: 187 C; 170 G; 127 T;
                                                                                                                                                                                                                                                                                                                                                                                181 TTCAGTGGGGAGTGTGGGGAGAGATTGACTGTGAGCATCAGCAGGAGTGGAGGGGGAA 240
                                                                                                                                                                                                 13-001-1996 (first entry)
pC3APN3 anti-tetanus tovoid jg light chain variable domain CDNA.
Mutagenesis Ig: immunoglobulin FB: Iframework region, variable. CDB,
complementarity determining region: light; heavy chain; PCR;
polymerase chain reaction; antibody library; diversity; affinity;
immunospecificity; ss.

    6) tyriagynecaatecaeaatettaaceagyareettageettageetggtaceageaaaaeetgge 129

                                                                                                          1 dantinacidasticionastranostranostranostranosasaassaasaacoronos 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gageteaegeagtetecaggeaecetgtetttgtetecaggggaaagagecaecetetee 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAGGTCAGGCAGTCTCCAGGCACCCTGTTTTTTTTGTCGAGGGAAA3AGCCACCGTCTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain gene CDR - useful for prodn, of Ig heavy and light chain examinatorial antibody libraries example 1; Page 84: 125pp; English.
T15202 and T15203 are the heavy and light chain variable domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 19; Indels 3: Gaps
                            Saps
                                                                                         Length 545;
                          [nde]s
Best Local Similarity 93.4%; Pred. No. 7.78e-158;
Matches 297; Conservative 6: Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 259; DB 22;
Pred No 1.88+-156;
                                                                                       as OF Rurton DP, Lernor PA-
96-171625/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .T 12
T15203 standard; cDNA; 646 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4904 accaaqqtqqaactcaaa 4921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ACCAAGTIGGAGATCAAA 318
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Local Similarity 93 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-1995; 911235;
02-SEP-1994; 98-300386;
(SCRI ) SCRIPPS RES INST.
Barbas GF Rutton DR. 1
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This sequence was pref dayd in the method of the lowering for the production of antibody libraries containing increased diversity. The sequences given in 97040 86 are primers which were used for induction of mutagenesis in a complementary determining tegton (CDR) of an immunoglobulin light chain gene. These primers contain a 3' terminus capable of hybridising to a first framework region, a 5' terminus capable of hybridising to a formation framework region, a 5' terminus capable of hybridising to a second framework region and a nothernorm sequence between the 5' and 3' termini having the formula (NNK). Where is 3.24. These primers may be used to produce antibods in the control of immunoglobulins heavy or light chains that are displayed on the surface of filamentous phane particles comprising the library. These primers prof. mutate the light chain CDR3. Sequence 645 BP. 152 A: 187 C: 177 C: 127 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligo-nucleotides - used as PCB primers for production increased diversity antibody libraries, for screening antibodes and page 84.85; 120pp; English.
This sequence represents the light chain coding sequence derived from this sequence represents the light chain coding sequence derived from the surface display phagement expression vector, pright, prightly contains the bacteriophage gene III and heavy and light chain variable domain sequences for encoding human Pah antibodies against Letanus Loxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64-APR-1995 (first entry)
Anti-tetanus toxoid light chain cDNA from vector, pG1AP313, Polymerase chain reaction; primer; mutagenesis; PCR; amplify; adviversity; antibody; complementarity determining region; GDR; framework; constant; light; heavy; phaye; immuneglobulin; library; ss.
                                                                                                                                                                                       181 tecagiggearigggietgggaeagaetteaeteteaeratoageageariqgauceigaa 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 tgcagggccagtcacagtgttagcayagcttagctagcttagcagcagaaactgg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
Local Similarity 93.1%: Pred. No. 1.88e-156;
es 296; Conservative C; Mismatches 19; Indels 3, Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-1993; US-174674.
(SCRI ) SCRIPPS RES INST.
Barbas CF, Barton DP. Lerner PA;
WPI: 94-279673/34.
                      THEFT HILL
                                                                                                                                                                                                                                                                                                                                                                                                                                170487 standard; cDNA; 646 BP
                                                                                                                                                                                                                                                                                      298 accaaggtggaactcaaa 315
                                                                                                                                                                                                                                                                                                                                   301 ACCAAGIIGGAGATCAAA 318
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02-FEB-1994: U01234.
02-FEB-1903: US-012566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 acgcagictccaggcacccigittitgictccaggggaaagagccacccictcctgcagg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 gecagicagagiatitageageagetactiagectiggiaeceageagageetiggeeagget 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 gattttgcagtgtactactgtcagcagtatggtggctcaccgtgg---ttcggccaaggg 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal human rheumatoid factor - obtd. by prodn. and secretion of hybridoma obtd. from cell fusion of human bone marrow derived lymphocyte and P301 mouse myeloma cell Disclosure; Page 5; 7pp; Japanese. The sequence shown encodes the variable region of the light chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 ACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCCCCCTCTCCTGCGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a human monoclonal antibody rheumatoid factor YES8C. The gene may be isolated from the bone marrow soln of a rheumatoid arthritis patient and used to produce hybridomas, allowing produ. of the rheumatoid arthritis factor at constant quality in large quantites.
                                        181 tecaqtggcagtgggtetgggacagaettcaeteteaceateageagaetggageetgaa
                                                                                                                                                                                                                                                                                                                                                                            Gene for Lv règion of human rheumatoid factor antibody.
Light chain; variable region; YESBC; arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   Q29766 standard; cDNA; 324 BP
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                                                                                                                                                                                                   298 accaaggtggaactcaaa 315
                                                                                                                                                                                                                                         301 ACCAAGTTGGAGATCAAA 318
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Local Similarity 96.7%;
nes 256; Conservative
                                                                                                                                                                                                                                                                                                                                                         18-MAR-1993 (first entry)
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/note= "leader seguence"
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22-FEB-1991; 048704.
22-FEB-1991; JP-048704.
(EZAK/) EZAKI K.
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/note= "encodes CDR1"
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/note= "encodes CDP2"
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/note= "encodes CDR3"
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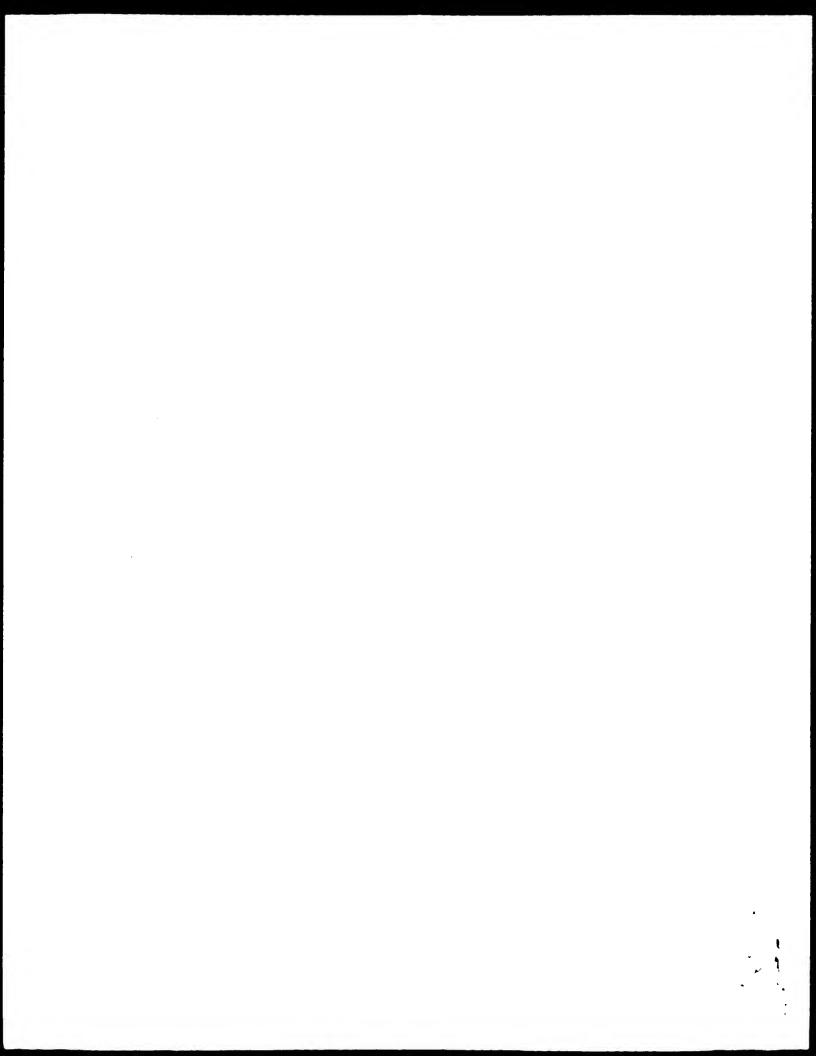
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187 GCCACTGGGTCTGGGACAGACTTCACTCTGACTACAGACTGAGACTGGAGATTTT 246
                                                                                                                                                                                                                                     27-FEB-1997 (first entry)
Ulcerative colitis-associated paNCA Fab 5-4 light chain cDNA.
Ulcerative colitis: anti-neutrophil cytoplasmic antibody: ANCA:
pANCA: UCPANCA: antibody engineering: phage display; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR3
/note= "complementarity determining region 3"
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/note= "complementarity determining region 2"
                                                                             289 gcagigtatiacigicagcagiatggtagcicaco 323
                                                                                                                     247 GCAGTGTATTACTGTCAGGAGTATGGTAGGTCACC 281
                                                                                                                                                                                                                                                                                                                                                                                                                 /product- UC-associated ANCA IgG light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "kappa light chain variable segment"
misc_RNA 286..327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Kappa light chain constant segment"
misc_RNA 4..66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "kappa light chain joining segment"
misc_RNA 328 .645
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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(REGC ) UNIV CALIFORNIA.
Baun J, Eggena MP, Targan SR;
WPI: 97-042866/04.
                                                                                                                                                                               T 15
144091 standard; cDNA; 645 BP
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/note= "framework region 2"
/note= "framework region 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= N-terminal tag
nisc_RNA 4..285
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05-JUN-1996; U08756.
06-JUN-1995; US-472688.
                                                                                                                                                                                                                                                                                                                                                                             1..645
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                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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/label= CDR1
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             Antibody material associated with ulcerative colitis - comprising anti-neutrophil cytoplasmic antibody, characterised by perinuclear neutrophil staining pattern

5 Action anti-neutrophil staining pattern

6 A CDNA clone (144091) derived from human gut-associated lymphoid tissue codes for the light chain (WO7615) of recombinant UCPANCA Fab clone 5-4. Anti-neutrophil cytoplasmic antibody characterised by perinuclear neutrophil staining pattern (pANCA) associated with characterised using a phage display technique. Libraries of VH-characterised using a phage display the immunoreactivity of Characterised using a phage display the immunoreactivity of methods for screening for UCPANCA and for isolating UCPANCA.
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Best Local Similarity 95 38: Pred No 1 29e-151;
Matches 265; Conservative 0: Mismatches 13; Indels 0;
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P-PSDB; W07616.
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Search completed: Tue Feb 24 07:57:01 1998 Job time: 82 secs.



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                                                                                                                                                                                                                        Direct Submission
Submitted (24-OCT-1994) Mahmoudi M , University of Western Ontario,
                                   Medicine and Microbiology and Immunology, University Hospital Room BRE-12, London, Ontario, Canada, NSA 5A5 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pratt I F., Passenfi,L., Larrick,J., Pobbins,B., Banks,P.M. and
Kipps,T.J.
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Human lymphocyte DNA, from patient BRA with small lymphocytic
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Vertebrata; Sutheria, Primates, Catarrhini, Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 294; DB 90; Length 387;
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0, Mismatches 9;
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                                                                                                                                                  /tissue_type="human tonsil"
                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                             /note="V kappa segment"
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1..>387
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116 c 98 g
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                                                                                                                                   /clone="BUD45"
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Best Local Similarity 97.1%;
Matches 303, Conservative
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/translation="VLTQSPGTLSLSPGEPATLSGPASQSVSSSYLAWYQQPPQQAP#
LLIYQASSPATGIPDPFSGSGSGTDFTLTISP!EPFPFAVYGQQYGSSPHTFQQGTX
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Chapman.C.J., Spellerberg.M.B., Hamblin.T.T. and Stevenson F.K.,
Partern of usage of the VH4-21 gene by B lymphocytes in a patient
With EBV infection indicates orgoing mutation and class switching
Mol. Immunol. 32 (5), 347-353 (1995)
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                                                       Draft entry and printed sequence for [1] kindly submitted by L P Pratt, 20-SEP-1989.
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H.sapiens immunoglobulin kappa chain V-J region (S17B VL).
Z46310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Ig kappa chain V-J2-region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 292; DR 99; 1
Pred. No. 2.33e-234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DP 90;
little or no somatic hypermutation J. Immunol 143 (2), 699-705 (1989)
                                                                                                                                                                                                                                                    /db_xref="GDB:G00-119-341"
/db_xref="PID:g185909"
                                                                                                                                  /organism="Homo sapiens"
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                                                                                               Location/Qualifiers
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Best Local Similarity 96.8%;
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Chapman, C.J.
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Direct Submission
Submitted (20-071-1994) Caroline J Chapman, Molecular Immunology
Submitted (20-071-1994) Caroline J Chapman, Molecular Immunology
Group, Tenovus Research Laboratory, Southampton University
Hospitals, Tremona Road, Southampton, SO16 6VD, United Kingdom
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Larrick, J., Robbins, B., Banks, P.M. and
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M28166
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Human lymphocyte DNA, from patient ROB with small lymphocytic
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Pratt.L.F. Passenti.L. Larrick, J. Pobbins, B., Banks, P.M. ekipps, T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                               /product="immunoglobulin, kappa chain, V-J region"
93.c 88.g 71.t
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Pred No 2 33e-234.
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/cell_line="heterohybridoma"
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7. Immunch. 143 (2), 699-705 (1989)
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/db_xref-"GDB:G00-119-341"
/db_xref-"FDD:q185907"
/translation-"VILGESTIESSPSERATISGEASUSVSSYLAWYOGKP:GAFR
LLIVGASSRATATPUPPSGSRSGIGFILT:SPIEPEGFAVYY**_QYSSPWTF3031K
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Submitted (02-001-1906) M Welschof, Universitaet Heidelberg.
Institute of Immunology, Department of Transplantation Immunology.
INF 305, 69120 Heidelberg. FRG
Pelated Sequence: L28046.
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Eukaryotae, Eutheria, Primates, Catarrhini, Hominidae; Homo.
1 (bases 1 to 324)
Welschoff, M., Tarness, P., Schoeneberg, A., Kipriyanov, S., Land, A.,
Kleist, C., Voyt, A., Pficonmaior, K., Little, M. and Mc. Smayor, D.
Isolation and characterization of a human anti-IId serv antibody
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H.saplens mPNA for 1g light chain anti-TId, variable region.
YORS94
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anti-TTd gene: immunoglobulin variable region light chain.
                                                                                                                                                                                                                                                                                                       Length 320;
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Pred. No. 1.63e-232;
0; Mismatches 11; Indels
/gene="IGKV"
/note="Ig kappa chain V-J1-region"
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                                                                                                                                                                                                                             /organism-"Homo sapiens"
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                                   /codon_start=1
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/gene="IGKV"
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Welschof,M.
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Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western Bank, Sheffield S10 20H, UK
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/translation="E1VLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQA
PRLL1YGASSPATG1PNPFSGSGSGTNPT1 TISRLPPRPFAVYYCQYSSPPTFGPG
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Colls, J.C., Pegg, C.A.S., Rees-Smith, B. and Burton, D.R.
Probing the human anti-thyroid peroxidase repertoire of a
Hashimoto's thyroiditis patient using combinatorial phage display
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                                                                                                                           /product="variable immunoglobulin anti-TTd light chain" /db_xref="PID:e274128"
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Hexham, J.M., Furmaniak, J., Pegg, C., Rurton, D.P. and Smith, R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 acgeagtetecaggeaccetgtetttgtetceaggggaaagagecacceteteetgeagg 72
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                                                                                                                                                                                                                                                                                                                                                                          Length 324;
/cell_type="peripheral B-cell"
/clone_lib="pSEX81 Ab expression library"
/clone="anti-TTd.clone1"
                                                                                                                                                                                                                                                                                                                                                                       Score 290; DB 91; Pred. No. 1.63e-232;
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Best Local Similarity 96.5%;
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Poben, P., O'Kennedy, P., Barbas, C.F. III. Rurton, D.R.
                                                                                                                                                                                                                                                                                                                                 /product="Ig kappa light chain variable region; subgroup
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae: Homo.
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                                                   Hexham,7 M., Partridge,L.J., Furmaniak,J., Fetersen,V.B.,
Colls,J.C., Pegg,C., Pees Smith,B. and Burton,D.R.
Cloning and characterisation of TPU autoantibodies using
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 324;
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Best Local Similarity 95.6%; Pred. No. 1.63e-232;
                                                                                                                                                                                                                                                            /cell_type="thyrcid lymphocyte"
/clone_lib="lambda phage"
/clone="C3"
1..324
                                                                                                        libraries
                                                                                                                                                                                        /organism≂"Homo sapiens"
/isolate="Hashimoto patient"
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                                                                                                      combinatorial phage display librario
Autoimmunity 17 (3), 167-179 (1994)
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 Autoimmunity 12 (2), 135-141 (1992)
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//translation="BLIQSPGTLSLSPGEPAILSCPASQSVISNYLAWYQXKPGGAPP
//translation="BLIQSPGTLSTSPLEPEDPAVSCQQYGTSPWTFGQGTK
VEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPPEAKVQWRW"
                                                                                                                                                                                                                                                                       /note-"This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal."
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Direct Submission
Submitted (08-FFR-1988) Kipps T.J., Scripps Clinic and Research
Foudation, 10666 North Torrey Pines Road, La Jolla, California
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    tgcagggccagtcagagtgttatcagcaactacttagcctggtaccagcagaaacctggc 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 14; Indels 0; Gaps
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1 (bases 1 to 402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 290; DB 99;
Pred. No. 1.53e-232;
                                                             /tissue_fype="bone marrow"
/tissue_lib="BMHIV"
/lab_host="XL1-Blue"
/map="14q32.33"
                  /organism="Homo sapiens"
                                                                                                                                                                          /note="G00-128-529"
/codon_start=1
                              /cell_type="I-cell"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                          117 g
                                                                                                                                                                                                                                                                                                                          /codon_start-1
                                                                                                                                                           /dene="IGHV3"
                                                                                                                                                                                                                            /dene="IGHV@"
                                                                                                                                                                                                                                                         /qene="IGHV@"
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Best Local Similarity 95.6%;
Matches 304; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          125 C
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Kipps,T.J., Tomhavé,E., Chen,P.P. and Carson,D.A.
Autoantibody-Associated & Light Chain Variable Pegion Gene
Expressed in Chronic Lymphocytic Leukemia with little or No Somatic
                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="METPAGXLFLLLLMLPD11GE1VLTGSPG1LSLSPGERATISGR
ASGSVSSSYLAWYQQKPGQAPPLL1YGASSPATG1PFFFFSGSGSG1LFT1T1SP1FPX
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M28169
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 godagtdagagtgttagdaggdagdtadttagdnttggtadnagdaaaaanntggnnaggnt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="mat peptide; variable region"
                                                                                                                    J. Exp. Med. 167 (1988) In press
see M15038 for corresponding genomic sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFAVYYCQQYGSSPWTFGQGTKVEIKRTVAAP"
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Best Local Similarity 96.2%; Pred. No. 1.37e-231;
Matches 300; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                             /note="Ig(k) L-chain precursor"
                                                                                                                                                                                                            /organism="Homo sapiens"
/cell_line="CLL B lymphocytes"
1..48
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                                                                                                                                                                                                                                                                                              /note="signal peptide"
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2 (bases 1 to 402)
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/translation="VLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPR
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1 (bases 1 to 320)
Pratt,L F., Passenti,L., Larrick,J., Pobbins,B., Banks,P M. and
Kipps,T.J.
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                                                                                                                                   Draft entry and printed sequence for [1] kindly submitted by L.F.Pratt, 20-SEP-1989.
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Bukaryotes, mitochondrial eukaryotes; Metazoa; Chordata;
Verrebrata; Putheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 324)
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                                                                                                                                                                                                                                                                                 /note="Ig kappa chain V-J3-region"
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/db_xref="PID:g185913"
                                                                             little or no somatic hypermutation
J. Immunol. 143 (2), 699-705 (1989)
89292697
                                                                                                                                                                                                          /organism="Homo sapiens"
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Best Local Similarity 96.2%;
Matches 300; Conservative
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/product="rearranged 1gM light chain V region"
/db_xxef="PiDi-g1673809"
/translation="EPVLTOSBOTISESPGEBATLSCPASOSBSSYLAWYOOKPTOA
PRLLIYGASSRATGIPPPFSGSSGSGTPFLITISPLEPEPFAVYCOOYSSPPFFSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 gecagticagagtgittageageagetaetiggeetiggitaeeageagaaaeetiggeeaggei 132
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Ripps.f.r., Tombave, E., Chen, P. P. and Fox, R.I. Molecular characterization of a major autoantibody-associated cross-reactive idiotype in Sjogren's syndrome
                                                  Submitted (30-Oct-1995) Aguilera I., Hospital W. Virgen del Br
Immunology, Manuel Siurot s/n, Seville, Seville, Spain, 41013
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ć-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa; processed gene.
Human salivary gland B lymphocyte cDNA to mRNA, clone NOV.
                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                        Score 288; DB 95; Length 324; Pred. No. 1.14e-230;
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M27025
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                                                                2 (bases 1 to 402)
Kipps,T.J Tomhave,E. Chen.P P and Carson,D A
Autoantibody Associated & Light Chain Variable Region Gene
Expressed in Chronic Lymphocytic Loukemia with Little or No Somatic
Vapites"ig kappa chain Virogion (V 11:0) signal peptide"
                                                                                                                                                             /note="Ig kappa chain V-region (V-JI-C) mature peptide'
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Foudation, 19666 Math Terrey Pines Pead, 1a Julia, California
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Vertebrata: Eutheria: Primates; Catarrhini: Hominidae; Homo
1. (bases 1 to 402)
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                                               /note="Ig kappa chain V-region (V-J1-C) precursor
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see M15038 for corresponding genomic enquence
Location/Qualifiers
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/coil_line="CLL B lymphocytes"
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/note="mat.pquk" L-chain precursor"
/codon_start=1
/db_xref="PID:q33291"
/translation="METPAQLELLILWLPDITGEIVL/OSP37LSLSPSFRTISCP
/translation="METPAQLELLILWARDITGEIVL/OSP37LSLSPSFRTISCP
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Light chain shuffling of a high affinity antibody results in a
facilit in epitope recognition.
Mol. Immunol. 33 (1), 47-56 (1996)
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L37307
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Best Local Similarity 96.2%: Pred. No. 1.14e-230;
Matches 300; Conservative 0: Mismatches iz: Indels 3
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/note="signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 324)
Oblin,M. Owman,H.,
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                                                                                  /note-"product combines with ITC88 immunoglobulin heavy chain variable region to form a binding site specific for the AD-2 epitope of cytomegalovirus gpl16" /codon_start*1
                                                                                                                                                                                                                                                                                                                                                 /note="This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo
1 (bases 1 to 324)
Danielsson, L. Furebing, C., Ohlin, M., Hultman, L., Abrahamson, M.
Carlsson, P., and Porrebaeck, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens immunoglobulin light chain (LH114) mRNA, V-region L43118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human monoclonal antibodies with different fine specificity for digoxin derivatives: cloning of heavy and light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 aggeteccaggetecteatetatggtgeatecageagggeeaetggeateceagaeaggt 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 tcagtggcagtgggtctgggacagacttcactctcaccatcagcagactggagcctgaag 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 attitgcagigiattacigicagcagiatggiagcicaccgggggacgitcggccaaggga 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 gcagggccagtcagagtgttagcagcagctacttagcctggtaccagcagaaacctggcc 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GCGGGGCCAGTCAGAGTGTTAGGAGCAACTACTTAGCCTGGTACCAGCAAAAACCTGGCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AGGCICCCAGGCICCICAICIAIGGIGIAICCAGCAGGGCCACIGGCAICCCAGACAGGI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TCAGIGGCAGIGGGTCTGGGACAGACTTGACTCTCACGATGAGGAGAGTGGGAGCCTGAAG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AGCTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCTCTCCT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         digoxin-specific immunoglobulin M: light chain; light chain
                                                                                                                                                                                                       'product="immunoglobulin kappa-chain V3a region"
                                                                                                                                                                                                                                                                            /note="differences originate from the use of a Vkappal-related primer to amplify this sequence"
                       /clone="pAC41"
/cell_type="peripheral blood mononuclear cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Homo sapiens cDNA to mRNA.
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Fred. No. 9.56e-230;
0; Mismatches 15;
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/organism="Homo sapiens"
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Immunology 74 (1), 50-54 (1991)
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Local Similarity 95.3%;
les 302; Conservative
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Direct Submission

Submitted (19-MAR-1996) to the DDBJ/EMBL/GenBank databases.

Mideyuki Ikematsu, Kyushu University, Department of General Medicine; 3-1-1 Maidashi, Higashi-ku, Fukuoka, Fukuoka 812, JAPAN (E-mail:ikemaisuepo.iijnet.or.jp, Tel:092-641-1151,
                                                                                                                                                                                                                                                                                             Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens B cell hybridoma cell_line:mAb55 producing hybridoma cell cDNA to mRNA.
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Vertebrata; Mammalia; Eutheria: Primates; Catarrhini: Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION HUMAN immunoglobulin (mABSS) light chain V region mRNA, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                         73 gecagicagagigitageageagetaetiageetigiaeeageagaaaacetiggeeagget 132
                                                                                                                                                                                                                                                                                                                                                                                                                           392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 gcagigitatiacigicagcagitatggiagcicacogcicacitioggoggagggascaag 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 acgocagicticcaggicaccotigitotitigitoticcaggiggaaagagocaccoticitocigoagg 72
                                                                                                                                                                                                                                                                                                                                                                    Score 286; DB 99; Length 324;
Pred. No. 8.00e-229;
0; Mismatches 13; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 cccaggctcctcatctatggtgcatccagcagggccactggcatcccaaacaggttcagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_line="mAb55 producing hybridoma cell" /cell_type="B cell hybridoma"
                                                                                                                                                                                    /product="light chain V-region"
                                                                      /cell_type="heterohybridoma"
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immunoglobulin light chain V region.
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                                                                                                                                              /gene="LH114 Vkappa"
                                                                                                         /gene="LH114 Vkappa"
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Location/Qualifiers
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                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                          Match 89.9%;
Local Similarity 95.8%;
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307 TTGGAGATCAAA 318
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PRULIYGASSPATGIPEPFSGSGSGTDFILTISRLEPEDFAVYYCQQYGSSPETFGQG
IKVEIK"
90 q 68 t
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<1...325</pre>
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Pred. No. 8.00e-229;
0: Mismatches 13; Indels 0;
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Search completed: Tue Feb 24 07:55:19 1998 Job time : 560 secs.

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Release 2.1D John F. Collins, Biccomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Tue Feb 24 07.42.43 1938, MasFar time 110.86 Seconds 710.962 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-16 (1-312) from US08844215.seq 312 Description: Perfect Score. N.A. Sequence.

1 GASCICACICAGITICASC CICGAGIGAGICAGAGGICS COMP.

OSACCAAGGIGGAGAIIAAA 312 POIGGIIOCACCICIAGIII

TABLE default Gap 6 Scoring table

333433 seqs, 126143548 bases x 2 Searched

Dhase 0, Query 0

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Nmat.:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:STS1 2:STS2 3.STS3 4.STS4 5.STS5 5.STS6 7.STS7 8.STS8 9:STS9 10:STS1 11:STS11 12:STS12 13:STS13 14:40.EST1 15:GNEST1 15:GNEST2 13:STS13 14:40.EST1 15:GNEST2 15:GNEST3 14:40.EST5 15:GNEST1 25:GNEST1 25:GNEST2 25:GNE

Mean 9.885; Variance 1.971; scale 5.015 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Pred. No.	0.00e+00 0.58e+293
Ssult Query No. Score Match Length DR ID Description Pred. No.	zwz7fll.rl Soares ova 0.00e+000 ngbsc07.sl NCL_CGALL 5.58e+297
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ult Query No. Score Match Length DB ID	400 60 418 33
Query Match	202 64.7
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07-JUN-1997 (Pel 52, Created)
07-JUN-1997 (Pel 52, Last updated, Version 1)
www.ffll.ri Soares ovary tumor NbHOT Home sapions opNA clone 770541
5' similar to gb:x06764 IG KAPPA CHAIN PPECUPSOR V-III PEGICN
(HUMAN):
                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson PK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Rox 8501. St. "ouis. Mo 63108 Tel: 314 286 1800 Fax: 314 286 1800 Exail: estawatson.wistl.edu This clone is available royalty-free through LLLL. contact the IMASE Consentium (informage ill) pry) for
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                                                                                                                                                                                         Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
HS1244850 standard, RNA; EST; 400 BP AA456778;
                                                                                                                                                                        Homo sapiens (human)
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ng69c07.si NCI_GGAP_Lip2 Homo sapiens cDNA clone 940044 similar to
gb.M5343R IG KAPPA CHAIN PPECUPSOR V-III PESION (HUMAN);
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Vertebrata; Mammalia; Eutheria; Frimates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 31; Indels 7; Gaps
further information. Trace considered overall poor quality Seq
primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                          Score 202; DB 60; Length 400; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                   /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                              mRNA <1..>400
Sequence 400 BP; 90 A; 120 C; 106 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                               /tissue_type="ovarian tumor"
                                                                            /organism≂"Homo sapiens"
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Email: Robert_Strausberg@nih.gov
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Matches 275; Conservative
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NCI-CGAP:
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A G.E Consortium/LUM.at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vertor pAMP10; mPNA made from liposarcoma, cDNA made by oligo-dI priming. Non- directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research
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4-JUL-1997 (Rcl. 52, Last updated, Version 2)
855C-07 s1 NCT_GRAP_LIP2 Home sapiens CDNA clone 940044 similar to
95-M63438 IG KAPPA CHAIN PRECUPSOF V-III PEGION (HUMAN);
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Robert_Strausberg®nih.gov Tissue Promyromont: I Teffroy Medeiros,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index";
Unpublished.
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Vertebrata, Mammalla, Eutheria; Primates, Catarrhini; Hominidae;
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                 cDNA Library Preparation: David B. Krizman, Ph.D.
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/tissue_type="liposarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 413.
Location/Qualifiers
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/clone="940044"
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Best Local Similarity 87 7%;
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7035605 rl shares ovary tumor NAHOT Home sapiens cona clone 739953
5' similar to gb-X06764 IG KAPPA CHAIN PPECURSOR V-III REGION
                                                                                                                                                                                                                                             /note-"Vector pawPl0; mRNA made from liposarcoma, cDNA made by oliqo-di prinning, Non-directionally cloned. Size-selected on agraces qel, average insert size 600 bp Peference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata: Mammalia; Euthoria; Primates: Catarrhini; Hominidae;
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Hillier.L., Allen.M., Bowles.L., Dubuque,T., Geisel,G., Jost,S. Krizman,D., Kucaba T., Lacy,M. Le.N., Lennon,G., Marra M., Martin,J., Moore,R., Schellenberg.K., Steptce.M., Tan.F., Theising.B., White,Y., Wylie,F., Waterston,R., and Wilson,K. WashU·NGI human EST Project
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Pred No 3.58e-297;
0; Mismatches 28; Indels 4; Gaps
M.D. Michael P. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizena. Ph.D. cLNA Library Arrayd by: Step Lennon. Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consertium/LIN at: Www.blo.linlgav/kbrg/image/image.html Insert Length 1070 Std Error: 0.00 Seq primer: -40ml3 fwd. El from Amersham High quality
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99 A: 127 C: 102 G: 90 T: 0 other;</pre>
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Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, 91 (
                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
                                                                                                                                                                                                                            /organism="Homo sapiens"
/note="Vector: pAMP10; m
                                                                                                                                                                  Location/Qualifiers
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Local Similarity 87.7%;
PS 228; Conservative
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@mage llnl gcw) for further information.
Seq primer - 28ml3 rev2 ET from Amersham.
Location/Qualifiers
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23-JUN-1997 (Pel. 52, Last pigdated, Version 1)
2u35b05.rl Scares ovary tumor NAHOT Home sapiens CDNA clone 739953
5' similar to gb:X06764 IG KAPPA CHAIN PPEUUPSOR V-111 REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jost S.,
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Vertebrata: Eutheria; Primates; Catarrhini; Hominidae: Homo.
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares ovary tumor NbHCT"
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Pred. No. 1.59e-272;
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91.4%; Pred. No.
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HES1268912 standard; PNA; EST; 242
AA419857;
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ORIGIN
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81 tecageagggeeactggeateceagaeaggtteagtggeagtgggtetgggaeagaette 140
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13-JUN-1997 (Rel. 52, Last updated, Version 1)
13-JUN-1997 (Rel. 52, Last updated, Version 1)
5. similar to gb:MI2740_cds1 IG KAPPA CHAIN PRECUPSOR V-III PRSION
(HUMAN);.
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available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 164; DB 64; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kucaba I., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore B. Schellenberg K., Stepfoe M., Tan F., Theising B.,
White Y. Wylie T., Waterston P., Wilson P.;
"WashU-Merck EST Project 1997";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 A; 66 C; 69 G, 53 T; 0 other;
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HS1258064 standard; RNA; EST; 324 BP.
                                                                                                Location/Qualifiers
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                                                                 rev2 ET from Amersham.
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AA464224 324 bp mPNA E21
zx83c06.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 810346
5' similar to gb:M12740_cds1 IG KAPPA CHAIN PRECURSOP V-III PEGION
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Hillier, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, P. and Wilson, P. Washi-Merck EST_Project 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Pharmacia). Library constructed by Bento Soares and /Clone="810346"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Fred. No. 1.59e-272;
0, Mismatches 15; Indels 2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.6%; Score 164; DB 63; Length 224; Best Local Similarity 91.8%; Pred. No. 1.59e-272; Matches 191; Conservative 0; Mismatches 15; Indels 2
                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                    /clone_lib="Soares ovary tumor NbHOT"
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Sequence 324 BF; 68 A; 102 C; 82 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                       /tissue_type="ovarian tumor"
                                                       /organism="Homo sapiens"
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Location/Qualifiers
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Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                     /sex="Female"
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01-JUN-1997 (Rel. 52 Last updated, Version 1)
7W27b1C.sl Soares ovary tumor NEHOT Homo sapieus CDNA clone 770491
31 stmilar to gb.M53438 I3 KAPPA CHAIN FREIURSGF V-III PESIGN
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nstlwdtson wustledu This clone is available royalty-free through LLNL: contact the IMAJE Enseitium (infollmage-liningsy) for futber information. See primer: -41ml3 [wd. El from Amersham Rey
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Eukaryotae: mitochondrial eukaryotes: Metasoa: Chordata:
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/sex-"Female"
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Local Similarity 91.8%; Pred. No. 1.59e-272;
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High quality sequence stop: 161.
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                      Socation/Gralifiers
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//organism="Homo sapiens"
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L-MAX-1997 (Rel. 52, Lost updated, Version 2)
ztflaall r1 Soares ovart tumer NBHOT Home sapiens 1DNA clone 712852
5' similar to gb-M67438 IG KAPPA CHAIN PRECÜBSOR V-IIT PEGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLNE, contact the IMAGE Consortium (info@image,iluf.gov) for
further information Seg primer: 28ml3 rev2 FT from Amersham
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Vertebrata, Eutheria, Primates, Catarrhini: Hominidae: Homo.
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Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
White Y., Wyller T., Waterston R., Wilson R.; Theising B.,
"Washy-Morck EST Project 1997".
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/lab_host="DH10B (ampicillin resistant)"
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Sequence 230 BP; 50 A; 79 C; 52 G; 49 T; 0 other;
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Fred, Nc. 5.45e-248;
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0: Mismatches
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Rest Local Similarity 97 (%)
Matches 155; Conservative
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Best Local Similarity
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Vertebrata: Mammalia, Eutheria, Primates, Catarrhini, Hominidae;
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This clone is avallable royalty-free through LLNL , contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
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the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                            Score 152; DB 52; Length 243;
                                                                                                                                                                   Indels
                                                                             /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                   /clone_lib="Soares ovary tumor NbHOT"
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                                                                                                                                                                                                                                                                                                             Sequence 243 BP; 55 A; 82 C; 56 G; 50 T; 0 other;
                                                                                                                                                       Fred. No. 5.45e-248;
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                                       /clone="713852
                                                                /sex="Female"
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ilarity 97.5%;
Conservative
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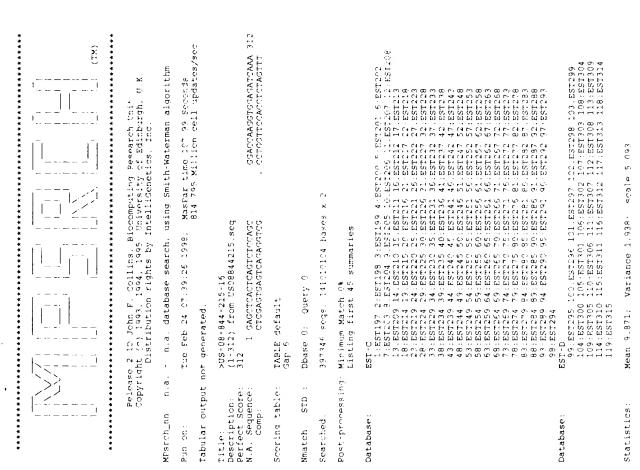
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/note=form convergence of the property of the property of the polytinker. Situal Not I. Situal. Edo RI: lst strand colons was primed with a Not I. - oligo(dT) primer [5 turner. Colons was primed with a Not I. - oligo(dT) primer [5 turner. Colons was primed size selected. Injurer [5 turner. Colons with a size selected. Injured to For RI adapters (Pharmacia), digested with Not I and coloned into the Not I and Edo RI sites of a modified pT713 vector (Pharmacia). Library constructed by Rento Scarcs and
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24-JUN-1997 (Rel. 52, Last updated, Version 1)
zv42c03.rl Soares ovary tumor NDHOT Home sapiens cDNA clone 755292
5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III PEGION
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Forest Park Parkway, Box 8501, St. Louis, Mn 63108 Tel: 314-286
1800 Fax: 314-286 1810 Email: est@watson wustl edu This clone is avallable royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml3
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Vertebrata, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/tissue_type="ovarian tumor" /lab_host="UH10B (ampicillin resistant)"
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56 A; 81 C; 56 G; 50 T; 0 other;
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                                                                                                                                                                        Score 152; DB 28; I
Pred No 5 45e-248;
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HS1272128 standard; RNA; EST; 243 BP
AA481842;
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Best Local Similarity 94.38,
Matches 149; Conservative
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                                                                                                           05-APR-1997 (Rel. 51, Created)
22-MAY-1997 (Rel. 52, Last updated, Version 2)
21-AAY-1997 (Rel. 52, Last updated, Version 2)
212-4933.rl Soares owar tumo: NEROT Home sapples on 20-no 714100
5. similar to qoiM63439 is KAPPA CHAIN PRECURSOR V-III PRESION
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Vertebrata: Eutheria: Primates: Catarrhini; Hominidae; Homo.
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S Mismatches 4, todels
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/lab_host="0Hl0R (ampigillin resistant)"
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/sex="Female"
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Local Similarity 96.3%; Pred. No. 7.70e-240;
es. 154; Conservation
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HS18086 standard; RNA; EST; 255 BP.
4A284662;
41927573
Matches 155: Conserlative
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AA485616 24° bp reha EST 24-"N-1997 zx90h01.rl Soares ovary tumor NbHOT Home sapiens CDNA clone 811957 5° similar to gb M1240_eds1 is KARPA CHAIR PRECISER V III HENION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 240)
Hiller, L. Allen, M. Boxles, L., Dubuque, T., Geisel, S., Bost, S., Krigman, D., Kroaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-NCI human, EST Project
                                                                                                                                                                                                                                                         Eukaryotae, mitochendrial eukaryotes, Metazoa. Chordata:
Vertebrata, Mammalla; Eutheria, Primates, Catarrhini; Huminidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est%watson.wustl.edu
This clone is available royalty-free through LLNL : confact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rov2 FT from Amorsham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park Parkway, Rox 8501, St. Louis, Mr 52108
Tel: 314-286-1800
Fax: 314-286-1810
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Pred. No. 1.38e-223,
0: Mismatches 9: Indels 0:
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK Washington University School of Medicine 4444
Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
BROO Fax. 314 286 1810 Email. est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer. 28mi3
                                                                                                                                                               27-JUN-1997 (Rel. 52, Created)
27-JUN-1997 (Pel. 52, Last updated, Version 1)
27-JUN-1997 (Pel. 52, Last updated, Version 1)
57-SUMMOLIS Source ovary tumor NbHOT Homo sapiens CDNA clone 811057
57-Similar to 9b:MI2740_cds1 IG KAPPA CHAIN PRECURSOR V-III PRSION (HUMAN);
                                                                                                                                                                                                                                                                                                                               Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier L , Allen M., Rowles L., Dubuque T , Geisel G., Jost S., Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White T , Wylie T., Waterston P., Wilson P.; "WashU-NCI human EST Project";
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/lab_host="DH10B (ampicillin resistant)"
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Local Similarity 94.3%; Pred. No. 1.38e-223;
Omismatches 9.
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127 ASSCICCICATCIAISAIGCAICCAACAGGGCCACIGG 164
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HS1227632 standard; RNA; EST; 244 BP.
AA430565;
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                                                                                              standard; ENA; EST; 240
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                                                                                            HS1280478
                                                                                                                     AA485616;
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double-stranded cDNAwas size selected, ligated to ECO RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco PI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M Fatima Panaldo."
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                                                           zw22h09.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 770081
5' similar to gb:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION
(HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Te): 314 286 1800 Fax: 314 286 1810 Email: estawatson wustl edu This clone is available royalty-tree through LLNL; contact the IMASE Consorrium (info@image.llnl gov) for further information. Seg primer: -28ml3 rev2 ET from Amersham. Key Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK WashM-Merck EST Project Washington University
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/lab_host="DH10B (ampicillin resistant)"
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/sex="Female"
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54 A; 82 C; 60 G, 48 T. C other;
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25-MAY-1997 (Pel 52, Created)
25-MAY-1997 (Rel. 52, Last updated, Version 1)
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                                                                                                                                                                                            Homo sapiens (human)
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es 149: Conser
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Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No.		PP-1997 milar to a: Hominidae: R.A., cayne,J.D., cayne,J.D., eayne,N.S., gen,N.S.,
cription	ESTION411 Pancreas to ESTION400 Pancreas to ESTION400 Pancreas to ESTION400 Pancreas to ESTION401 PANCREAS TO	sapiens CDNA 5' end sin, VJ legions. primales: Metazoa; Chordat Primales: Catairhini. schmann, P. D., Fuldher. F., Weinstock, K. G., So., Brandon, R. C., Man-Wain, M. D., Earle-Hapkes J. Eritchman, J. C., Googha C., Hedhlom, E., Hinkle,
SUMMARIES	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	mena mena light chai light chai drial eukar Flancess, E Blake, J.A. Blake, J.A. Blake, J.A. T.R., Cotto
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Kelley, T.M., Kelley, J.C., Liu, L.-T., Marmaros, S.M., Merrick, J.M., Moreno, Palangues, P.F., Mchomald, L.A., Nguyen, D.T., Palligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Lii, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E. J. Dimke, D. Feng, D.-F. Ferrie, A. Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungja, A., Fischer, J., Hudson, P., Kim, A.K., Rozak, D.L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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//nutw="Grydu. pancreas, Vector. pBluescript SK., Site_1.
EcoR1: Site_2: XhoI"
/clone_lib="Pancreas tumor I"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Pred. No. 0.00e+00;
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<1...>328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
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Local Similarity 90.0%;
Hes 244, Conservative
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Adams M. Rerlavog, A. P. Fleischmann. B. D. Fuldner. B. A. Weitster, K. R. G. G. Agrer, J. A. Brandon, R. C. J. Lee, N. H. Kirkness F. F. Weitster, K. R. G. G. Agrer, T. D. Mhite, J. Sutton, G. Blake, J. A. Brandon, R. C. Man-Wal, C. Fine, L. D. Clayton, P. A. Cline, T. B. Cotton, M. D. Earle-Hughes, J. Fine, L. D. Fitzgerald, L. M. Fitzhugh, W. M. Fritchman, J. L. Geoghagen, N. S. Glodek, A. Gnehm, C. L. Hanna, M. C. Hedblom, E. Hinkler, S. Jr. Kelley, J. M. Kelley, J. C. Hanna, M. C. Hedblom, E. Hinkler, S. Jr. McDonald, L. A. Nguyen, D. T. Pelligrino, S. M. Morreno-Palanques, R. F. McDonald, L. A. Nguyen, D. T. Pelligrino, S. M. Bednarik, D. P. Cao, L. Cepeda, M. A. Coleman, T. A. Collins, E. J. Bednarik, D. P. Cao, L. Cepeda, M. A. Coleman, T. A. Collins, E. J. Dimke, D. Fengio, P. Ferrie, A. Fischer, C. Hastings, G. A. Kozak, D. L. Kunsch, C. Hungjun, J. Li, H. Meissner, P. S. Olsen, H. Fraser, C. M. and Venter, J. C. Pareno, A. Maseltine, M. A. Fields, C. Fraser, C. M. and Venter, J. C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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/note="Organ: pancreas; Vector: pBluescript SK-; Site_l:
EGORI, Site_l: MhoI"
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidae.
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Pred; No 0 00e+00;
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Rest Local Similarity 90 5%;
Matches 237; Conservative
                                                        (hases 1 to 370)
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RESULT

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Adams. M.D. Kerlagage, A.P., Fleischmanb, R.D., Fuldner, R.A., Rult. C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayee, J.D., White, O., Sutton, O., Blake, J.A., Brandon, R.C., Man-Wall, C., Clayton, R.A., Cinne, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., T., Kelley, J.M., Kelley, J.G., Mornardos, S.M., Merrick, J.M., Moreno-Palaques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R. Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Shirley, R., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Hashirl, C.M., Manson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Rymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Flalds, C., Fraser, C.M., and Venter, J.C., Haseltine, W.B., Fields, C., Fraser, C.M., and Venter, J.C.
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                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                  21-APR-1997
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EcoR1: Site_2: XhoI"
/clone_lib="Skin tumor I"
/dov.staqe="adult"
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AĀ379044 349 bp mRNA EST 21-APR-1
EST91999 Skin tumor I Homo sapiens cDNA 5' end similar to
immunoglobulin kappa light chain. VJ regions.
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9712 Medical Center Drive, Rockville, MD 20850 USA
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zw27f11.rl Soares ovary tumor NbHOT Home Sapiens con close 770541
5' similar to qb:x06764 IG KAPPA CHAIN PRECURSOR V-III REGION
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Hiller., Allen,M., Bowles.L., Dubuque,T., Geisel.G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.qov) for further information. Trace considered overall poor quality Seq primer: 28ml2 ror2 ET from Amersham High quality sequence stop: 1.
70 acgcagictccaggcacccigictitatciccaggggaaagagreaccrictroigcagg 129
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Vertebrata: Mammalia; Butheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washu-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fex; 314 286 1800
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/lab_host="PHIOB (ampicillin resistant)"
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/sex="Female"
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Best Local Similarity 87.9%; Pred. No. 0.00e-00;
Matches 275, Conservative 0; Mismatches 31
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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BooR; Site_2: XhoI"
/clone_lib="Festis tumor"
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                                                                                                                                                                                                                                                                                                                                     57 GCCAGICAGAGIGITAACA--AG-TACTTAGCCIGGIACCAACAGAAACCIGGCCAGGCT 123
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DEFINITION EST13427 Testis tumor Homo sapiens CDNA 5' end similar to
immunoglobulin kappa light chain, VJ regions.
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/dev_stage="adult"

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S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Stadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirke, S.E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Randon, R.C., Man-Wai.C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhudh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C., Hanna, M.C., Hadblom, E., Hinkle, P.S.,
Kelley, J.M., Kelley, J.C., Lün, L.-I., Marmaros, S.M., Merier, J.M.,
Moreno-Palanques, R.F., McDonald, A., Nguyen, D.T., Pelligrino., S.M.,
Phillips, C.A., Ryder, S. Sorrt, J.L., Sandek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, T.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisener, P.S., Olsen, H.,
Raymond, L., Wei, P.F., Ferrie, A., Fischer, C., Puppen, S.M.,
Phillion, P.J., Fahren, G.A., Hoseltine, W.A., Fields, C.,
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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AA367405
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018694056
                                10 others
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a 92 c
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Adams, M.D. Kerlavage, A.P., Fleischmann, P.D., Fuldher, P.A.,
Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldher, P.A.,
Bult.C.J., Leee, N.H., Kirkness, E.F., Weinstock, F.G., Gegraphe, J.D.,
White, D.S., Sutton, G., Blake, F.E., Weinstock, F.G., Gegrapes, J.D.,
White, D.S., Cline, T.P., Corten, M.D., Earle-Hughes, J., Fine, I.D.,
Flizerald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, L.E., Hanna, M.C., Hedby, M. Merrick, J.M.,
Morenn-Palanques, P.S., McConald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Pyder, S.E., McConald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Bednarik, D.P., Greene, J.M., Gruber, J., Hatings, G.A.,
Rymend, D., Wenty, F., Ferrie, A., Fischer, C., Hatings, G.A.,
Rymend, L., Welly, Greene, J.M., Gruber, J., Hatings, G.A.,
Blillon, P.J., Fannon, M. Gruber, J., Hating, M.A., Fischer, S.M.,
Billion, P.J., Fannon, M.P., Posen, C.A., Haselline, W.A., Fischer, S.
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                                                                                                                   /Organism="Homo sapiens"
/note="Organ: parcreas: Vector: pBluescript SK-; Site_1:
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Vertebrata; Mammalla; Eutheria; Primates; Catarrhini: Hominidae;
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Local Similarity 83.7%; Pred. No. 0.00e+00;
ics 252; Conservative 0. Mismatches 46,
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                                                               FEATURES
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/note="Organ: lymph node: Vector: pBluescript SK-: Site_1:
ECORI: Site_2: XhoI"
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<1..>405
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Adams, M.D., Rorlavage, A.R., Eleischmann, R.D., Fuldnet, R.A.,
Bult, C.D., Lee, N. H., Kirkess F. F., Weinstock K. G., Gocayne, J.D.,
White, O., Suton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayten, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Finc, L.D.,
Firgerald, L.M., Fuldnah, W.C., Healboom, E., Harle, P.S., J.,
Kelley, J.M., Kolley, J.C., Liu, L.J., Belboom, E., Harle, P.S., J.,
Moreno-Palanques, F. Mohonald, L.A., Naryen, D.T.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
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                                                                                                                                                                                                                                                        For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human General Index (http://www.tigr.org/tdz/ig./hgl.html)
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Vertebrata, Mammalia, Eutheria: Frimates; Caturrhini: Hominidae:
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The Institute for Genomic Research
9712 Medical Center Drive, Pockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
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Pred. No. 0.00e+00;
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tased upon 43 millon nod
Nature 377 (6547 Suppl).
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Matches 224; Conservative
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Small,K.V., Spriggs,T A., Utterback,T R., Weidman,J.F., Li,Y., Dimarik,D P., Cao,L., Cepeda,M A., Coleman,T.A., Collins,E.J., Dimke,D., Fengio, -F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J M., Gruber,J., Hudson,P., Kim.A.K., Kozak,D L., Weis,Y.F., Wing,J., Li,H., Melssner,P.S., Olsen,H., Baymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Farser,C.M. and Venter,J.C., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C., Rosen,C.A., Haseltine,W.A., Fields,C., Faser,C.M. and Venter,J.C., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Nenter,J.C., 1011al assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 agggecactggcateceagaeaggtteagtggcagtgggtegggaeagaetteaetete 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 ccaggggaaagagccgccctctcctgcagggccagtcagcgtgttagcagcagtcactta 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 geetgatateageagaaaeetggeeaggeteeeaggeteeteatetatgtggtgegteeagg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AGGGGGACTGGGATGGGAGGGAGGTTGAGTGAGTGGGGTGTGGGACTAGGACTTGACTTGTG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 accateageagaetggageetgaagattttgeagtgtattaetgteageagtatggtgae 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 ACCATCAGCAACCTAGAGCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCGAC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: gall'bladder; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI" /clone_lib="Gall bladder II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 CCAGGGGAAAGAGCCACCTCTCTGCAGGGCCAGTCAGAGTTTAACA--AGT-ACTTA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 188; DB 73; Length 403; Pred No 0 00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 TGGG-TC--ACTITCGGCGGAGGGACCAAGGIGGAGATCAAA 312
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 bp
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Local Similarity 88.7%;
nes 250; Conservativo
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COMMENT
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Homo.

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A (Wassa L. Cala)

A (Wassa L. Cala)

Bult, C.J. Lee.N. H., Kirkness, E.F., Weinstock, K.G., Gorayne, J.D.,
White, O., Sulton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E.Hinkle, P.S.Jr.,
Kelley, M., Kelley, J.C., Liu, L. J., Marmaros, S.M., Merrick, J.M.,
Morenc-Palanques, R.F., McDenald, L.A., Nguyen, D.T., Pelliqrino, S.M.,
Phillips, C.A., Fyder, S.E., Scott, J.L., Sandek, D.M., Shirley, R.,
Bednarik, D.P., Cac, L., Cepeda, M.A., Coleman, T.A., Chilins, F.J.,
Dimke, D., Roggo, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,
Paymond, L., Welly F., Rosen, C., Maseltine, W.A., Fields, C.,
Friser, C.M., And Venter, J.C.,
Friser, C.M., Cannon, M.P., Posen, C., Ruben, S.M.,
Friser, C.M., And Venter, J.C.,
Friser, C.M., A., Fields, C.,
Friser, C.M., Friser, C.M., Fields, C.,
Friser, C.M., Friser,
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EST101165 Thymus III Homo sapiens cDNA 5' end similar to similar to
immunoglobulin kappa light chain, V region (GB:Y00640).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGP Human Gene
Index (http://www.tigr.org/tdb/hgi/hqi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Site_1 Fook: Site 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 agagtgitagcagaaacttagcctggitccagcagaaacciggccagccicccaggeicc 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 AGAGTGTTAACAAGTACTTAGGGTGGTAGCAAGAAAQGTGGGGGAAGGTGAGGTAAGTAGGGTGGAGGTGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
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Pred. No 8.06e-277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/note="Vector pRluesoript SK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTS: THC168243
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Best Local Similarity 90 9%;
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(bases 1 to 283)
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REFERENCE
AUTHORS
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Admin M. Kerlangera P., Fleischmann, F. Fuldroffeld.

Rult G. J. Lee, N. H., Kirkness F. F., Weinstock, K. G., Gocayne, J.D.,

Rult G. J., Sutton, S., Plake, J. Braden, R.J., Man-wall, C.,

Clayton, P. A., Cline, T. P., Cotton, M. D., Earle-Highes, J., Fine, D.D.,

Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. J., Gocahagen, N.S.,

Gledek, A., Gnebb, C. L., Hanna, M. C., Harkler, P. S. J.,

Kelley, J. M., Kelley, J. C., Lu, L. J., Marmarcs, S.M., Merick, J. M.,

Moreno-Palanques, F. McDonald, L. A., Nguyen, D. T., Pallintino, S.M.,

Rednark, D. P., Fright, J. M., Mayer, D. T., Pallintino, S.M.,

Rednark, D. P., Ferrie, A., Hischer, C., Hastings, G.A.,

Billon, D. J. G., Geene, J. M., Gruber, C., Hastings, G.A.,

Rozak, D.L., Kunsch, G., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,

Phillon, P. J., Shopper, P. Posen, C.A., Haseltino, W.A., Fields, T.,

Phillon, P. J., Shopper, P. Posen, C.A., Haseltino, W.A., Fields, T.,

Phillon, P. J., Shopper, P. Posen, C.A., Haseltino, W.A., Fields, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillion, P.J., Fannon M. P., Posen, C.A., Haseitine, W.A., Fields, T., Fraser, C.M. and Venter, J.C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                            Būkaryotae, mitoobondrial Aukaryotes, Metazoa, Chordata;
Vertebrata, Mammalia, Butheria, Primates, Catarrhoni, Hominidao;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: thymus; Vector: pBluescrip, Sk-; Si'e_1:
EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 catotatogitgoatooacoaggicoactgitatoocaggittoaggigtoaggagit. 237
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    EST97387 Thymus II Homo sapiens cDNA 5' end similar to
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Tel: 3018699056
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Best Local Similarity 93.9%; Pred. No. 2.01e-266;
Matches 170; Conservative 0; Mismatches 11;
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                Adams, M.D., Kerlavage A.P., Fleischmann, P.D., Fuldner, P.M.,

Bult, C.J., Lee, N.H., Kirkees, E.F., Weinsterk, K.G., Gorayne, J.D.,

Bult, C.J., Lee, N.H., Kirkees, E.F., Weinsterk, K.G., Gorayne, J.D.,

Clayton, P.A., Ciner, T.F., Cotton, M.D., Earle-Hughes, J., File, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, T.L., Geoghagen, N.S.,

Glodek, A., Gorben, C.L., Hanna, M.C., Howhle, P.S., Moreno-Palanques, P.F., McDonald, L.A., Nguyen, D.T., Pelligtino, S.M.,

Moreno-Palanques, P.F., McDonald, L.A., Nguyen, D.T., Pelligtino, S.M.,

Phillips, C.A., Byder, S.E., Scott, J.L., Saudek, D.M., Shirley, P.,

Small, K.V., Spriggs, T.A., Interface, T.P., Weidman, J.F., Lity

Bednarik, D.P., Cao, L., Gepeda, M.A., Coleman, T.A., Collins, E.J.,

Blimke D., Feng D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hastings, G.S., Olsen, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dimke D. Feng D. F. Ferrie, A. Fischer, C. Hastings G.A., He, W.W., Hu, J.S., Greene, J. M., Gruber, J., Hudson, P. Kim, A. K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissen, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C.L., Puben, S. M. Dillion, P. J. Fannon, M.P., Rosen, C. A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (5547 Suppl), 3-174 (1995)
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                                                                                       Eukaryotae: mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidae;
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// Clone_iib-"Thymus II!"
//dev_stage-"adult"
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ms.M.D., Kerlavage A P., Fleischmann P D ,
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Best Local Similarity 88.5%, Pred. No. 9.72e-275,
Matches 20, Chestrative C. Miscalthes 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 bp
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wail, C.D.,
Clayton, R.A., Cline, T.F., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.I., Marmanos, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., Moronald, L.A., Ngnyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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ECORI; Site_2: XhoI"
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.
Raymond,L., Wei,Y.P., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,R.P., Rosen,C.A., Haseltine,W.A., Fields,C.
Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this ESI, please check the ILGF Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                    Eukaryotae, mitochondrial eukaryotes, Metazoa; Chordata;
Vertebrata; Mammalia, Eutheria, Primates, Catarrhini, Hominidae;
                                                                                                                  EST100538 Pancreas tumor I Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VJ regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Pred. No., 2.876-262;
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Contact: Kerlavage, AR
                                                                                              277 bp
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Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gorayne, T.D.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gorayne, T.D.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J. Fine, J.D.,
Fliggerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glode, A., Genehu, C.L., Hanna, M.C., Handlow, E. Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.T., Marmaros, S.M., Morrick, J.M.,
Moreno-Palanques, R.E., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scort, J.L., Saudek, I.M., Shiley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.F., Weidman, J.F., Li, Y.,
Bednarik, D.P., Gao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Fengy, D.-F., Ferrie, A., Fischer, C., Hassings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Fraser, C.M., and Venter, J.C.,
Dillion, P.J., Fannon, M.E., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.G.,
Initial assessment of human gene diversity and expression patterns
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Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata:
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                     AA327218 20-APP-1997 EST 20-APP-1997 EST30586 Colon I Homo sapiens CDNA 5' end similar to similar to immunoglobulin kappa light chain, VNJ regions (GB:211894).
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                            /note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI: Site_2: XhoI"
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9712 Medical Center Prive, Pockville, MD 20850 USA
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Best Local Similarity 90.4%;
Matches 188; Conservative
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AA43419C 239 bp mPNA EST 29-MAY-1997 zw27b10.si Soares ovary tumor NDHOT Homo sapiens cDNA clone 770491 3' similar to qb:M53438 IG KAPPA CHAIN PRECURSOR V-III PEGION
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Vertebrata: Mammalia; Eutheria; Primates; Gatarrhini: Hominidae;
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                      142 agagigitaigagoggetaettageetggiaeeagoagaaaeetggeeaggeteeeaggg 201
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Fax 314 286 1810
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/lab.hosr="tH10H (ampicillin resistant)"
complement(<1..>230)
/dh_vref="npk-saans44"
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48.78; Score 152; DB 873; L
Best Local Similarity 97.5%; Pred. No. 6.68e-252;
Matches 156; Conservative 6; Mismatches 4
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Washington University School of Medicine
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LOCUS AA284584 243 bp mRNA EST 15-MAY-1947
DEFINITION 2122all rl Soares ovary tymer NbHOT Home sapiens cDNA clone 714852
5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III PESTON
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Hillier, L. Allen, M., Howles, L., Dubuque, F., Geisel, G., Jost, S., Kiraba, T., Lary, M., Le, N., Lennron, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Walle, T., Waterston P. and Wilson, P., Theising, B., Washir-Merck EST Project 1947
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Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidae:
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This clone is available röyalty free through LLNL : contact the
IMAGE Consortium (info@image.lini.gov) for further information.
Seq primer: -28ml3 rev2 EI from Amersham.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Mp 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Matches 156; Conservative C. Winning
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/sex="Female"
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132 bp mPNA EST 06-SPP-1445
EST7181 Homo sapiens cTNA 5' end similar to inmunoribbulin kappa
110th chain, V region (SE:M29469) (HI:3056).
20342
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                                                                                                                       Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
163:EST193
168:EST188
143:EST193
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y18aco3.rl Homo saple
yryff10.rl Homo saple
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EST69430 Home saplens
FST14707 Home saplens
EST99871 Home saplens
182:EST182
187:EST187
192:EST192
                                                                                         scale 5.129
180:EST180 181:EST181
185:EST185 186:EST186
190:EST190 191:EST191
195:EST195 194:EST196
                                                                                         Variance 1.931;
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184:EST184
189:EST189
194:EST194
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human primer=M13 Reverse library-Human Panoreas

ACCESSION NID KEYWORDS SOTROE

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                         Haseltine, W.A., Fields, C., Fraser, C.M. and Verter, J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
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DOFINITION y)82409.rl Hodd Sapiens CINA clode 155249 5' similar to gb:M63438
IG KAPPA CHAIN PRECURSOR V-111 PEGION (HUMAN);
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                Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata,
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Pred No 0 000+00;
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Best Local Similarity 95 1%; Pred No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 3018699423
   Homo sapiens
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modified pT7T3 vector (Pharmacia) Library went through one round of normalization to a Cot = 230 Library constructed by Rento Soares and M.Fatima Bonaldo.
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Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osfeichthyes:
Sarcopterygii: Choanata: Tetrapoda; Amniota: Mammalia: Theria:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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1 (bases 1 to 463)
Hilliar,L., Clark,N., Fubuque,T., Elliston,K., Hawkins,M.,
Helman,M., Hultman,M., Kuraha,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Fifkin,L., Pohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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WashU-Merck EST Project
Washington University School of Medicine
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/clone="155249"
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Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project
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Fax: 314 286 1810
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For clone availability, additional sequence and expression
intendion related to this EST, please contact the 115% batabase
(tdbinfo?tdb.tigr.org).
                                                                                                                                                                                                  esteichthyes:
                                                                                                                                           Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Churdata; Verrebrata; Grathostomata; Esteichthys
Sarcopteryqii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae, Homo.
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                                                                                              human primer=Ml3 Reverse library=Human Lymphoid tissue.
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Pred. No. U.due+00;
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Pel: 3018699056
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                                                                                                                                    Homo sapiens
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Buttarostomia: Chordata: Vertebrata; Gnathostomata: Osteichthyes:

Barcopteryota.

Euthoria: Archonta: Primates: Catarthin; Hominidae. Homo.

Euthoria: Archonta: Primates: Catarthin; Hominidae. Homo.

I (bases 1 to 383)

S Adams. M. Ferlavage. A. P. Fleischmann. P.D. Fuldner. R.A.

Bult. C. J. Lee. N. Kirkness. E.F. Weinstock. K.G. Gogane. I. P. White, O., Sutton. G., Black. J.A. Brandon. R.C. Chiu. M.W.

Clayton. P. Clinc. T. Cetton. M. Fritchman. J. L. Gocahagen. R.S. K.

Relley. J. M. FitzHugh. W.M. Fritchman. J. L. Gocahagen. R.S. M.

Meriday. J. M. Moreno-palangues. P. Moronald. L. T. Marmaros. S.M.,

Meridan. I. F. L. Y. Hedder. S. E., Scott. J. L.

Saudex. D. M. Shirley. P. Small. K.V. Spriggs. T. A. Trerbary. T. R.

Weiden. T. H. Washor. P. Homarik. D., Cao. L. Cepeda. M. A.

Collins. E. - T. Dillins. E. - T. Dinke. D. Ferrie. A.

Fischer, C. Hastings, G. A., He. W. - W., Hu. J. - S., Greene. J. M.,

Fischer, C. Hastings, G. A., He. W. - W., Hu. J. - S., Greene. J. M.,

Meisaner, D. S., Olsen, H., Reawood, L. Weinst, C. Ji, H., Li, H.,

Meisaner, D. S., Olsen, H., Raymond. L. Wein, Y. - F., Wing, J. S.

Haselline. W. A., Fields. C., Francon, M. P., Posen C. A.,

Haselline. W. A., Fields. C., Francon, M. P., Posen C. A.,

Haselline. W. A., Fields. C., Francon, M. P., Posen C. A.,

Haselline. W. A., Fields. C., Frascr. C. M. and Verter, J. G.

First A. A., Fields. C., Frascr. C. M. and Verter, J. M. and Soner. D. M. and Conter, J. M. and Soner. D. A. M. A. Fields. C., Frascr. C. M. and Verter, J. M. and Soner. D. M. and Soner. D. M. A. B. A. M. A. Fields. C., Frascr. C. M. and Verter, J. M. and Soner. D. M. A. B. A. M. A. Fields. C., Frascr. C. M. and Verter, J. M. and Verter. J. M. and Soner. D. M. A. B. A. M. A. Fields. C. Frascr. C. M. and Verter. J. M. and Verter. J. M. A. B. A. M. A. M. A. B. A. M. A. M. A. M. A. M. A. M. A. M. A.
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For clone availability, additional sequence and expression
information related to this ESI, please contact the TISF Talabase
                                             to immunoalobulin kappa
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36 - SEP - 1495
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0: Mismatches 19; Indels 5; Gaps
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                                                      light chain V region (GB:X05753) (HT:3087).
T27870
T27870 383 bp #RNA ES
ESI19007 Homo sapiens CDNA 5' end similar
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Pred. No. 0.00e+00;
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20
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Other_ESTs: THC24452
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Local Sim-
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DEFINITION EST9981 Homo sapiens CDNA 5' end similar to immunoglobulin kappa ACCESSION 729916
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                                                                                                                                                              Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ACTICAGILITODAGO CACCOTGICITIGICIO CAGGGAAAGAGAGO COTOTOCOGAGGA EE
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                                                                                                               human primer-Ml3 Reverse library-Human Pancreas.
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932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
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Best Local Similarity 85.7%;
Matches 269; Conservative
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double-stranded obbA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a medified pTT1 vector (pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Pento Soares and M.Patima Ronaldo.
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Deuterostomia; Chordata: Vertebrata; Gnathestomata Ostaichthyes;
Saronpherygii: Choanata Tetrapoda, Ammista: Mammalia Theria:
Eutheria; Archonta: Primates; Catarrhini: Hominidae: Homo.
1 (bases 1 to 385)
Hiller, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le. M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                  H25475 385 bp mPNA FST 10-JHL-1995
y151g05.rl Homo sapiens cDNA clone 161816 5' similar to gb:M63438
IG KAPPA CHAIN PPECUPSOR V-T11 PEGION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                               Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                            human clone=161816 library=Soares breast 3NbHBst vector=pT7T3D
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred No u nue+nu;
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local_Similarity H7.0%;
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Fax: 314 286 1810
                                                                                           351 aaggtggaagtcaa 364
                                                                                                                                       298 AAGGTGGAGATCAA 311
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Eucaryotae; Metazoa; Chordata; Vertebrata; Guathostomata; Mammalla;
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                                                                                                                                                                              DEFINITION yel5d10.rl Homo sapiens cDNA clone 117811 5' similar to gb:M12740_cds1 IG FAPPA CHAIN PPECUPSOP V-III PESION
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Pred. No. 0.00e+00.
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Source: IMAGE Consortium, LLNL
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Best Local Similarity 90.9%,
Matches 229, Conservative
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yj81d08.rl Homo sapiens cDNA clone 155151 5' similar to db:X06764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
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Sarcopterygii; Choanata, Tetrapoda; Amniota, Mammalia, Theria;
Eutheria: Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stops: 316 Source: IMAGE Consortium, LLNL This clone is available royalty-free through UINL : contact the IMAGE Consortium (info@image iln1 gov) for further information.
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Hillier, L. Clark, N. Dubuque, T. Flliston, K. Hawkins, M.,
Holman, M. Hultman, M. Kucaba, T. Le, M. Lennon, G. Marra, M.,
Parsons, J. Rifkin, L. Pohlfing, T. Scares, M., Tan, F.,
Trevaskis, F. Waterston, P. Williamson, A., Wohldmann, P. and
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Pred No. 4.70e-193;
0, Mismatches 27, Indels
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Washington University School of Medicine
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                                                                                                                                                                        y161g7.rl Homo sapiens cDNA clone 162780 5' similar to gb-x06764
IG KAPPA CHAIN PPECUPSOR V-III PEGION (HUMAN):
H27642
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Sarcopterygii; Choanata, Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                   High quality sequence stops: 186 Source: IMAGE Consortium, LLNL This clone is available robalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Eucaryotae, Metazoa, Chordata, Vertebrata, Gnathostomata; Mammalia: Butheria; Primates; Catarrhini, Hominidae, Homo.

[ (bases I to 401)

Hillier.L., Clark,N., Dubuque,T., Flliston.K., Hawkins,M., Pholman,M., Ruchan,M., Roares,M., Tan,F., Marra,M., Treyaskis,E., Waterston,P., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vertor=pT7T3D (Pharmacia) with a modified polylinear host=LHLDa temptollar resistant) primer MISPET Estel=Pac I PSite2=Eco PI Liver and spleen from a 20 week-post conception male fetus. Ist strand cDNA was primed with a Pac I - oligo(dT) primer [5' ACTGGARGATTAATAAAGATTTTTTTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3
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yf3la06 rl Homo sapiens cDNA clone 128434 5' similar to gb-X06764
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human clone-188346 library-Soarns broast 3NbHBst vector-pT7730 (Pharmacia) with a modified polylinker host-tH108 (ampicillin resistant) primer-M3RP1 Rsitel-Not I Psite2-Eco El Adult human. List strand cDNA was primed with a Not I - oligo(d) primer 5' double-stranded cDNA was ligated to Eco El adaptors (Pharmacia), double-stranded cDNA was ligated to Eco El adaptors (Pharmacia), algested with Not I and cloned into the Not I and Eco El sires of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot - 20. Library constructed by Hente Scarns
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5 5 Similar to quixie?44
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Deuterostomia, Chordata, Vertekrata, Gnathostomata, Osteichthy
Sarcopterygii: Choanata: Tetrapoda, Amniota: Mammalia: Theria:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria: Archonta: Primates: Catarrhini; Hominidae: Homo.

(bases 1 to 399)
Hillari, Clark, D. Dubuque, T., Flliston, K., Hawkins, M., Holman, M., Kuraba, T., I.P., M., Lennon, G., Marra, M., Parsons, J., Fifkin, L., Folliflay, T., Soares, M., Tan, F., Trevaskis, E., Waterston, P., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK washu warek EST Project Washu warek EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 54108 Tel: 314 286 1800 Fax: 314 286 1810 Fax: 314 286 1810 Fax: 314 286 1810
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87,7%; Fred. No. 2,32c-255;
vative 0; Mismatches 23; Indels 9;
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IG KAPPA CHAIN PPECUPSOP V-III PESION (HUMAN);
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The Washu-Merck EST Project
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Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Renth Shares and M Patina Panaldo
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Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes,
Sarcoptorygii, Choanata, Tetrapoda, Amniota, Mammalia, Theria,
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189 IGGGICTGGG-ACAGACTTCACTCI-CACCAI-CAGAAACCIAS-AGGCTGAAGATTT- 243
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                                                                                                                                                                                                                        K/9907 360 bp mRNA EST 09-JUN-1995 yiR5f01.rl Home sapiens CDNA clone 146041 5' similar to db:MN274(L-ds) 1G KAPPA GHAIN PRECHRSOR V-III REGION (HUMAN): P27407
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1 (bases 1 to 360)
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4444 Forest Park Parkway, Box 8501, St. L∩uis, M∩ 63108
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WashU-Merck EST Project
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii: Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 iggggtetggggaeagagtteantiteaecateageageetgeagtettgaagattitge 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS R51922 361 bp mRNA EST 18-MAY-1995
DEFINITION yj71b07.rl Homo sapiens cDNA clone 154165 5' similar to
qb:M12740_cds1 IS KAPPA CHAIN PRECURSOR V-III PE51UN (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 agaqtgttqccaacaacttagcctggttccagcagaaacctgggccaggctcccaggctc 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AGAGIGITAACAAGIACIIAGCCIGGIACCAACAGAAACCIGG-CCAGGCICCCAGGCIC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 149; DB 28; Length 3£1;
Pred. No. 5.05e-247;
0; Mismatches 25; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 OFFICASORACITSTOTITISTUNCAGGSSAAASAGCACORFICERGCAGGCAGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 53108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 others
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Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="154165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
310 atttttgcagtgtattactgt 330
                                    239 ATTTT-GCAGITTATIACIGI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.0%;
Matches 220; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
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                                                                                                                                                                                           9813824
                                                                                             RESULT 13
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JOURNAL
                                                                                                                                                                         ACCESSION
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                                                                                                                                                                                                             KEYWORDS
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Eukaryotae, medazao Eumecazoa Bliateria, occionadas Deuterostomia, Chodadas, Petrebrata, Gnathostomata, Theria: Eutheria, Archonta; Primates, Catarrhini, dominidae, Home.

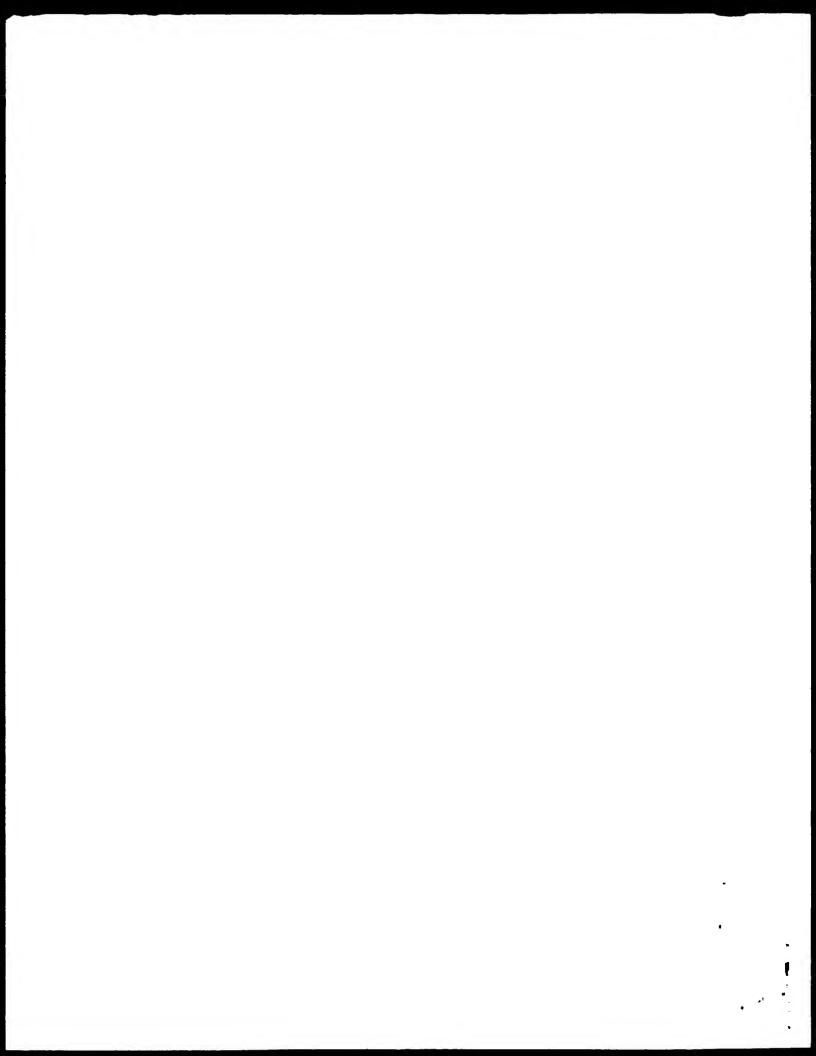
Eutheria, Archonta; Primates, Catarrhini, dominidae, Home.

I (bases I to 393)

S Adams,M.D., Kerlavage,A.R., Fleischmann,P.D., Fuldner,R.A., Mitrkees,E.F., Weinstrock, G. Gorayne, I.D., White,O., Sutton,G., Blake,I.A., Britchmann,P.D., Entle-Hughes,J. Fine,L.D., Flitchnon,P.D., Calyon,R.D., Catron,M.D., Earle-Hughes,J. Fine,L.D., Glodek,A., Gnehm,C.I., Hanna,M.C., Homellow, E., Hinkel Jr.P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Fiu,L.I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nquyen,D.T., Pelley,J.C., Fiu,L.I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Uttryback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Collins,R.J., Pimke,D., Feng,P., Ferrick,A., Grober,J.M., Gruber,J.M., Hudson,P., Kim,A., Koyak,D.L., Knnsch,C., Hastings,R.A., Meiser,P. Weigman,J.S., Gleen,H., Paymond,I., Weil,Y.F., Wing,T., Xu,C., Yu, C., L., Peuben,S.M., Dillow,P.J., Fannon,M.P., Penger,J.C., Markellow, M., Alloch,P., Meisener,P.S., Meiser,P.C., Markellow, M., Promon,M.P., Penger,J.C., Hasting,M.A., Koyak,D.L., Knnsch,C.L., Priben,S.M., Dillow,P.J., Fannon,M.P., Penger,J.C., Markellow,P.M., Meisener,D.S., M., Dillow,P.J., Fannon,M.P., Penger,J.C., Markellow,P.M., Meisener,P.S., Olsen,H., Paymond,I., Weil,Y.-F., Wing,T., Xu,C., Faser,C.M., and Venter,J.C.
                           EST100653 Homo sapiens cDNA 5/ end similar to immorrogiologic Aappa 1995t chaip, V region (GR-L01279) (HT·3043).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial Assessment of Human Gene Diversity and Expression Fatterns Based Upon 52 Million Basepairs of CDNA Sequence Impublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 agaiganceagictecaiceinnigictgeatriglaygagarayaginaerrinanii 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 cecetaagotectgatetetgetgeatecaatttgegaagtggggteeeateaagg+tea 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GCAGGGCCAGTCAGAGTGTTAACAAGTACTTAGCCTAGCAACAAAAACTGGCCAGT
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Loral Similarity 75.2%; Pred No. 6 67e-216;
les 200; Conservative 0; Mismatches 66; Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 geogggeaagteagageattageaeetttttaaattggtateaggaaaeeagggaeag
                                                                                                                                                                                                                                                                                                                                                             Sukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                 human primer-M13 Reverse library-Human Pandreas.
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
61.
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393 bp
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double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector (Pharmacia). Library went through one round of normalization to a Cot - 20. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae: Metazoa: Eumetazoa: Bilateria; Coelomata:
Deuterostomia: Chordata: Vertebrata; Gnathostomata: Osteichthyes:
Sarcopteryqii; Choanata; Tetrapoda; Amniota: Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                       Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H27031 218 bp mRNA EST 12-JUL-1995 y165d01.rl Homo sapiens cDNA clone 163105 5' similar to 9b:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN); H27031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 ctocaqcoaccetgtetgtgteteccaggggaaagagcoacceteteetgcagggecagte 125
240 giggostetggaaic gggaeagaitteaeteteaecateagaicigoaacetgaaaeig 299
                                         182 SISSEANTANNELDASSACACATICATICICACCAICASCAACCIAGAGGCTGAAGATT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 218)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultnan,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 133; DB 64; Length 210,
Pred. No. 7.75e-214;
Transches 9; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria: Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
WashJ-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MD 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project
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73 c
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Best Loral Similarity 94.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                             9897021
                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                           DEFINITION
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Search completed: Tue Feb 24 07:39:04 1998 Job time : 279 secs.



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* 4.7	se 2.1D John F. Collins, Biocomputing Pesearch Unit. ight (c) 1993, 1994, 1995 University of Edinburgh, U K Distribution rights by Intelligenetics, Inc.
MPsrch_nn n n	- n a database search, using Smith-Waterman algorithm
Run on:	time 410 lo seronds a weinster contractor
Tabular cutput n	542 Million ce.
Title: Description: Perfect score:	>US-08-844-215-16 (1-312) from "S08844215 soq 312
N A Sequence:	1 PAGETENETRAZIONES GANCEANGEGRAGATORA 312 CIGGAGAGAGAGAGA 312
Scoring table:	TABLE default Gap 5
Nmatch STD:	Dbase 0; Query 0
Searched:	430261 seqs, 710217276 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	embl-new7 1:8CT 2:FUN 3:GEN 4:HTG1 5:HTG2 6:HTG? 7:HTG4 8:HUM1 9:HDN2 10:HTM3 11:INT 12:END 13:GENG 14 MAR 15 VRT
Database:	1. BGT2 25. BCT3 25 BCT4 27. BGT5 28 1. BGT9 32. BGT10 33. BGT11 34. BGT12 1. GEN2 38. GEN3 39. GEN4 40. GEN5 41 1. HTG3 45. HTG4 46. HTG5 47. INV 1 48 1. INVS 52. INVS 54. INVS 56 1. B6. INV12 59. MAM1 60. MAM2 61. MAM3 6 1. VRT3 65. VBT4 66. PAT1 67. PAT2 68 1. FAT5 72. PAT7 73. FHG 74. FLN1 75. P. 1. FAT5 72. PAT7 73. FHG 74. FLN1 75. P. 1. FAT5 79. FAM5 80. FLN7 81. FLN8 82
	85.PLN12 86.PP11 87.PP12 88.PP13 89.PP14 17.PP16 92.PP17 93.PP18 94.PP19 95.PP110 103.PP112 98.PP113 4 100.PP115 10 103.PP11 104.PP18 105.PP18 104.PP1 109.PP17 110.PP18 111.PP19 112.STR 113.SY
Database:	114:0NA genbanb101 115:VRL1 116-VPL2 117-VPL3 118-VP14 119-VP15 120-VPL5 131:VB17 133:VP10 133:VP10 134:VP110 135:VP11
Database:	Dank-new7 Dank-new7 12: VRI 127: GEN 128: HIGH 129: HIGH 131: PNV 131 13: VRI 133: PHG 134: PINI 135: PNX 136: PRII 13
Database:	9:SYN 140:UNA 141:VRL 143:part2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

Mean 9 94%; Variance 4 455; scale 2,232

Statistics:

and is derived by analysis of the total score distribution.

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LLIYDASNRATGIPARFSGSGSGTDFTLIISSLEPEDFAVYYCQQRSNWPPSFGGGTK
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Ohlin,M., Sundyist,V.A., Mach,M., Wahren,B. and Borrebaeck,C.A.
Fine specificity of the human immune response to the major neutralization epitopes expressed on cytomegalovirus gp58/116 (gB), 3. Virol. 67 (2), 703-710 (1993)
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Homo sapiens (clone pAG21) Ig kappa chain mRNA, V-region, partial
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Light chain shiftling of a high affinity antibody results in a
darift in epitope recognition.
Mol. Immunol. 33 (1), 47-56 (1996)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                  89, 3175-3179 (1992)
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Pred. No. 4.76e-225;
0; Mismatches 8;
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/isolate="JM"
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/tissue_lib="JM14"
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Best Local Similarity 96.5%;
Matches 304; Conservative
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Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata, Butheria, Primates, Catarrhini, Hominidae, Homo (kase) 1 to 321)

(hases 1 to 321)

(hilli, M., Sundayist, V. A., Mach, M., Wahren, B. and Borrehaerk, C. A. Fine specificity of the human immune response to the major neutralization epitopes expressed on cytomegalovirus 9p58/116 (9B), as determined with human monoclonal antibodies

T. Virol. 67 (2), 703-710 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="PID:9845532"
/translation="DIQMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP
RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPLIFGGGT
                                                                                                                                         /note="product combines with ITC88 immunoglobulin heavy chain variable region to form a binding site specific for the AD-2 epitope of cytomegalovirus gpl16"
                                                                                                                                                                                                                                                                                                                                                                                                                            translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal."
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Homo sapiens (clone pAGZIB) Ig kappa chain mFNA, V-region, partial
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                                                                                                                                                                                                                                                                                                                                                    VkappaI-related primer to amplify this sequence"
                                                                                                                                                                                                                                                                                                                                                                                                    /note="This CDS feature is included to show the
                                                                                                                                                                                                                                                                                                                          /note="differences originate from the use of a
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Pred. No. 3.05c-222;
0; Mismatches 9;
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                                               /organism="Homo sapiens"
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Socation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  /note="this sequence has been corrected for primer-encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="EIVLTQSPATLSLSPGEPATLSCPASQSVSSYLAWYQQKPGQAP
RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPLTFGGGT
                                                                                                                                                                                                                                      /note-"product combines with IIC88 immunoglobulin heavy chain variable region to form a binding site specific for the AD-2 epitope of cytomegalovirus gpl16" /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anote—"This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal." /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H.sapiens mRNA for immunoglobulin kappa light chain VJ region (ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoqlobulin: immunoqlobulin kappa ohain: immunoqlobulin liqht
               (Kases 1 to 22)
chlin,M., Cwman.H., Mach,M. and Borrebaeck,C.A.
Light chain shuffling of a high affinity antibody results in a
drift in epitope recognition
Mobi. Immunol. 33 (1), 47-55 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differences (in comparison to most VkappaIIIa-related sequences) carried by the AG21 scFv Vkappa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 gecaateagaatgttageagetaettageetggtaeeaacagaaaoetggeeaggeteee 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 GCCASICAGASTSIIAACAAGIACIIASCCISSIACGAASASAAACGIGGGCASGCICCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 Aggerecrearerargearerageaseassanageseareragearerageassaneassan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 aqtgugictqqqacagacticactctcaccarcagcagcctagagcctqaagatittgca 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 AGTGGGTGTGGGAGAGATTGACTGTGAGGATGAGGAAGGTAGAGGGTGAAGATTTTGGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 acroagictocagecaecetqtotttgtetocagagaaaagagocaeetetectgeagg 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                                                                                                                                                                               /cell_type="bone marrow-derived mononuclear cells" <1...>321
                                                                                                                                                                                                                                                                                                                          /product="immunoglobulin kappa-chain V3a region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 274, DB 99, Length 321,
Pred, No. 2.54e-221;
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human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                     /organism="Homo sapiens"/clone="pAG218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:q845534"
                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 96.9%;
Matches 299; Conservation
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SOURCE

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anti-DNA autoantibody; constant region; immunoglobulin light chain;
joining region; kappa-immunoglobulin; variable region.
Homo sapiens cDNA to mRNA.
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DEFINITION Human immunoglobulin Pappa light chain (16KV) mPNA variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-JAN-1996) Juul L., Dept. of Clinical Immunology Kl
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
2200 Copenhagen N, DENMARK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="sequence goes out of frame in the Vi junction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 aggeteeteatetaigaigeaigeaineeaaeagggeeearigena'eneaaeeagaileagiige 258
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C. Mismatches 15; Indels 1; Gaps
                                                                                                                                                                                                                                                                                               Jull. Hougs, L., Andersen, V., Svergaard, A., and Barington, T. The normally expressed kappa immunoglobulin light chain gene repertoire. Frequent occurence of features often assigned to
Eskaryotan; mitochondrial mukanyntns; Metanna: O'nriata;
Vertebrata; Lutheria; Primates; Catarrhini; Hominidae: Homo.
1. (bases 1 to 388)
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/isolate="PBMC pooled from ten healthy advits"
/tissue_type="blood"
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/chromosome="2"
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67 388
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Best Local Similarity 94.8%:
Matches 291, Conservative
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Juul,L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xreff="PID:9619622"
/translation="EIVLTQSPATLSLSPGEPATLSCPASQSVSSYLAWYQQKPGQAP
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                                                                                                                                                                                             Direct Submission
Submitted (09-NOV-1994) Joyce Pauch, Montreal General Hospital
                                                                                                                                                                                                                                 Research Institute, McGill University, Rheumatology, Montreal, Quebec, H3G 1A4, Canada
Location/Qualifiers
                  1 (bases 1 to 387)
Prioux,J D., Zdarsky,E., Newkirk,M.M. and Pauch,J
Anti-DNA and anti-platelet specificities of SLE-derived
autoantibodies: evidence for CDR2H mutations and CDR3H motifs
Mol Immunol 32 (10), 683-696 (1995)
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/codon_start=1
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                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/cell_line="B8815"
/cell_Lype="B-lymphocyte"
/tissue_type="blood"
/map="2p12"
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JOUPNAL
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/translation="warpa]ilfiliiwi.puttgeivligepatisispgerati.scr
asqsvssylawyooppgappiiiiynasnpatgipapfsgssgsgtdftiissleped
Favyycoorsnwpltfgggtkveik"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig D-segment; Ig kappa light chain; Ig light chain; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vettebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 381)
Silberstein, L.E., Litwin, S. and Carmack, C.E.
Relationship of variable region genes expressed by a human B cell
lymphoma secreting pathologic anti-Pr2 erythrocyte autoantibodies
U. Exp. Med. 169 (5), 1631-1643 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GCCAGTCAGAGTGTTAACAAGTACTTAGCCIGGTACCAACAGAAACCIGGCCAGGCICCC 126
                                                                                                                                                                                                                                                                                          172 aggetecteatetatgatgeatecaacagggecaetggeateecageeaeetteagtgge 231
                                                                                                                                                                                                                                                                                                                                 232 agigggicigggacagaciticacicicaccateagcagcciagagccigaagattitgca 291
                                                                                                                                                                                                                                                                                                                                                                                                                 187 AGTGGGTCTGGGACAGACTTGAGTCTCACCATCAACAAACCTAAAAGCTGAAAATTTTGCA 246
                                                                                                                       52 acacagtotecagecaccetgtetttgtetecaggggaaagagecaccetetectgcagg 111
                                                                                                                                                                                                         112 gecagiragagigitagcageiantiageeiggianeaaeagaaaneiggnnaggeinee 171
                                                                                                                                             31-MAR-1995
                                                                                  3: Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS HSIGVLLS 381 bp RNA PRI 31-MAR-1
DEFINITION Human mRNA for LSI/EVB 19 V(kappa), autoantibody with RBC
                                       Length 387
                                                                                Indels
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/product="LS1 1g light pre-chain"
/db_xref="P1D;g33757"
                                                                                ·.
                                    Score 272; DR 99; I
Pred. No 1.97e-219;
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                                                                                Mismatches
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/note*"V(kappa) segment"
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C
                                    Query Match

Best Local Similarity 46 4%;
Matches 298; Conservative
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Direct Submission
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X15987 Y00652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 GAGATCAAA 312
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/db_xref="PID:q1335190" |
/translation="PIV:TQSPATESISPGFPATESCPASQSVSSYLAWYQQKPGQAP
RLLIYDASNPATGIPAPFSGSGSGIDFTLIISSLEPEDFAVYYQQGSNWFWIFSQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-JAN-1992) ©. Tsaiwei, Department of Medicine - 0663,
University of California, San Diego La Jolla, California
92092-0663, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Author-qiven protein sequence is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae, mitochondrial eukaryotes; Metacoa; Chordata; Vertebrata, Eutheria, Primates, Cataithin; Heminidae; Heme (Dases 1 to 33)

"lee; T. Lu, E.M. Huang, D.F., Soty-Gill, P.M., Leftes, M., Kozin, F., Carson, D.A. and Chen, P.P. Genetic analysis of self-associating immunoglobulin G rheumatoid factors from two rheumatoid syncvia implicates an antigen-driven
                                                                                                                               73 anahagtothnagocachotgtotttgthttgthtcdgggggaaagagocaccotottotgcagg 132
                                                                                                                                                                                                       133 gecagticagagigitiagcagitiacitiagectiggiaecaacagagaectiggecaggetieec 192
                                                                                                                                                                                                                                                                                               253 agtgggtctgggacagatttcactctcaccatcagcagcctagagcctgaagattttgcg 312
                                                                                                                                                                                                                                                                                                                                                                                       187 ASTISISICISSSACASACITCACTCTCACCATCAGCAACCTAGAGCCTGAAGATTTTGCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                            313 gittattacigicagcagcgiagcaaciggccgcicacticggcggaggagcaaggig 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                67 GCCAGTCAGAGTGTTAACAAGTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSKA3D11G 333 bp RNA PPI 10-JUN-1992
H.saplens rearranged Humigka3d1 gene encoding IgG light chain.
X59705
                                                                                                                                                                7 ACTOAGTOIGGAGGGTGTGTTTGTGTGCAAGGAAAAAAGGCCACCCICTGCAGGAGG
                                                                                           Gaps
                                                                                                                                                                                                                                                                                3;
                                                      Length 381,
                                                                                          0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin; J-segment; light chain
                                                    Score 268, DB 91, 1
Pred. No. 1.08e-215;
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                                                    Ouery Match
Best Local Similarity 95.8%:
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Tsalwel, 0.
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                                                                                          295; Conservative
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/translation="MPAPAQLIFLIHIWLPPTIGFIVITGSPAILSLSPGERATLSOR
ASQSVSSYLAWYQQXPGQAPRLLIYDASNKATGVPARFSGSGSGTDFTHIISSLHIFD
FAVYYCQQSSKWPLIFGGGTKVEIKG"
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T Immunel 144 (7), 2921-2828 (1949)
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gene, variable region subgroup VK-IIIa.
Buman (patient POP) hybridoma AB6-5 DNA, chome pRosepVK, derived
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                                                                                                                                                                                                                                                                                                                                                                                                               193 agtgggtetgggacagaetteaeteteaecateageageetagageetgaagattttgna 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Ig rearranged anti-myelin kappa-chain mRNA V-34-region, hybridoma AE6-5, 5' end.
                                                                                                                                                                                    Gaps
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Spatz. L.A., WongX.K., Williams.M., Desai,R., Goller,J., Berman,T.E., Alt.F.W. and Latov.N.
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                                                                                                                                      Length 333;
                                                                                                                                                                                  0; Mismatches 11; Indels
                                                                                                                                   Score 266; DB 91; I
Prod. No 8.04e-214;
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/db_xref="PID:q185923"
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                   /gene="Humigka3d1"
/note="J-segment, Jk"
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Rest Local Similarity 95.5%;
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Direct Submission
Submitted (01-DBC-1943) Pojen P. Chen, Medicine, University of
California San Diego, 9500 Gliman Dr., La Jolla, CA 92093-0663. USA
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Defining the genetic origins of three rheumatoid synovium-derived
Igs rheumatoid factors
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Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 627)
                                                                                                                                                                                                                                                          Score 266; DB 99; Length 407; Pred. No. 8.04e-214;
                           /gene="IGKV"
/note="Ig kappa-chain signal peptide"
/codon_start=1
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/cell_line="D1 hybridoma"
/cell_type="lymphocyte"
/tissue_type="synovium"
                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                            /note-"Ig kappa-chain"
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/product="rheumatoid factor Dl 1gG light chain VK3 region" /db_xref="PID:g520413"
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                                                                                                                                                                                                                                        ASOSVSSYLAWYQOKPGQAPPILITYDASNRATGIPARFSGSGSGTDFTLTISSLEPED
FAVYYCQQRSNWPWTFGQGTKVEIKRTVA"
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H.sapiens mRNA for immunoglobulin kappa light chain VJ region (ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Vertebrata: Eutheria: Primates. Catarrhini, Hominidae, Homo.
1 (bases 1 to 384)
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                                                                    join(114..162,332..>675)
/gene="humka3d1"
/dev_stage="adult"
join(114..162,332..>342)
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189 c 157 g
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The progeny of a single virgin B cell predominates the human recall
B-cell response to the capsular polysaccharide of Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS HSSIM044 342 bp LNA PRI 12-SEP-1996 DEFINITION H.Sapiens mRNA for Kappa immunoglobulin light chain (V-J-C region; clone HSSIM044).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 265; DB 93; Length 384;
Pred. No. 6 92e-213;
0: Mismatches 10; Indels 3: Gaps
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Batington,T., Hougs,L., Juul,L., Madsen,H.O., Ryder,L.P.,
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                                                       /isolate="PRMC pooled from ten healthy adults"
/tissue_type="blood"
/cell_type="mononuclear cells"
//hromosope="2"
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                 1..384
/organism="Homo sapiens"
Location/Qualifiers
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40
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                                                                                                                                                                                                                                                                                                                                           Query Match

Best Local Similarity 95.8%;
Matches 293; Consorvative
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Heilmann,C. and Svejgaard,A.
The progeny of a single virgin B cell predominates the human recall
B-cell response to the capsular polysaccharide of Haemophilus
influenzae type b
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Submitted (01-DD2-1995) Torben Barrington, Tissue Typing Laboratory
7431, Pigsbospitalet, National University Hospital, Tagens"() 20.
DK-2200 Ocpenhagen M. DENMARK
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H.sapiens mPNA for Kappa immunoglobulin light chain (V-J-C region:
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Vortebrata: Butheria: Primates: Catarrhini; Hominidae; Hom
1 (bases 1 to 345)
Barington, I., Hougs, L., Juul. L., Madsen, H.O., Ryder, L.P.,
                                                                                                                                                                       /note="variable region and joining region" /product="immunoglobulin kappa light chain"
                                                                                                                                                                                                                                                                                                                                                                           Length 342;
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Pred No 5 % e-212,
0, Mismatches 21;
                                                                                                                                                                                                                                        /gene="V-kappa-L6 and J-kappa-4"
                                                                                                                                                     /gene="V-kappa-L6 and J-kappa-4"
/organism="Homo sapiens"
/tissug_type="peripheral blood"
/cell_type="B lymphocyte"
/clone="SiMO44"
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Barington,T.
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Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata: Eutheria: Primates; Catarrhin; Hominidae, Homo.
1 (bases 1 to 384)
Nickerson.K G. Tac.M -H. Chen.H -T., Larrick,J. I. and Kabat,E A
Misserson.K G. Tac.M and antibodies to blood group A substance
Which are nearly identical immunochemically, use radically
different primary sequences
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Homo sapiens anti-A monoclonal antibody IgK chain mPNA, V-region
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light chain; monoclonal antibody.
Homo sapiens hybridoma cDNA to mRNA.
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                                                                                                                                      /gene-"V-kappa-L6 and J-kappa-2"
/note-"variable region and joining region"
/product-"immunoglobulin kappa light chain"
                                                                                                                                                                                                                                                                                                                                            Length 345;
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Pred. No. 5.95e-212;
0: Mismatches 12; Indels
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/tissue_type="hybridoma"
/map="2p12"
                                                                                                                                                                                                 /gene="V-kappa-L6 and J-kappa-2"
325. >345
                /tissue_type="peripheral blood"
/cell_type="B lymphocyte"
/clone="SIP055"
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/organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                          Match 84.6%;
Local Similarity 95.1%;
Hes 294; Conservative
                                                                                                       /rearranged
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HIMIKORF 294 bp mPNA PPI 10-MAY-1996
HOMO Sapiers (clone ITPBL2) immunoqiobulin kappa light chain mRNA,
partial cds.
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 294)
Bridges,S.L. Jr., Lee,S.K., Johnson,M.L., Tavelle,J.C.,
Fowler,P.G., Knopman,M.J. and Schroeder,H.W.Dr.
Somatic mutation and CDR3 lengths of immunoglobulin kappa light
chains expressed in patients with rheumatoid arthritis and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 aggeteeteatetatgatgeatecaacagggeeactggeateecageeaggtteagtage 252
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                                                                                                                                                                                                                                                                                                                            Length 384;
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                                                                                                                                                /function="anti-A monoclonal antibody"
                                                                                                                                                               /evidence=experimental
/product-"immunoglobulin kappa chain"
                                                                                                                                                                                                                                                                                                                          84.0%; Score 262; DB 99; L: 94.8%; Fred. No. 4.40e:210; vative 0; Mismatches 13;
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95362845
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                                                                                         /standard_name="HUAVK"
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                                                                        /dene="IGK"
/gene="IGK"
                                    /gene="IGK"
                                                                                                                                                                                                                                                                                                                                                            293; Conservative
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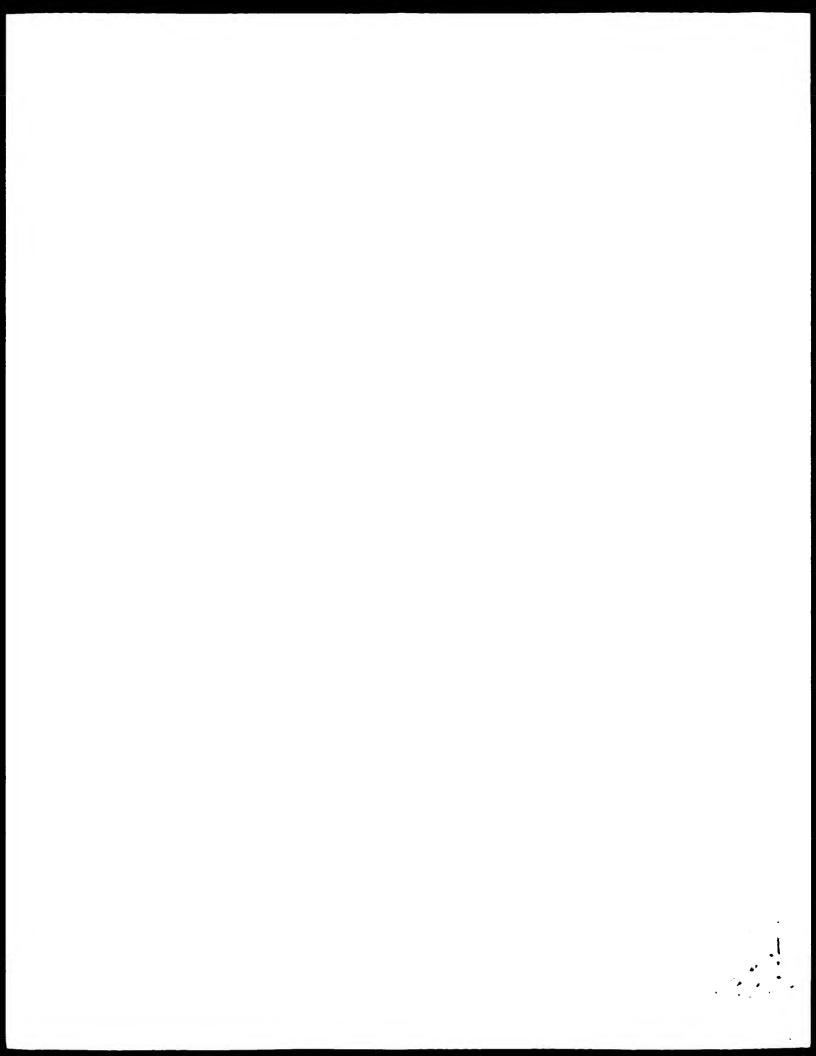
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                                                                                                                         /product."immunogiobulin kappa chain."
/dx.xref-rpiD:q722482
/translation="ALTSICEPEPATIS"PASGSVSSFLAWYQQPPGGAPFLLIYDAS
NRAIGIPAPPSGSGSCINFILLISSLEPEPFAYYQQGSNWPIFGGGIKVEIK."
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1 (bases 1 to 321)
Ohlin,M., Sundqvist,V.A., Mach,M., Wahren,B. and Borrebaeck,C.A.
Fine specificity of the human immune response to the major neutralization epitopes expressed on cytomegalovirus qp58/116 (qB), as determined with human monoclonal antibodies
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Homo sapiens (clone: pAC33) cDNA to mRNA; and Homo sapiens (clone:
pAC36) cDNA to mRNA.
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Homo sapiens (clones pAC33, pAC35) 1g kappa chain mRNA, V-region,
partial cds.
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Ohlin,M., Owman,H., Mach,M. and Borrebaeck,C.A.
Light chain shuffling of a high affinity antibody results in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 GITARCARSTRUTTERSOCIAGOARCARSARACOTARSOCIAGOSTOFOCAROTARS 138
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                                                                                                                                                                                                                                                                                              Overy Match 83.3%; Score 260; DR 99; Length 294; Best Local Similarity 94.2%; Pred. No. 3.25e-208; Matches 277; Censerrative 0; Mismatches 17; Indels 9;
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                                                 /note="putative"
/citation=[1]
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/translation-"ETVLTGSPAILSISPGFPATI SCPASCESVESSLAWYGGRFGGAP
RLLVYDTSNRATGIPARFSGSGSGIDFTLTISSLEPEDFADY)CGGRSEWPLTFG3GT
KVEIK"
                                                                                                               translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal." /codon_start=1
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Pred. No. 3.256-208:
0: Mismatches 14: Indels 3: Gaps
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/product="immunoglobulin kappa-chain V3a region"
                                                                                   /note="This CDS feature is included to show the
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Matches 292; Conservative
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***************************************	(E)	Release 2.1D John F. Collins, Biodomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U K Distribution rights by Intelligenetics, Inc	nn n.a n.a. database search, using Smith-Waterman algorithm	Tue Feb 24 13.56 3R 1998. MasPar time 19 34 Seconds output not generated.	>US-08-844-215-16 Score: 312 1-3A3CTZACTCAGTCAGGCCCAGGTGGAGGTGGAAGGTGAAA 312 quence: 1-3A3CTZACTCAGTCAGGCCCCCCCAGGTGGAGGTGAAA 312 mp:	table: IABLE default
****			MPsrch_nn	Run on. Tabular out	Title: Description: Perfect Score: N.A. Sequence: Comp.	Scoring table:

Dbase 0; Query 0 TABLE default Gap 6 STD : Nmatch 87531 segs, 22996021 bases x 2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

n-issued 1:backi 2.51 2.52 4.53 5.54 6.55 7.56 8.PCT90 9 PCT91 10:PCI92 11:PCI93 12-PCT94 13-PCT95 14-PCT96 Database:

Mean 7.521: Variance 4.215; scale 1.808 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Match	Length	ď.	1.0	Description	Pred No
7	258	82.7	912	7	08-08-053-	Sequence 178, Applicat	1.750-173
2	252	80.8	006	7	US-08-053-	180,	6 696-169
ĸ.	228	73.1	646	13	PCI-US95-1	2, Ap	1
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17	140	44.9	381	¢	- 12- 00-Si	C4	3 230-94
18	140	44.9	e.	7	US-08-487-	Sequence 82, Applicati	3 230-04
91	140	44.9	381	S	US-07-634-	Sequence 82, Applicati	3.23e-84

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600, APPLICATION A	74. Application Ap	92, Applica 93, Applica 2, Applicat 14, Applicat 1, Applicat 35, Applicat	34, Applicati 2, Applicati 3, Applicati 3, Applicati 69, Applicati
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ALIGNMENTS

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Sequence 178, Application US/08053131.
Sequence 178, Application US/08053131.
Sequence 178, Application US/08053131.
Sequence 178, Application US/08053131.
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Pobert M.
IIILE OF INVENTION: Transpenic No. 5661016-Human Animals for ITILE OF INVENTION: Producing Heterologguis Antibodies NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                               SEE: Townsend and Townsend Khourie and Crew: One Market Plaza, Steuart Tower, Suite 200 San Francisco
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENTING SYSTEM: PC-DCS/MS-DOS
SOFTWAPE: Patentin Pclease #1.0. Version #1.25
         US-08-053-131-178 STANDARD; DNA; UNC; 812 BP.
                                                                                                                                                                                                                                                                                                                                                                                     CUPRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,131
FILING DATE: 26 APR-1993
CLASSIFICATION BOD
FILING DATE: 26 APR-1993
CLASSIFICATION BATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 16 DEC 1992
FILING DATE: 17 DEC-1991
FILING DATE: 17 DEC-1991
FRICK APPLICATION NUMBER: US 07/853,408
FILING DATE: 17 DEC-1991
FRICK AFFLICATION NUMBER: US 07/853,408
FILING DATE: 18 MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, MILITAM M.
REGISTRATICN WIMBER: 30.223
FREEFENTHY/POOTKET NUMBER: 14643-9-3
FREEFENTHY/POOTKET NUMBER: 14643-9-3
FREEFENTHY/POOTKET NUMBER: 14643-9-3
FREEFENTHY/POOTKET NUMBER: 14643-9-3
                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                 E: California
PR: USA
94105
                                                                                                                                                                                                                      ADDRESSEE:
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                                              01-JAN-1900
RESULT
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502 GCCAGICAGAGIGIIAGCAGCIACTIAGCCGGGIACCAACAGAAACCIGGCCAGGCTCCC 561
                                                                                                                                                                                                                                                                                                                           622 AGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCA 681
                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5651016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CORPRESPONDENCE: 197
CORPRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                         Score 258; DB 7; Length 812;
Pred, No. 1.76e-173;
                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                    <u>LOCATION join(199 246, 418, 714)</u>
Sequence 812 RF: 201 A: 22F C: 187 G: 399 T: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-053-131-180 STANDARD; DNA; UNC; 900 BP.
                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            682 GITTATTACTGTCAGCAGCGTAGCAACTGG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                           247 GITTATTACTGTCAGCGTAGCGACTGG 276
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26-APR-1993
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Sequence 180, Application US/08053131
Patent No. 5661016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATINS SYSIEM; PC-DOS/MS-DOS
TELEPAX: 415-326-2400
TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 178-
SEQUENCE CHARACTERISTICS.
LENGTH: 812 base pairs
                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 16-DEC-1992
PRIOP APPLICATION DATA-
APPLICATION NUMBER: US 07
                                                                                                                                                                          Ouery Match 82.7%;
Best Local Similarity 97.8%;
                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPITER READABLE FORM:
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California
                                                                nucleic acid
                                                                                       linear
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                                                                                                                            NAME/KEY: CDS
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                                                                        STRANDEDNESS
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                                                                                       TOPOLOGY
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01-JAN-1900
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GENEPAL INFOPMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: HISTORY FOR PRODUCING ANTIRODY LIBRARIES
TITLE OF INVENTION: HISTORY HAVIOEPSAL OF FANISCHIZED IMMUNICATIONHILD INSTITUTE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 AGTGGGCCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCTGAAGATTT1GCA 660
                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 252; DB 7; Length 900;
Pred. No. 6,69e-169;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                               LOGATION - join(180 227, 397 693)
Sequence 900 BP: 225 A: 244 G: 204 G: 227 T: 0 other:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: The Scripps Research Institute
STREET: 10666 North Forrey Pines Road, TPCR
                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-11235-2 STANDARD; DNA; UNC; 646 BP.
                                                                                           14643-9-3
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IS 07/853,408
FILING DATE: 18-MAP-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 GITTALIACIGICAGCAGAGGACGACTGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9511235
Sequence 2, Application PC/TUS9511235
                                                                 NAME: Smith, William M. PEGISTRATION NUMBER 30,223 PEFERENCE/DOCKET NUMBER 14(TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                             INFORMATION FOR SEQ ID NO: 180: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      LENGIH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SECUENCES 70
                                                                                                                                 415-326-2422
                                                                                                                                                                                                                                                                                                      Query Match 80.8%;
Best Local Similarity 96.7%;
Matches 261; Conservative
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                                                                                                                                                                                                               linear
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IILLE OF INVENTION. METHODS FOE PACHOCOING ANTIBODY LIPEARIES
TILLE OF INVENTION: USING UNIVERSAL OF PANDOMIZED PACHOCOIN LIBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 CAGGCTCCCAGGCTCCTCATCTATGATGCAICCAACAGGGCCACTGGCAICCCAGGCGG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GATITIGGAGIGIACIACIGIAGOGASTAIGGIGGOTGAGGGIGGIJGGGAAGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IGCAGGGCCAGTCACAGTGTTAGCAGGGCCTACTTAGGCTGGTAGCAGCAGCAGAAAACCTGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGCTCACGCAGTCTCTCAGGCACCTGTCTTTGTCTCCAGGGGAAAGAGCACCCTCTCC 60
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Pred. No. 1.30e-150;
0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURPENT APPLICATION DATA-APPLICATION NUMBER-PGT/US94/01258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 646 BP, 162 A, 187 C, 170 G, 127 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                       PMRER: PCT/US94/01258
02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ris 08/174,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 08/012,566
                                                                                                    NUMBER OF SEQUENCES: 61
COMPUTER PEACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Richard A
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-FEB-1994
PPIOP APPLICATION DATA:
APPLICATION NUMBER: US 08/0
FILING DATE: 02-FEB-1993
PPIOP APPLICATION DATA:
APPLICATION NUMBER: US 08/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28-DEC-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.68;
Matches 279, Conservative
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Lerner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbas,
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APPLICANT: Barbas
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APPLICANT:
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Sequence 646 RP: 162 A: 187 C: 170 G: 127 I: 0 other:
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PCT-US94-01258-2 STANDAPD; DNA; UNC; 646 BP.
APPLICATION NUMBER: POLZUSSEJILZES
FILING DATE: 01-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08, 100, 186
FILING DATE: 02-SEP-1994
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                                                                                                                                                                                                                                         TIS 08/174,674
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Sequence 2, Application PC/TUS9401259
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/PACKET NUMBER: TSK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OR
                                                                                                                                                                                                                                                                             FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
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LENGTH: 646 base pairs
TYPE: nucleic acid
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Rest Local Similarity 88.6%;
Matches 279; Conservative
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181 TCCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAGTGGAGCTGGAGCTGAA 240
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            ADDRESSBE: The Scripps Research Institute
STRRET: 10666 No. 5667948th Torrey Pines Road, TPCA
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Fred No 1 108-150,
0; Mismatches 33; Indels
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                                                                                                                                                     SOFTWARE: Patentin Folease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,186A
FILING DATE: O2-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         PEFERENE DOCKET NUMBER: TSPI 409.1 TELECOMMUNICATION INPURMATION: TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                UMBER: US 08/012,566
02-FEB-1993
                                                                                                                                                                                                                                                                                                 FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012.566
                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBEP- US OR/174,674
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBEP: US 07/826,623
                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTEP: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO. 2-SEQUENCE CHARACTERISTICS:
LENGTH 646 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFOPMATION:

    646 base pairs
nucleic acid

                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fitting, Thomas PEGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     619-554-6312
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Local Similarity 88.6%;
les 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:

    301 AAGGTGGAACTCAAA 315

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                                          La Jolla
                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                     COUNTRY:
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                                          CITY: STATE:
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435 GCCAGTCAGAGTGTTAGCAGGTACTTAGCGGGTACCAGAGAGAAACTGACTAGAGT 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 ACGCAGICITCCAGGCACCCIGICITIGICICCAGGGGAAAQAGCACCACCTCTCTTGTAGA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 GCCAGTCAGAGTGTTAACA--AG-TAGTTAGGCTGGTACCAACAGAAAGGTGGCAGGT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ACTCASTCTCCAGCCACCTSTCTTTGTCTCCCAGGGGAAAGAGCCCCCTCTCCTGCAGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 11; Indels 3; Gaps
                                                                                        SENERAL INFORMATION:
APPLICANI: Lonberg, Nils
APPLICANI: Ray, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 218; DB 7; Length 900; Pred. No. 5.22e-143;
                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend Khourie and Crew STREET. One Market Plaza, Steuart Tower, Suite 200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: join(115.163, 351..650)
Sequence 900 BP: 220 A: 241 C: 201 G: 238 T: C cther:
                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.25
          US-08-053-131-182 STANDARD; DNA; UNC; 900
                                                                                                                                                                                                                                                                                                                                                                                            PLORA PELLICATION ON OUR PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 16-DEC-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NIMBER: 14643-9-3
                                                                                                                                                                                                                                                                                                                                        CURPENT APPLICATION DATA-APPLICATION NUMBER-US/08/053,131
FILING DATE: 26-APR-1993
                                                    Sequence 182, Application US/08053131. Sequence 182, Application US/08053131
                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Smith, William M. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415-326-2400
415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900 base pairs
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LENGTH: 900 base pairs
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                                                                                                                                                                                                                                                                         COMPUTER READARLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247; Conservative
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                                                                                                                                                                                                                                  California
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                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26 CLASSIFICATION:
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                                                                                                                                                                                                                                                  USA
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                                                                              Patent No. 5661016
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                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                STATE:
                                       01-JAN-1900
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JT 8
US-08-276-852-152 STANDABED, DNA; UMT: 729 BP
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FILING DATE: 30-SEP-1993
APPIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTPATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/OB/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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01-JAN-1900
Sequence 152, Application US/08276952.
Sequence 152, Application US/08276952
Patent No. 5652138
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
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TYPE: nucleic acid
STRANDEDNESS: double
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51.9%:
Rest Local Similarity 83.9%
Matches 219: Conservative
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LOCATION: 9.715
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                                                                                PRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY PROPERTY SAME ASSETT TO THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 CCCASSOTOCIOALCIAISAISCALCIAARASASSOCACTASCATOCCASCCAGGIICAGI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19. BGCASTGGGICTGGSACAGACITCACICICACAICAGAAGAGGGGGAGGCIGAAGAIIII 252
     124 OCCASSULGOLGALGIAISALGCAACOGAAGAGGGGGATTGGGATGTGAGGAAGTTGAGT 183
                                                          555 GGGAGTGGGGTGTGGGAAGAGAGTTGAGTGGAGGAGAGAGAGAGAGAGGGGAGAGATTTI 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 - ACGGAGIGT GCAGGCAGCCTGTGTTT TGTPCTGCAGGGAAAAAGAGCGAGCCTGTGCTGCTGCAGGAGG
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Pred. No. 6.70e-134;
0; Mismatches 32; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
Sequence 325 BP; 79 A; 93 C; 79 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Hi Density Diskette
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                        PCT-US93-12501-1 STANDAPP DNA UNC: 325 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DGS, Version 3.30 SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCI/US93/12501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Tanox Biosystems, Inc. STREET: 10301 Stella Link Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INX92-3
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application PC/TUS9312501
Sequence 1, Application PC/TUS9312501
GENERAL INFORMATION.
APPLICANT: CADRG, ISE Wen
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STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mirabel, Eric P.
REGISTRATION NUMBER: 31,211
REEDRUCLYPOTET NUMBER: TN)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-664-2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACIERISTICS:
                                                                                                                                                                 615 GCAGIGIAIIACISICAGCAG 635
                                                                                                                                                                                                                    244 SCACITIATIACIGICAGCAG 264
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ATTORNEY/AGENT INFORMATION
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TELEPHONE: 713-00.
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Local Similarity 87.8%;
es 274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: SOFTWARE: Wordper
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COUNTRY: USA
ZIP: 77025
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244 GCAGIIIAIIACIGICAGCAGCGIAGCGACIGG--GIC-ACTIICAGCGAGCGAGGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Burlon, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
IIILE OF INVENTION: HUMAN NEUTFALIZING MONOCLONAL ANTIBUDIES
IIILE OF INVENTION: 10 HUMAN IMMUNORFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET 10666 No. 5652138th Torrey Pincs Foad, Suite 120. STREET: Mail Drop 1PC8 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ~~>
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Prod No 1 100-100;
O; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 729 BP: 173 A: 208 C: 192 G: 156 T: 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEPATIN: SYSTEM: PF-14/5/MS-L4/5
SOFTMARE: Patentin Pelease #1 0, Version #1.25
CURRENT APPLICATION DATA:
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121 GCTCCCAGGCTCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGGCTGCTGTC 180
                                                                                                                                                                                                         78 CTCACSCASTCTCCASSCACCOSTCTCTGTSTCTCASASAAAAAACACTTCTCCTST 137 [HTH HTHH HTHH HTHHH HHHHH HHHHH
                                                             138 AGGICCAGICACACOTICACAGOGCOGCGGTAGCTGGIACCACACAAAACCIGACAAA 147
                                                                             198 GCTCCAAGGCTGGTCATACATGGTGTTTCCAATAGGGCCTCTGGGCATGTCAGACAGGTTC 257
                                                                                                                                                                                       258 AGCGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCACCAGAGTGGAGCCTGAAGAC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 CTCACGCAGTCTCCAGGCACCCTGTCTCTGTCTCCAGGGGAAAGAGCCACCTTGTCCTGT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 AGGTGCAGTCAGAGCATTGGGAACTGGGGGGGTAGGTGGTAGGAGAGAAAAGGTGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AGGGGGAGTGGGGTGTGGGACAGACTTCACTCTCACCATCACCAGAGTGGAGCGTGAAGAC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CTCACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCACCCTCTCCTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN NEUTPALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-POS
SOFTWARE: Patentin Pelease #1.0, Version #1 25 (EP?)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 51.9%; Score 162; DB 13; L. Local Similarity 83.9%; Pred. No. 1.10e-100; les 219; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-08743-152 STANDARD; DNA; UNC; 729 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USG5/0R743
FILIND DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 152, Application PC/TUS9508743. Sequence 152, Application PC/TUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 08/276,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO- 152:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                    318 IITGCACTGIACTACTGTCAG 338
                                                                                                                                                                                                                                                                                  241 TITGCAGITIATIACIGICAG 261
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nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1'
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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LOCATION: 9 715
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251 CTGACAGTAATAAACTGCAAAATCTTCAGGCTCTAGGTTGCTGATGGTGATGAGGTGAAGTC 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 TGTCCCAGACCCACTGCCGCTGACCTGTCTGAGATGCCAGAGGCCCTATTGGAAACAC 511
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                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN NEUFALIZING MONGCLONAL ANTIFCOLES TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS NUMBER OF SEQUENCES: 170 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jenath 729,
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC_DOS/WS-DOS
SOFTWAPE: Patentin Release #1 9, Vorsion #1 25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
PILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 162, DB 13, Length 729
Pred. No. 1.10e-100,
0; Mismatches 39; Indels
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                                                                                                                                           T 10
PCT-0S95-08743-168 STANDAPD: DNA: UNC: 729 BD.
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                                                                                                                                                                                                   01-JAN-1900
Sequence 168, Application PC/TUS9508743.
Sequence 168, Application PC/TUS9508743.
APPLICANT
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Sequence 168, Application US/08276852
Patent No. 5652138
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                                                                                                                                                                                                                                                                                                                                                                                                          IRM PC compatible
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SEQUENCE CHAPACTERISTICS:
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Carlos F
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                                        318 TTTGCACTGTACTACTGTCAG 338
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                                                              LENGIH: 729 base pairs
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83.98;
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EDNESS: double
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les 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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APPLICANT: Burton,
APPLICANT: Barbas,
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                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER
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261 CTGACASTAATAAAGTGCAAAATGITCASSCTCTAGSITGCTGATSSTGAGTGAASTC 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 CTGACAGIAGIACAGIGGAAAGIGIIGAGGIGGAGIGIGGIAAIAGIGAGAGIGAAGIG 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LETDER, RICHARD A LILLE OF INVENTION: HUMAN NEUTRALIZING MCHOCOGNAL ANTIBODIES LILLE OF INVENTION: HUMAN NEUTRALIZING MCHOCOGNAL ANTIBODIES FOR SEQUENCES: 170 HUMAN IMMUNDEFICIENCY VIRUS COPRESPONDENCE ADDRESSE: ADDRESSE: ADDRESSE: Patent Counsel STREET: 13666 No. 555178th Torrey Fines Road, Suite 120, STREET: Mail Drop TPCR STREET: A Jolla STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 51.9%; Score 162; DB 7; Length 729; Local Similarity 83.9%; Pred No. 1.10e-100; hes 219; Conservative 0; Mismatches 39; Indels
                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: TRM PF comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Pelease #1.0, Version #1 25
CURRENT APPLICATION DATA:
FILING DATE: 18-JHT-10.
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Sequence 729 BP: 156 A: 192 G: 208 G: 173 T: 0 o*ther:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-5EP-1992
ATTORNEY/AGENI INFORMATION:
NAME: Fitting, Thomas
PEGISIPATION NUMBER: 34,163
REFERENCE/COCKET NUMBER: SCR1452P
TELECHNOR. 619-554-2937
                                                                                                                                                                                                                                                       CLASSIPICATION LAFA.
PRIOR APPLICATION NIMPER.
FILLING
                                                                                                                                                                                                                                                                                                                            APPLICATION NIMBER: US 08/178,302
FILING DATE: 30-EEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 168: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GGTGGGTGGGAGAGTGAGTGAG
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ZIP: 92037
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RESULT 12 ID 19-00-276-902-106 STANDARD, UNA, CMS, 13254-86

01-14N-10

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NAMES CONTROLLARIA DE CARACTERIO DE CONTROLLA DE CONTROLL
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Sequence 156, Application US/08276852.
Sequence 56, Application US/08276852.
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burbon, Dennis R
APPLICANT: Burbon, Dennis R
APPLICANT: Lerner, Richard A
TITLE CF INVENTION HUMAN NEUTPALLIZING MONEYL MAI ANTIBOTIES OF SEQUENCES: 170
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: The Scripps Posearch Institute, Office of ADDRESSE: Patent Counsel STREET: 10666 No 5452138th Torrey Pines Road Suite 22%, STREET: Mail Drop TPC8 (TTY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 39; Indels 3:
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Sequence 13254 BP; 3204 A 3550 C, 2251 G, 3238 T, C (ther:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Pelease #1 0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/276,852
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Pred. No. 1.10e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSFICATION DATA:

PRIOF APPLICATION NUMBER: US 08/178.302
FILING DATE: 0.55EP-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178.302
FILING DATE: 0.55EP-1993
APPLICATION NUMBER: US CT.

FILING DATE: 30.00
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COMPUTER: IBM PC compatible
OPEPATING SYSTEM: PG-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: SCR14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-2937
INFORMATION FOR SEC ID NO: 156:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
TOPOLOGY: circuit
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Best Local Similarity 83.9%;
Matches 219; Conservative
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MEDIUM TYPE: Floppy
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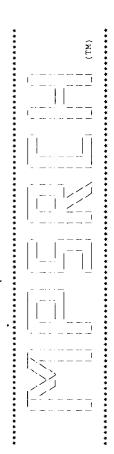
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01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12566 AGGICCAGICACACCAITICGCAGCCGCGCGTAGCCIGGIACCAGCACAAACCIGGCCAG 12725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12726 GGTTGGAAGGGTGGTGATACATGGTGTTTTGAATAGGGGTTGTGGGATGTGAGAGGTTT 12785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AGTGGCAGTGGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGGCTGAAGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 162; DB 13; Length 13254;
Pred. No. 1.10e-100;
0; Mismatches 39; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CTCACTCAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGC 63
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                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIRODIES TITLE OF INVENTION: TO HUMAN IMMINODEFICIENCY VIRUS NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
Sequence 13254 BP; 3206 A; 3559 C; 3251 G; 3238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Pelease #1.0, Version #1 25 (EPO) CURRENT APPLICATION DATA.
.T 13
PCT-0S95-08743-156 STANDARD; DNA; UNC; 13254 RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .T. 14
PCT-US95-08743-170 STANDARD: DNA; UNC; 13254 RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1900
Sequence 170, Application PC/TUSSS08743.
Sequence 170, Application PC/TUSSS08743.
APPLICANT:
                                                                                                                                                            Sequence 156, Application PC/TUS9508743.
Sequence 156, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/276,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TTTGCAGTTTATTAGTGTGG 261
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Local Similarity 83.9%;
les 219; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy C
COMPUTER: IBM PC COMP
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                                                                                                                          01-JAN-1900
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389 CTGACAGTACAGTGCAAAGTCTTCAGGCTCCACTCTGGTGATGGTGAGAGTGAAGTC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 TGTCCCAGACCCACACTGCCCTGTCTGTCTGAGATGCCAGAGGTCTTATTGAAAATACA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 ATGTATGACCAGCCTTGGAGCCTGGCCAGGTTTGTGCTGGTACCAGGA7TAAGGGGGAGT 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTPALIZING MONOCLONAL ANTIRODIES
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORPESPONDENCE ADDRESS.
ADDRESSEE: The Scripps Pesearch Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652194th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                      Length 13254:
                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
Sequence 13254 BP; 3238 A; 3251 C; 3559 G; 3206 T; 0 other;
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-4TL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 170:
SEQUIMENT CHARACTERISTICS:
LENGTH: 13254 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 GURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    Score 162; DB 13; I
Pred. No. 1 10e-100;
0. Mismatches 39.
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FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 170, Application US/08276852
Sequence 170, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis P
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Carlos F
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Local Similarity 83.9%;
es 219, Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                        TOPOLOGY: circular MOLECULE TYPE: DNA (9
                                                                                                                                                                                                                   nucleic acid
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389 CIGACAGIAGIACAGIGCAAAGICIICAGGCICCACICIGGTGGIGGIGAGAGIGAAGIC 448
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                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
Sequence 13.254 BP: 3.238 A; 3.251 C; 3559 G; 3206 T; 0 other;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TS 08,178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 30-SEP-1992
ATTORNEY/ASENT INFORMATION:
NAME: FILLING, THOMAERING:
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: SCD1452P
TELEPHONE: 619-54-2937
TELEPHONE: 619-54-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: Tue Feb 24 13:57:30 1998 Job time : 52 secs.
                                                                                                                                                                   INFORMATION FOR SEC 1D NO: 170: SEQUENCE CHARACTERISTICS: LENGTH: 13254 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   629 GGTGCCTGGAGACTGCGTGAG 649
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Release 2 1D John F Collins, Riccomputing Possorch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, "Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Tue Feb 24 97 19:58 1998, MasPar time 112.35 Seconds 714.026 Million cell updates/sec

Tabular output not generated.

>US-08-844-215-15

(1-318) from US08844215.seq 318 1 GAGCICACGCAGICICAGG Description: Perfect Score:

CTCGAGIGCGTCAGAGGICC. Sequence: Comp: Z Z

SCACCAAGGTGGAGATCAAA 318 CCTGGTTCCACCTCTAGTTT

TABLE default Gap 6 Scoring table:

Dbane ht. Query 0 STD Nmatch

332433 seqs, 126143548 bases x 2

Minimum Maich 0% Listing first 45 summaries Post-Promossing.

Database:

STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 9:STS9 9:STS9 10:STS81 0.1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 9:STS9 9:STS9 10:STS81 0.1:STS1 1.2:STS2.1.2:STS12.1.3:STS13.1.3:STS12.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1.3:STS13.1

Mean 9.875; Variance 2.009; scale 4.916 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by unalysis of the total score distribution.

SUMMARIES

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C C
1 272 85.5 400 67 HS1244856 7W27411 F1 Scarcs ora 0 00c-00 2 239 75.2 418 39 AA515239 ng69c07.s1 NCL_CGAF_L 0.00c-00
F 50
5W27f1
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                                                                           DEFINITION ng69c07.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone 940044 similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-JII PEGION (HUMAN);
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Pred. No. 0.00e+00;
0; Mismatches 17; Indels 1; Gaps
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further information. Trace considered overall poor quality Seq
primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1
                                                                                                                                                                                                                                              /tissue_type="ovarian tumor"
/lab_host="DH10R (ampicillin resistant)"
                                                                                                                                                                                                                      /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                           mRNA <1..>400
Sequence 400 BP; 90 A; 120 C; 106 G; 84 T; 0 other;
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Email: Robert_Strausberg@nih gov
                                                                    /organism="Homo sapiens"
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                             Location/Qualifiers
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/clone="770541"
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CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Senome Sequencing Center
Clone distribution: WILGARP chone distribution information on the
found through the I M A G E Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pAMP10; mRNA made from liposarcoma, cDNA made by oligo-dr priming, Non-directionally cloned. Size-selected on agarcose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research
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24-JUL-1997 (Rel. 52, Last updated, Vorsion D)
rq56-07-51 NCL CGAF_Lip2 Home Sapiens CDNA Clone 340044 similar
gb-M63438 IG KAPPA CHAIN PPECUPSOP V-111 PEGION (HUMAN);.
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael P.
Emmert-Ruck, M.D., Ph.D
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Best Local Similarity 89.1%; Pred No 0.006+00;
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/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
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/organism="Nomo capiens"

/orte="Vertor: pamplo: mBNA made from liposarroma cDNA
made by oligo-dr priming Non--directionally cloned
Size-selected on agrose gel, average insert size 600 bp.

Reference: Krizman et al (1996) Gancer Pesearch
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                                                Contact: Pobert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Pobert_Strausberg/Phih, gov Tissue Procuement: L. Jeffrey Modelros, M.D. Michael B. Emmert-Buck, M.D. Ph.D. CNN Library Preparation: David B. Krizman, Ph.D. CENA Library Arrayed by Green Lennon, Ph.D. David B. Krizman, Ph.D. Char Library Arrayed by Green Endown, Ph.D. Clone distribution: NIT-GAP Under distribution: NIT-GAP Under distribution: Information can be found through the I.M.A.G.E. Consortium/LNL at:
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23-JUN-1997 (Rel. 52, Last updated, Verston 1)
23-SDOS.11 Soaries Ovary timer NEHOT Home sapiens CDNA clone 739953
5' Similar to de:X06764 IG KAPPA CHAIN PPECHPSOP VIII PEGION
                                                                                                                                                                                                                                    www-bio.llnl.qcv/Abrp/image/image/image/image/image/it.lgngth-1970 Std
Error: 0.00 Seq primer: -40ml3 fwd. El from Amersham High quality
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Vertebrata, Eutheria: Primates, Catarrhini, Hominidae, Homo
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/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH108"
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AA479857;
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                                                                                                                     Contact: Wilson PK Washington University School of Medicine 4444
Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314-286
1800 Fax. 314-286 [810 Email: estimatiscu musti edu This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@image lini.gov) for further information. Seq primer: 28ml3 rev2 ET from Amersham.
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  Lennon G., Marra M.,
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Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
Martin T., Moore R., Schellenberg K., Steptoe M., Tan F.,
Theising B., White Y., Wylle T., Waterston R., Wilson R.,
"WashU-NCI human EST Project".
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/sex="Female"
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Hillier,L., Allen,M., Rowles,L., Eubuque,T.
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lenn
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Lennon.G., Matra.M.

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                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham.
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01-JUN-1997 (Rel. 52, Last updated, Version 1)
02-SEOL: Soarrs every tumer NEMPT Home sapiers cDNA clone 770329
5' similar to gb:zll894 IG KAPPA CHAIN PRECUPSOP V-III PEGION
(HUMAN);.
Theising, B., Woore, R., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/lab_host="DH10B (ampicillin resistant)"
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/sex="Female"
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Washington University School of Medicine
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LOCUS AA476101 171 bp mPNA EST 19-THN-1997 DEFINITION 2W29409.51 Soares ovary tumor NDHOT Homo sapiens CDNA Clone 770705 3' similar to gb.X06754 IG KAPPA CHAIN PREFURSOR V-III PEGION
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini: Hominidae;
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| Hillier, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Tost
| Krizman, D., Kuraba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
| Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
| Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
| WashUruhuman Est Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Confact: Wilson RK WashU-Morck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108 Tol: 314 286 1800 Fax: 314 286 1812 Email: estiwateson.wustl.edu This clone is available royalty-free through LLNL.; contact the IMAGE Consortium (info@imaqe:llnl.gov) for further information. Seq primer: ~28m13 rev2 Er from Amersham.
                                                                    Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S. Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wylie T., Waterston P., Wilson R.; "Washu-Merck EST Project 1997";
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/lab_host="DH10B (ampirillin resistant)"
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Sequence 269 BP; 59 A; 90 C; 67 G; 53 T; 0 other;
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nes 168; Conservative
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This chore is available royalty-free through ILNI,; contact the
IMAGE Consortium (info@image.linl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham.
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23-JUN-1997 (Rel. 52, Last updated, Version 1)
28-JUN-1997 (Rel. 52, Last updated, Version 1)
28-JUN-1997 (Rel. 50-JUN-1997) (Rel. 1997) (Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact. Wilson RK Washington University School of Medicine 4444
Forest Park Farkway, Box 9701, St. 10.13 MT 67100 Tol. 314 286
1800 Fax: 314 286 1810 Email: estWatson.wustl.edu This clone is
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                                                                             4444 Forest Park Parkway, Box 8501. St. Louis, MO 63108
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Vertebrata: Eutheria: Primates: Catarrhini: Hominidae: Homo.
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97.7%; Pred. No. 4.27e-255;
vative 0: Mismatches 3.
                                               Washington University School of Medicine
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Matches 167, Conservative
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                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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AA454224 324 bp mRNA ESI 10-JUN-1997 2X83906.rl Scares ovary tumor NbHOT Home sapiens obna clone 810346 5° similar to gb.MIZT40_cds1 13 KAFPA DHAIN FEEDRESP V III HUSI N
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Hiller, L. Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kuraba, T., Tary, M. He, N., Tennon, G., Marra, M., Mortin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Waish, Werk, K., Wylle, T., Waterston, R. and Wilson, R. Wash, Werk EST Project 1997.
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Vertebrata, Mammalia, Eutheria, Primates: Catarrhini: Hominidue;
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Prod. No. 4.27e-255;
0; Mismatches 3; Indels 1; Gaps
available royalty-free through LLNL; contact the IMAGE Consortium (infe@image.llnl.gov) for further information. Seg primer: -41ml2 fwd. ET from Amersham.
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/lab_host="DH10B (ampicillin resistant)"
complement(<1..>171)
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/sex="Female"
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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Bost Local Similarity 97.7%;
Matches 167; Conservative
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DEFINITION
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13-JUN-1997 (Rel. 52, Last updated, Version 1)
2x83c06.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 810346
5' similar to gb-M12740_cds1 rg KAPPA CHAIN FFECURSOR V-III FEGION
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Mo 63108 Tel: 314 286 1800 Fax. 314 286 1810 Email.

Est@watson.wustl.edu This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 EI from Amersham High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK WashU-Merck EST Project Washington University
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chördata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                         Length 324;
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Moore B., Schellenberg K., Steptoe M., Tan F., Theising R.
White Y., Wylle T., Waterston R., Wilson R.;
"WashU-Merck EST Project 1997";
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                          /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1 >124
                                                                                                                                                                  /clone-"810346"
/clone_lib-"Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                      Pred. No. 4.34e-251;
0; Mismatches 10;
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                                                                                                                                                                                                                                                                                                          Score 156;
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Location/Qualifiers
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Matches 196; Conservative
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/note="Organ: ovary: Vector: pT7T3D (Pharmacia) with a modified polylinker: Sito_1: Not I; Sito_2: Eco RI: lst. strand cDNA was primed with a Not I: oliqo(dT) primer [5: TGTARCGAATCTGAAGTGGGASCASCASIIITITITITITITITITITI 3: double-stranded cDNAwas size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution. NCI-CGAP Clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA494059 217 bp mPNA EST 10-JUL-1997 ng61b01 s1 NCI_GGAP_Lip2 Home sapiens reNA clone 979241 similar toge:x06764 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);;
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Vertebrata, Mammalia, Eutheria, Frimutes, Catarrhid: Hemididae;
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                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 324 BF; 68 A; 102 C; 82 G; 72 T; 0 other;
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/organism="Homo sapiens"
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/clone="810346"
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92.98;
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/note="Vector" pamplo; mena made from liposarcona, cDNA made by oligo-dr priming, Non- directionally cloned. Size-selected on agarose go!, sverage insert; size for the Reference. Rilaman et al. (1996) Cancer Pesearch 56:5380-5393.
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/notex="Vector pAMP10" mENA made from liposarcoma, "DNA
made by allga. If priming Nea. directionally cloned
Size-selected on agrose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
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Contact: Robert Strausberg-hih gov Tissue Procurement: L. Jeffrey Medeiros,
M.D. Michael R. Emmert-Ruck, M.D., Ph.D. CONA Library Preparation:
David R. Wrizmen: Ph. D. GDNA Library Arrayed by Greg Lencon, Di.D.
DNA Sequencing by: Washington University Genome Sequencing Center-
Clone distribution: Not-CDAP clone distribution information can be-
found through the L.M.A.G.E. Consortium/LLNL at:

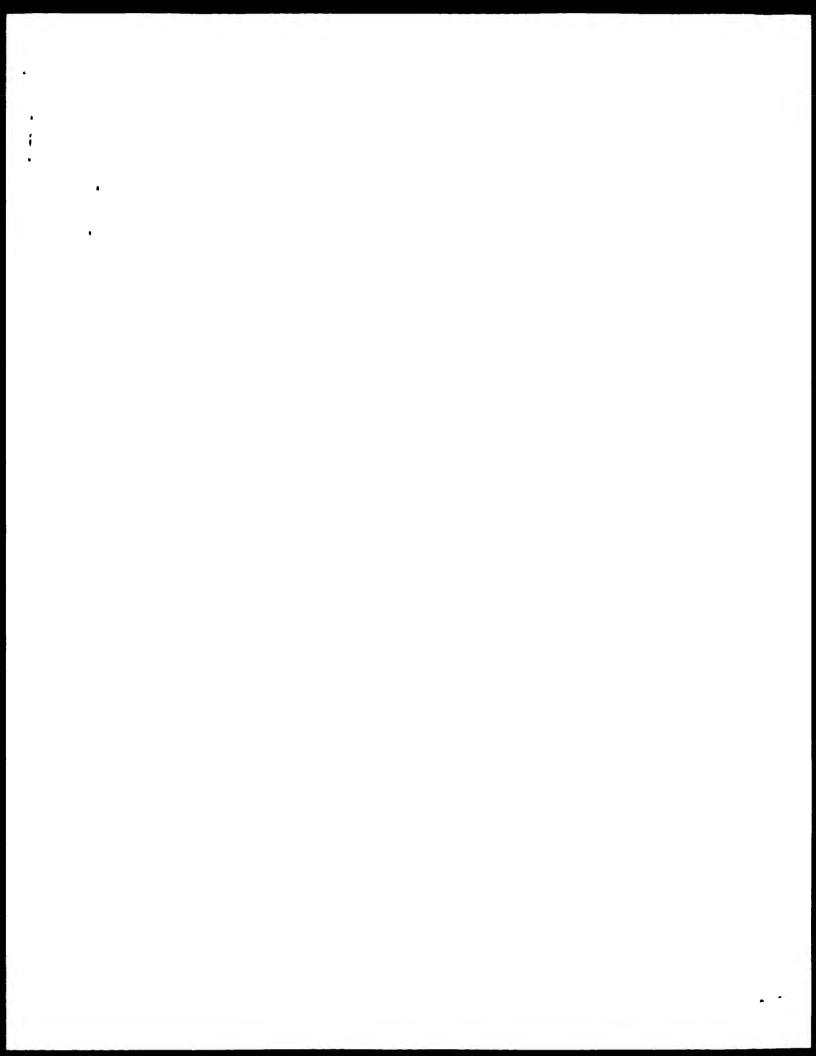
www-blo.lini.gov/bbfp/image/image.html insert Length, 322 Std
Error: 0.00 Seq primer: -40mil fwd ET from Amersham
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12-VUL-1997 (Rel. 52, Last updated, Version 2)
ng61b01.s1 NCI_CGAP_Lip2 Homo sapiens CDNA cione 939241 similar :
qb:XCK744 in KRPPA CHAIN PRECIPSOR V-III PEGION (HPMAN):
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Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla: Eutheria: Primates; Catarrhini, Hominidae;
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Fred. No. 4.36e-241;
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/tissue_type="liposarcoma"
/lab_host="DH108"
                                                                                                                             /clone='939241"
/clone=lib="NCI_CGAP_Lip2"
/tissue=type="liposarcoma"
/lab_host="DH108"
              /organism-"Homo sapiens"
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                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.2%;
Matches 151; Conservative
                                                                                                                                                                                                                                     75 C
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Unpublished.
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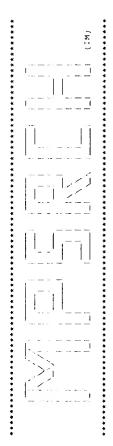
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adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMPIO by the Und-chonding method (Life Technologies) Average freatt size is 500 bp. NOTE. NOT directionally closed, This library was constructed by David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /noise_Vertor pampin Site_1 Not1, Site_2: BroFF: 18: Stand CoDNA was primed with bilon(407) 7 on 50 nd of primed NotNate treated, total of ellipar ENA challed from 5,000-10,000 microdissected, histologically normal prostat
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                                                                                                                                                                                                                                            47 acgeagetegeaggeacetgtetttgtetteagggggaaacageeacetgterfgragg i06
                                                                                                                                                                                                                                                                                                                                                                                                                                                67 GCCAGTCAGAGTGIIAGCAGCAAIIACTIAGCCTGGIACCAGCAGAGACCTGGCAGGCI 126
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Contact: Fokert Strauskerg*nh.gov Tissue Procurement: W. Marston Linehan.
M.P. Fodrigo Chuaqui, M.D. Michael Emmert-Ruck, M.D., Ph.D. CDNA
Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed
by Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by:
MCLGGAP Chome distribution information can be found through the
T.M. A G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1997 (Rel. 51, Created)
25-711-1927 (Rel. 51, Last grafited, Version 5)
26-711-1927 (Rel. 62, Last grafited, Version 5)
30-711894 IG KAPPA CHAIN PPECIPSOR V-III PESION (HUMAN);
                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1065 Std
Error: 0.00 Seq primer: -41ml3 fwd. ET from Amersham High quality
sequence stop: 250.
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Tumor Gene Index";
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 151; DB 67; Length 217; Prod Nr 4 PCe:241;
                                                                                                                                                                   Mismatches 14. Inde.s
                                Sequence 217 BP; 44 A; 75 C; 55 G, 43 I; 0 other;
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/clone_lib="NCI_CGAP_Prl"
/sex="Male"
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/lab_host="DH108"
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AA225858;
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                                                                                                     Query Match
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/organism="Homo sapiens"
/note="Vector: pAMPIO; Site_1: Not1; Site_2: EccRI: 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
strand cDNA was primed with oligo(dT)17 on 50 ng of
bNAse-treated, totaal cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
CDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMPIO by the UDG-cloning
method (Life Technologies). Average insert size is 500
bp. NOTE: Not directionally cloned. This library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.B. Consortium/Linl at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata,
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA225858 260 bp mRNA EST 20-JJN-1997 nc27d05.sl NCI_CGAP_PrI Homo sapiens cDNA clone 3490 similar to gb:z11894 IG KAPPA CHAIN PPECURSOR V-III PEGION (HUMAN):
                                                                                                                                                              90 egcagnetecaggeaecetgtetttgtetecaggggaaggageeaeceteteetgeaggg 149
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                                                                                                                                                                                                                                                                                                    68 CCAGTCAGAGTGTTAGCAGCAATTACTTAGCC-TGGTACCAGCAGAGACCTGGCCAGGCT 126
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    mRNA <1..>260
Sequence 260 BP; 57 A; 84 C; 66 G; 49 T; 4 other;
                                                                                                                  0, Mismatches 12;
                                                                      Score 137; DB 49, |
Fred. No. 3.33e-213,
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High quality sequence stop: 250.
Location/Qualifiers
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/clone_lib="NCI_CGAP_Pr1"
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/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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<1..>260
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                                                                      Query Match 43.1%;
Best Local Similarity 92.2%,
Matches 154, Conservative
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NCI-CGAP.
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Unpublished (1997)
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       mRNA
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SOURCE
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be-
found through the T.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA492131 262 hp mPNA EST 10-JUL-1997 0960902.sl NCI_CGAP_Lip2 Homo sapiens cUNA clone 939218 similar to gb.zl1894 IG KAPPA CHAIN PPECUPSOP V-III PEGION (HUMAN). ĀA492131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae, mitochondrial eukaryotes, Mctazoa; Chordata;
Vertebrata; Mammalia, Eutheria, Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                   90 egcagnetecaggeaecetgiettigieiceaggggaaggageeaecetrificaggg 149
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                                                                                                                                                                                                                                                                                                                                         68 CCAGTCAGAGTGTTAGCAGCAATTAGTTAGCC-TGGTAGCAGGAGAGAGAGAGAGAGAGGTGAGGGT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 262;
                                                                             Length 260;
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                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               127 CCCAGGCTCCTCATCTATGGTGCATCCAGGGGCCACTGGCATCCC 173
                                                                                                                                  0; Mismatches 12;
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                                                                          Score 137; DB 27; I
Pred. Nc. 3 33e-213;
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Location/Qualifiers
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Fred. No. 2.95e-207;
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
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Search completed: Tue Feb 24 07:22:48 1998 Job time : 170 secs.





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n.a. - n a databash search, using Smith-Waterman algorithm MPSrch_nn Tue Feb 24 07:15:48 1998: MasPar time 115.99 Seconds 773.214 Million cell updates/sec >US-38-844-215-15 (1-318) from US^8744215 seq 318 not generated Tabular output Run on:

Description: Perfect Score: N.A. Sequence: Comp:

GGACCAAGGTGGAGATCAAA 318 1 GAGCTCAGGCAGTGTGGAGG CICGAGIGGGICAGAGGIGG

TABLE default Gap 5 Scoring table:

397346 segs, 141010104 bases x 2 Searched:

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Minimum Match 0% Listing first 45 summaries Post-processing:

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EST107 2:EST109 3:EST109 4.EST200 5:EST201 6.EST202 13:EST203 14:EST204 9:EST204 15:EST204 11:EST201 15:EST201 15:EST201 11:EST201 12:EST201 15:EST201 11:EST201 12:EST201 12:ES

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77004 Bukaryotae: mitochondrial eukaryotes: Metazoa: Chordata: Vertebrata; Mammalia: Eutheria: Primates; Catarrhin: Hominidue: Hillier, L., Allen, M., Bowles, L., Dubuque T., Geisel G., Post, S. Rucaba, T., Lary, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisiud, H., Walte, Y., Walerston, R., and Wilson, R., WashU-Merck EST Project 1997 AM#OD/78 400 bp mRNA EST (%-U/N-1997 2*27)2.rl Suares commy limit NHOT Humb sapiens (VNA - lone 77 5 similar to glinieff is EAPPA CHAIN FRECHESUB VIII FEII NA456778 92177199 Homo sapiens human. Ношо. LOCUS ORGANISM PEFERENCE AUTHORS ACCESSION KEYWOFES SOURCE RESULT

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                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.ilnl gov) for further information.
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                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 272; DB 116;
Pred No. 0 00e+00;
                            Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
                                                                                                                                                            Trace considered overall poor quality Seg primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
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Adams, M.D., Kerlavage, A.R., Fleischmann, P.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Rrandon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Octton, M.D., Earle-Hughes, J., Fine L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Giode, A., Gehem, C.L., Hanna, M.C., Haddlow, E.P., Billey, J.C., Liu, L. J., Marnaros, S.M., Merrick, J.M.,
Kelley, J., Kelley, J.G., Liu, L. J., Marnaros, S.M., Merrick, J.M.,
Moreno-Palanques, P.F., McDonald, L.A., Ngiyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hudson, P. L.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissener, P.S., Olsen, H.,
Paymond, L., Welly, Wing, J., Xu, G., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Farner, M., Morsen, C.A., Hassener, P.S., Olsen, H.,
Praser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
For clone avallability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
                          Eukaryotae; mitochondrial eukaryotes; Metazoa: Chordata;
Vertebrata; Mammalia, Eutheria, Primates, Catarrhini, Hominidae:
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EcoRI; Site_2: XhoI"
/clone_lib="Testis tumor"
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Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser.C.M. and Venter,J.C. initial assessment of human gene diversity and expression patterns based upon 8.3 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdp/hdi/hdi/hdi/hdi/hdi/Seq primer: M13 Reverse.
                                                                                                                                                  LOCUS AA345486 403 bp mENA EST 21-AFR-1997 DEFINITION FORTS1655 Gall bladder II Home sapiens obnA 5' end similar to be similar to immunciciballo kappa light chain, V region (38 X09763) ACCESSION AA345466
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Site_1: RcoRI; Site_2: XhoI"
/clone_lib="Gall bladder II"
/scx="fenale"
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Tel: 3018699056
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The Institute for Genomic Research
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Adams. M. D., Kerladage A. P., Fleischmann, P. D., Fuldner, R. A., Hult, C. T., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, D. C., White, O., Sutton, G., Flake, J. A., Brandom, R. C., Mann Wai, G., Gocayne, D. C., Sutton, G., Flake, J. A., Ernedom, R. C., Enter-Hughes, J., Flore, E. Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, I. I., Googlager, N. S., Glodek, A., Gabhar, C. L., Hanna, M. C., Heddhom, E. Hinklo, P. G., T., Kelley, J. M., Kelley, J. C., Liub, L. T., Marmaros, S. M., Merrick, J. Moreno-Palanques, R. F., McDonald, L. A., Nauyen, D. T., Pelligrino, S. M., Phillips, C. A., Fyder, S. E., Scott, J. I., Saudek, D. M., Shriesy, P., Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y., Bednarik, D. P., Googla, M. A., Kolley, D., Feng, D. F., Ferrie, A., Fischer, C., Hadson, P. Kim, A. K., Kozak, D. L., Kunsch, C., Hungjun, J. L. H., Meissnor, P. S., Greene, T. M., Gruber, C., Hadson, P. Kim, A. K., Kozak, D. L., Wei, Y. F., Wing, J. Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Fannon, M. P., Rosen, C. A., Haseltine, W. A., Firlds, C. M., Eraser, C. M., and Venter, J. C., Anna, Garden, J. M. M., Anna, General and Seessment of human qene diversity and expression patterns and a seessment of human qene diversity and expression patterns
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For chone avallability, additional sequence and expression
information related to this EST. please check the TIGR Human General
Index (http://www.rigr.org/tdb/hgi/hgi.html)
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Vertebrata, Mammalia, Eutheria, Primates, Cafarrhini, Hominidue;
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EST91999 Skin tumor I Homo sapiens cDNA 5' end similar to
immortajebulin kappa light chain, VI regions.
AA379044
based upon 83 million nucleotides of cDNA sequence.
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
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9712 Medical Center Drive, Pockville, MD 20850 USA
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/clone_lib="Skin tumor I"
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Other_ESTs: THC169106
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                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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Adams, M.D., Kerlavage, A.P., Fleischwann, P.D., Fuldner, P.A.,
Bult., C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, S., Blake, J.A., Brandon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earla-Hughes, J., Fine, I.D.,
Flizgerald, L.M., Fitzbugh, W.M., Fritchman, J.L., Geoglagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, T.M.,
Moreno-Palanques, R.F., McConald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Pyder, S.F., Scott, J.L., Saudek, D. M., Shiley, P.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D. Fenria, A. Fischer, C., Huschn, S.M.,
Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Paymond, L., Wang, J. F., Wing, J., Xu, C., Yu, G.L., Puben, S.M.,
Paymond, L., Wang, J. F., Wing, J., Xu, C., Yu, G.L., Puben, S.M.,
Paymond, L., Wang, Y.F., Wing, J., Xu, C., Yu, G.L., Puben, S.M.,
Pillion, P.J., Fannon, M.P., Rosen, C.A., Haseltine, M.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
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For clone availability, additional sequence and expression
information related to this EST, please check the TISR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION EST69341 Lymph node I Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region.
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Vertebrata; Mammalia, Eutheria, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                              88 gccactgagagtgttagcaacacctacttagcctggtaccaacagaaacctggccaggct 147
                                                                                                                                                                                                                                                                                                                                                                 148 cccaggetecteatetatggtgeatecageagggeeactggeateceagaeaggtteagt 207
                                                                                                                                                                                                                                                                                                                                                                                                                              127 CCCASSCIOCIFAICITAIGSIGCAICCAGASSGCCACIGGCAICCCAGACASGIIGASI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 ggcagtgggtetggggacagaettcaetetcaecatcagcagactggageetgaagatttt 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 gcagtatattactgtcaagcagtatggtagtttacccctcaantttcggccctggggacc 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 GCAGIGTATTACTGTCA-GCTTTATGGTAACTCACGT-TGGACGTTCGGCCAAGGG-ACC 303
                                                                                                                         28 actragicticoaggeaccetgicitiqueteceaggggaaagagecaccetetectgeagg 87
                                                                                                                                                                                     7 ACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG AA
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Tel: 3018699056
Score 245, DB 59,
Pred. No. 0.00e+00;
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   Ouery Match
Best Local Similarity 91.1%;
Matches 287; Conservative
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CE Adams.M.D., Kerlavage,A.P., Fleischmann.P.D., Fuldner.R.A., Adams.M.D., Kerlavage,A.P., Fleischmann.P.D., Fuldner.R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock.R.G., Gacayne,J.D., White,O., Sutton.G., Blake,I.A., Brandon.R.C., Man-Wal,C., C., Kalton.R.A., Cline,T.R., Cotton.M.D., Earle-Hudbes,J., Fine,L.D., Fltzgerald.L.M., Fitzbugh,W.M., Fritchman,J.L., Geoghagen.N.S., Glock,A., Gnehm.C.L., Hanna.M.C., Hanna.M.C., Hanna.M.C., Hanna.M.C., Hanna.M.C., Hanna.M.C., Hanna.M.C., Hanna.M.C., Halley,J.C., Liu,L.-I., Marmaros.S.M., Merrick.J.M., Morenc.Palanques,R.F., McDonald,I.A., Nguyen.D.T., Pelligitin.O.S.M., Phillips,C.A., Ryder,S.E., Scott.J.L., Saudek,D.M., Shirley,R., Small.K.V., Spriggs,T.A., Interback,T.R., Weidman,J.F., Lin,Y., Hednarik,D.P., Cao,L., Cepeda,M.A., Coleman T.A., Collins,E.J., Hew.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P.S., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Colsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben.S.M., Dillion,P.J., Fanne,M.M., P., Posen,C., Yu,G.L., Ruben.S.M., Praser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns hased upon 83 million nucleotides of CDNA sequence
NE BOCOLECT.
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Vertebrata: Mammalia; Eutheria: Primates: Catarrhini: Hominidae:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 tecteatetatggtgeatecageagggeeactggeateceagatesatggeata 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 agactgitaggagetteteettageetggtaeeageagaaaeetggeeeaggeteeeagge 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 TCCTCATCTATGGTGCATGCAGGAGGACCAGCATGGCATGCCAGACAGGTTCAGTGGAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 CTCCAGGCACCCTGTCTTGTCTCCAGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 21; Indels
Index (http://www.figr.org/tdb/hgi/hgi.html)
Seq-primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 231; DB 52;
Pred No 0 00e+00:
                                                                                                                                        /organism="Homo sapiens"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 attactgtcantggtatggtagctca 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 ATTACTGTCAGCTTTATGGTAACTCA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION EST100471 Pancreas tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245; Conservative
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                                                                                                                                                    For clone availability, additional sequence and expression information related to this ESI, please check the TIGP Human Gene Index (http://www.tigr.org/tdb/hgi/hgi html) seq primer MI3 Reverse
                                                                                                                                                                                                                                                                                                                          /hote="organ: pancieas. Vector. phiuescript SK+, Site_i.

BCORI: Site_2: XhoI"

/clone_lib="pancreas tumor I"

/dev_stage="adult"

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Vertebrata: Mammalia: Eutheria: Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 ggcagtgggtctgggacagagttcactctcancatcagcatcctgcagtctgaagatttt 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 acqcagntincagccaccctgtctgtgtntccaggggaaaaqagccacccntcctgcagg 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 gecagicagagitatiageageaa---etiageciggiaecageagaaaeciggecaggei 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 GCCAGICAGAGIGITANGAGATTACTTAGCCIGGIACCAGGAGAGACCTGGCCAGGCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 GGCAGIGGGIFIFGGAGACTICACTICACTICAGGAGACTIGGAGGTITT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTIGO400 Pancreas fumer I Home sapiens cDNA 5' end similar co
Similar to immunoglobulin kappa, variable region (GB:Y00640),
AA295093
41947582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 328;
                                                               9712 Medical Center Drive, Reckville, MD 20850 USA Tel: 3018699055
                                                                                                                                                                                                                                                                                                                                                                                                                                       7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 211; DB 24;
Pred No. 0.00e+00;
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                   Bioinformatics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                     Email: arkerlav@tigr org
Contact: Kerlavage, AP
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Adams,M.D. Kerlavage,A.R., Fleischmann.B.D., Fuldnor,R.A.,
Robit,G.T., Lee,N.H. Kirbnoss E.F., Woinstock,P. G., Godayne,J.D.,
White,O. Sutton.G. Hake, J. A., Brandon,P. G., Man.Wal.G.,
Clayton,R.A., Cline,I.R., Cotton,M.D., Earle-Hubbes J., Fine.L.D.,
                                                                                                                                                                                                                                                                                                                                                                          Email: arkerlavatigr.org
For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human here
Index (http://www.igr.org/tdb/hgi/hgi.html)
Seq primer: MIS Reverse.
Kozak,D.L., Kunsch,C., Hungjun,J., 11,H. Meisseer P.S., Creet,H.,
RaymenG.L., Welly F., Wing,J., Xu.C., Yu.G.L., Buhen,S.M.,
Dillion P.J., Fancen M. R., Poseen C.A., Haseltino,W.A., Ficids.C.,
Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"organ: pancreas; Vector: pBluescript SK-: Sitr_):
EcgEL, Site_2, XhoI"
/clone_lib="Pancreas tumor I"
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Vortobrata; Mammalia; Eutheria; Primates: Catarrhini: Hominidue;
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EST10638 Pancreas tumor I Home sapiens cDNA 5' end simila:
immunoglobulin kappa light chain, VJ regions.
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0: Mismatches 23; Indels
                                                                                                                                                                                                                                                                           The Institute for Genomic Research
9712 Medical genter Drive, Rockville, MD 20850 USA
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Pred. No. 9
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<1..>370
                                                                                                                                                                                                     Other_ESTs: THC168243
Contact: Kerlavage, AR
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es 233; Conservative
                                                                                                                                                                                                                                                                                                                           Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                          Fax. 3018699423
                                                                                                                                                                                                                                                      Ricinformatics
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (5547 Suppl), 3-174 (1995)
Fitzgerald, L. M., Fitzhugh, M. M., Fritchman, J. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hedblom, E., Hinkle, P. S., Jr., Kelley, J. M., Kelley, J. M., Liu, L. L., Marmaros, S. M., Merrick, J. W., Moreno-Palanques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrin, S. Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, P. M., Shirley, F., Bednarik, D. P., Cao, L., Gepeda, M. A., Coleman, J. F., Li, Y., Bednarik, D. P., Cao, L., Gepeda, M. A., Coleman, T. B., Collins, F. J. Dimke, D., Feng, D. -F., Ferrie, A., Fischer, C., Hastings, G. A.,
                                                                                                                                                                                                                            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.I., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,I., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Puben,S.M.,
Dillion,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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EcoPI; Site_2: XhoI"
/clone_lib="Pancreas tumor I"
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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The Institute for Genomic Research
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<1 >277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
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Best Local Similarity 94.7%;
Matches 198; Conservative
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Pult.C.J. Lee, N.H. Kirkness, F. P. Weinstock, K. G. Gorayne J.D. White, D., Sutton, G. Rlake, J. A., Brandon, P. C., Man-Wei, C. Gorayne J.D. White, D., Sutton, G. Rlake, J. A., Brandon, P. C., Man-Wei, C. Grayne J.D. Fitzgerald, L.M. Fitzhugh, W. W., Fritchman, J. J. Googhagen, N.S. Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, F., McConald, L.A., Nguyen, D.T., Pelligrino, S. M., Phillips, C. A., Pyder, S. E., Scott, J.I., Saudek, D. M., Shirley, P. Spriggs, T.A. Greena, M. Colleman, T. P. Li, Y. Bednarik, D. P., Ferrie, A., Pischer, C., Hastings, G. A., Liw, M., Hu, J.S., Greene, J.W., Colleman, T. M., Maissner, P. S., Olsen, H., Rozak, D.L., Wei, Y. F., Wing, J. Xu, C., Yu, G. I., Ruben, S. M., Praymond, L., Wei, Y. F., Wing, J. Xu, C., Yu, G. I., Ruben, S. M., Praser, C. M. and Venter, J.C.
Indical assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression information related to this EST, please check the IIGR Human GeneIndex (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer M1% Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: pancreas: Vector: pBlueScript SK:, Site_1:
BCORI, Site_2: XhoI"
/clone_lib="Pancreas tumor III"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 etecagecaceetgtetgtgtetecaggggaaagagteaceeteteetgeagggeeagte 60
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                          Adams.M.D., Kerlavage, A.R., Fleischmann.R D., Fuldner R A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 82.6%;
(bases 1 to 363)
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Admas M.D. Retlavage, A.B. Fleischmann, R.D. Fuldher, R.A.,
Bult, C.T. Lee, N.H. Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, J. Satton, G. Blake, J.A. Brandon, R.C., Manwah, C.
Clayton, R.A., Cline, T.R., Carton, M.D. Earle-Hughes, J. Fine, D.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J. I., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, F. Hinklep, F.J.T.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.
Morenc-Palanques, R.F., McDenald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, A.B., Psyler, S.E., Scott, J.E., Saudek, C.M., Shriley, R.,
Small, K.V., Spriggs, T.A., Putterback, T.R., Weldman, J.F., Lin, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Cioleman, T.A., Collins, E.J.,
Dimker, D. Beng, D.-F. Ferrie, A. Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J. L. Li, H., Meissner, P.S., Olsen, H.,
Raymond, S., Well, Y.E., Wing, J., Kosen, C., Yu, G.L., Pilhen, S.M.,
Fraser, C.M. and Venter, J.C., Rosen, C.A., Haseltine, W.A., Fields, C.,
Loston, B. M. Million, D. L., Kosen, C., A., Maseltine, W.A., Fields, C.,
Loston, B. M. Million, B. M. Million, B. M. Hillon, D. L., Markelles, G. ChNA, Sequence
                          LOCUS AA295941 253 bp mRNA EST 18-APR-1997 DEFINITION ESTI01165 Thymus III Homo sapiens cDNA 5' end similar to similar to immunoslobulin kappa light chain, V region (GB:Y00540).
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EcoRI: Site_2: XhoI"
/cione_lib="Thymus III"
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    6 acttagcctggtaccagcagaaacctggccaggntcccaggetcctnatctatggtgcat
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.2%;
Best Local Similarity 89.4%;
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 253)
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                                                                                                                      AA295941
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      RESULT
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Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A.,

Rodams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A.,

Bullt, T., Lee, N. H., Kirkness, E. Wahnston, K. A.,

Glayton, F. A., Cline, I. R., Cotton, M. D., Farlo-Hughes, J., Fine, L. D.,

Flizgeraid, L. M., Flizhugh, W. M., Fritchman, J. Gavabagen, N. S.,

Glodek, A. Gnehm, C. Lin, L. Hannan, M. C., Hadbon, E. Hinkle, P. S. Jr.,

Kelley, J. M., Kelley, J. C., Lin, L. -I., Marmaros, S. M., Merrick, J. M.,

Moreop Palanques, P. M., Moronaid, L. A., Nuysen, D. T., Pelliorins, S. M.,

Phillips, C. A., Pyder, S. E., Scott, J. I. Sandek, D. M., Shirley, K.,

Rednarik, D. V., Cao, L., Capeda, M. A., Coleman, J. A., Collins, F. I.

Dimke, D., Feng, D. F., Ferrie, A. C., Coleman, J. A., Collins, F. I.

Buywond, L., Wusch, C., Hungjun, J. Li, H., Melsener, E. S., Cisen, H.,

Raymond, L., Welly, E., Wing, J., C., Vy, G. I., Puber, S. M.,

Palmon, D. L., Fannon, M. P., Rosen, C. A., Haseltine, M. A., Fleids, C.,

Fraser, C.M. and Venter, J. C.

Initial assessment of human gene diversity and coveression patterns

hased upon 83 million noter, J. C.

L. Matures 377 (6547 Suppl), 3-174 (1945)
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Seq primer: MI3 Reverse
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae, mitochondrial eukaryotes, Metazoa; Chordata;
Vertebrata, Mammalia, Eutheria, Primares, Catarrhini: Hominidae;
                                                                                                                                                              AA327218 289 bp mRNA EST 20-APP-1997 EST30586 Colon I Homo sapiens CDNA 5' end similar to similar to immunoglobulin kappa light chain. VNJ regions (GB:211894).
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/note="Urgan: colon: Vector: pbiuescript sK-: Site_i:
EcoRi: Site_2: XhoI"
/clone_lib="Colon I"
/dcv_stage="adult"
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01 3%; Pred No 1 55e 299;
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The Institute for Genomic Research
9712 Medical Center Drive, Porkville MD 20850 USA
186 aaaactggccagaggaggttcggccaaggggagccaaggtggaaatcaaa 232
                                                272 SIAMOTEAGITEGGAGGITEGGGCAAGGGAGGTGGAGATCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 200: Conserv
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                                                                                                                                                                                            DEFINITION
                                                                                                                                        RESULT 11
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131 gecaginagagigitagcagcagetaetitageetigitaceageagaaaeetiggeeaggei 190

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Adams, M D. Kerlavage, A.P., Fleischmann, B.D., Fuldner, R A., Bades, M D., Kerlavage, A.P., Fleischmann, B.D., Fuldner, R A., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R A., Cline, T P., Cotton, M D., Earle-Hughes, J., Frine, L.D., Fitchyan, J. T., Googhagen, S., Glodek, A., Gnehm, C. L., Hanna, M.C., Heddlom, E., Hinkle, P. S., T. Kelley, J. M., Kelley, J. W., Kelley, J. C., Hun, L.-I., Marmaros, S. M., Merrick, J. M., Moreno, Pelanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S. M., Phillips, C.A., Pyder, S. E., Scott, J. L., Saudek, D. M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J., He, W. W., Hu, T. S., Grone, J. M., Gruber, T., Hustings, G. A., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Paymond, L. Wel, Y. F., Wing, J., Xu, C., Yu, G.L., Puben, S. M., Pillion, P. J., Fannon, M. R., Chen, J. C., Welling, J., Ku, C., Yu, G.L., Puben, S. M., Pillion, P. J., Fannon, M. R., Chen, J. C., Kosen, C. A., Haseltine, W. A., Filleds, C., Litter, J., Sannon, M. R., Sosen, C. A., Haseltine, W. A., Filleds, C., Litter, J., Sannon, M. R., Sosen, C. A., Haseltine, W. A., Filleds, C., Litter, J., Sannon, M. R., Sosen, C. A., Haseltine, W. A., Filleds, C., Litter, J., Sannon, M. R., Sosen, C. A., Haseltine, W. A., Filleds, C., Litter, J., Sannon, M. R., Sosen, C. A., Haseltine, W. A., Filleds, C., Litter, J., Sannon, C. A., Maseltine, W. A., Filleds, C., Litter, J., Sannon, C. A., Maseltine, W. A., Filleds, C., Litter, J., Sannon, C. A., Maseltine, W. A., Filleds, C., Litter, J., Sannon, C. A., Maseltine, W. A., Filleds, C., Litter, J., Sannon, C. A., Maseltine, W. A., Filleds, C., Litter, J., Sannon, C. A., Maseltine, W. A., Filleds, C., Litter, J., Sannon, C. A., Washing, J., K., Sannon, C. A., Washing, J., K., Sannon, C. A., Washing, J., Sannon, C. A., Sannon, C. A., Washing, J., Sannon, C., Sannon, C., Sannon, C., Sannon, C., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial assessment of human gene diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For clone availability, additional sequence and expression information related to this EST, please check the TLGK Human Gene Index (http://www.rigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESTIO0122 Pancreas Fumor I Home sapiens cNNA 5' end similar to immunoglobulin kappa light chain, VJ regions.
63 CAGGGCCAGTCAGAGTGTTAGCAGCAATTACTTAGCCTGGTACCAGCAGAGACCTGGCCA 122
                                                                            191 ggeteccagggtegteatetatgagacatecagaagggecaetggeattecagacaggtt 250
                                                                                                                18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24;
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Pred No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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<1 >264
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Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.78;
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Best Local Similarity 94.3%;
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ن 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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Adams, M. D., Kerravage, A.P., Fleischmann, P. D. Fuldher, P. A.,
Bult, C. J., Lee, N. H., Kirkness, E.F., Weinstock, K. G., Gorayne, T. D.,
White, D., Sutton, G., Blake, J. A., Frandon, R.C., Mannami, J.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Foldek, A., Gnehm, C. L., Hanna, M. C., Hedblom, F. Hinkle, P.S. Jr.,
Kelley, J. M., Kelley, J. G., Libi, L. I. Marmanco, S. M.,
Moreno-Palanques, P. F., McDonald, I. A., Nguyen, D.T., Pelligatino, S.M.,
Phillips, C. A., Pyder, S. E., Scott, J. L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T. A., Ulterback, T.P., Welden, J. E., Li, Y.,
Bednarik, D.P., Cao, L., Gepeda, M.A., Coleman, J.E., Li, Y.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G. A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser, C.M. and Venter, J.C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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ECORI: Site_2: XhoI*

/clone_lib="Pancreas tumor III"

/dev stage="adult"
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Kozak,D.L., Kunsch,C., Hungjun,J., Li,L., Melsser,P.S., Olsen.H.
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Pillion,P.J. Fannon,M.R. Fosen, A. Haseltine W.A., Fields,C.,
                                                                                                                                                                                                                                                                                          EST7468 Pancreas tumor III Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini: Hominidae;
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 401869066
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zw25f01.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 770329
5' similar to qb:211894 IG KAPPA CHAIN PRECURSOR V-III FEGION
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Vertebrata; Mammalia; Eutheria; Primates, Catarrhiol, Hominidae,
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lengon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan F., Theising,R., White,Y., Wylie,T., Waterston,F. and Wilson,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl gov) for further information Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                  85 acgeaatetecaqeeaeeetgtetgtgtgteteeaggggaaaagageeaeeeteteetgeagg 144
                                                                                                                                                                                                  145 gecaginagagigitaggagagaaeciaetiageciggiaeceageagaaaeciggecagget 204
                                                                                                                                                                                                                                           57 GCGAGTCAGASIGITAGCAGCAAITACITAGGCIGGIAGCAGCAGAGAGCIGGGCAGGGT 126
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4444 Forest Park Parkway. Box 8501, St. Louis, MO 53108
Tel: 314 286 1810
Fax: 314 286 1810
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Length 294;
  Score 170: DB 55: Length 294
Pred No. 3.55e-202:
0: Mismatches 18: Indels
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/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                      265 agcadtgggtctggggacagaattca 289
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y Match
Loral Similarity 91 2%:
has
                                                  197; Conservative
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Manual M. Meriavage, A. B., Fleischmann, P. D., Fuldner, P. A.,

Rull, C. J. Lee, N. H., Kirness, E. F., Weinston, K. B., Greaphe, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C.,

Clayton, R. A., Cline, T. B., Cotton, M. D., Earle-Hughes, J., Fibe. L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J. L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hannan, M.C., Hadblon, E., Hinkle, P. S., Ur.,

Kelley, J.M., Relley, T. G., Liu, L. I., Marmaros, S.M., Morrick, J. M.,

Moreno-Palanques, F. F., McDonald, L. A., Novyen, D.T., Pelligrino, S.M.,

Phillips, C. A., Pyder, S. E., Scort, T. L., Saudek, D.M., Shirley, R.,

Small, K. V., Spriggs, T. A., Uterback, T. R., Wedman, J.F., Li, Y.,

Bednarik, D. P., Cao, L., Cepeda, M. A., Eccher, C., Hastings, G.A.,

He, W.W., Hu, J. S., Greene, T. M., Grüber, T., Huston, P., Kim, A. K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H.,

Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Phillion, P. J., Fannon, M. P., Rosen, C. A., Haseltine, W.A., Fields, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone availability, additional sequence and expression information related to this EST, please check the TiGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA361678 283 bp mRNA EST 21-APR-1997 EST70983 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to immunoglobulin Kappa, variable region (GR:Y0064A), AA361678
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   Length 269:
Query Match 51.9%; Score 165; DB 87; Length 269
Best Local Similarity 98 2%; Prod No. 5.64e-273;
Matches 168; Conservative 0; Mismatches 3; Indels
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Tel: 3018699056
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/1. \283
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Query Match 47.8%; Score 152; DB 53; Length 283;
Best Local Similarity 91.0%; Pred. No. 1.52e-246;
Matches 182; Conservative 0; Mismatches 15; Indels 3; Gaps 2;
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                                                                                                            Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995, University of Edinburgh, U-K Distribution rights by IntelliGenetics, Inc.
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scale 5 018 Variance 1 472; Mean 9 494; Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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156:EST151 156:EST156 161:EST161

166:EST166 171:EST171 176:EST176

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Adams, W.D. Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A., Blatt, G. G. Grayne, J.D., Whitheres, F., Wainstock, K.G., Gorayne, J.D., White, O., Sutton, G., Blake, A.A., Brandon, P.C., Chiu, M.M., Fine, L.D., Flayton, P.A., Cotton, D., Earle-Hughes, J., Fine, L.D., Flayton, P.A., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr., P.S., Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Penley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelleqrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Shirley, R., Small, K.V., Spriggs, T.A., Tterhack, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Pengy, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Weisler, S.M., Dillon, P.J., Fannon, M. P., Pesen, J. M., Chaselline, M.A., Fields, C., Fraser, C.M. and Venter, J.C., Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence
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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
                                                    Deuterostomia, Chordata, Vertebrata, Grathostomata, Osteichthyes,
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Gatarrhini; Hominidae; Homo
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932 Clopper Rd, Gaithersburg, MD 20878
Tel: 301869056
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Admis M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldher, P.A., Rirhness, E.F., Weinstock K.G., Gocoyne, J.D., Mult.C.J., Lee, N., Kirkness, E.F., Weinstock K.G., Gocoyne, J.D., Clayton, P.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J. Fine, L.D., Flizderald, L.M., Flizdenhan, J.L., Geoghaden, N.S.M., Glode, A., Gnehm, C.L., Hanna, M.C., Hedblow, E. Hinkle Jr.P.S., Kelley, J.M., Klimek, K.M., Kelley, J.G., Liu, L.-I., Marmaros, S.M., Merine, P. M., Moreno-Palanques, R.F., McDonald, L.A., Mayen, D.T., Pelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Mayen, D.T., Pelleyrino, S.M., Phillips, C.A., Pyder, S.E., Scrit, T.L., Mayen, D.T., Weidman, J.F., Li, Y., Bednarik, D.P., Capeda, M.A., Colman, J.F., Li, Y., Bednarik, D.P., Capeda, M.A., Colman, J.F., Li, Y., Bednarik, D.P., Capeda, M.A., Colman, J.F., Min, A., Kazak, D.J., Kong, C.L., Feng, P., Errie, A., Kim, A., Kazak, D.J., Kung, J., Ku
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Deuterostomia: Chordata: Vertebrata: Gnathostomata; Ustoichthyes:
Sarroptarygii: Choanata: Tetrapoda: Amniota: Nammalia: Theria:
Butheria: Archonta: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 381)
                            EST69430 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V(III),J(V) regions (GB 727170) (HT 3121).
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Email: tdbinfo@tdb.tigr.org
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12/8/U 383 bp mRNA ESI U6-SEP-1995
ESI19027 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
114ht chain V regine (GB-XOA763) (HT-3087)
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                                                                                                                                                         Eukaryotae: Metazoa: Eumetazoa; Bilateria; Coelomata;
Deuterostomia: Chordata; Vertebrata; Gnathostomata; Ostelchthyes;
Saroopterygii: Choanata; Tetrapoda; Amniota; Mammalia: Ineria;
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Pred No 0 00e+00;
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Other_ESTS: THC24452
Contact: Venter_JC
The Institute for Genomic Research
932 Clopper Rd Gaithersburg MD 27
Tel: 3018699055
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Duman clobe-155151 library-Soares breast 2NhHBst vector-pTTT30 (Pharmacia) with a modified polylinker host-HB10B (ampleillin resistant) primer-MTRP1 Relief-Not I Relief-PEO RI Adult (emale.) Its strand cDNA was primed with a Not I - 0100G/HJ primer (5 ISTIACCAATCTSAAGGGGGGGGGCGTIIIIIIIIIIIIIIIII s), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), adosted with Not I and cloned into the Not I and For RI sites of modified pTTT Vector (Pharmacia) Library won' through one round of normalization to a 7ct + 220 Library constructed by Beitto Scares and M Patima Bonalde
                                                                                                                                                y)81d08.rl Homo sapiens cDNA clone 155151 5' similar to qb:x06744
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.
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( pases: In 570)
Hiller, Clark, N. Dubuque, T. Elliston, K. Hawkins, M. Holman, M. Hulman, M. Kucaba, T. Le, M. Lennor, G. Marra, M. Parsons, T. Piffing, T. Soares, M. Tan, F. Trevaskis, E. Waterston, P. Williamson, A. Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 316
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for turther information.
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318 gtattactgtcagcattatggta 340
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Local Similarity 84.7%;
Nes 261; Conservative
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Fax: 314 286 1810
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strand cDNA was primed with a Pac I - Oligo(dT) primer [5].

AACIGGAAGATTAATTAAGACTITITITITITITITITI 3 ], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the medified p1713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 199; DB 40; Length 401;
Pred. No. 0.00e+00;
0; Mismatches 14; Indels 13; Gaps 13;
                                                                                                                                                                                                                                                                                                  5' similar to qb: X06764
                                                                                                                                                                                                                                                                                                                                                                                                                               human clone-128434 library-Soares fetal liver spleen INFLS vector-pT7T3D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-M13FP1 Rsitel-Pac I Rsite2-Eco FI Liver and spleen from a 20 week-post conception male fetus. 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stops: 239 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info*image linlagev) for further information.
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333 tigcagigitatiacigiticagogatatigatgaggeteancectititinggecetgggace 392
                          245 TIGCAGTGTATTACTGT-CAGCTTTATGGTAACTCACGTTGGACGTTCGGCCAAGGGACC 303
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(bases 1 to 401)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Poblifing,T., Scares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Igrappa CHAIN PRECURSOR V-III REGION (HUMAN);.
P10529
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yj82d09.rl Homo sapiens cDNa clone 155249 5' similar to gb:M63438
1G KAPPA CHAIN PRECUPSOP V-III PEGION (HUMAN);.
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254 tgggtctggggaaagatttcactcttcaccattcagcaqactgggagcctgaagatttt 313
                                        192 TGGGFCFGGG-ACAGACTFCACFCF-CACCAF-CAGCAGACFGG-AGCCFGAAGAFFFF- 246
                                                                                  314 gcagigiatitiacigiticagcagiatiggiagcicaccgiticacititicgggcggaggga 373
                                                                                                          89 etecagecaccetgtetgtgtetecaggggaaagagcacceteteetgeagggeagte 148
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Source: IMAGE Consortium, LLNL
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Fax: 314 286 1810
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digrested with Not I and cloned into the Not I and Eco RI sites of a modified pI713 vector (Pharmacia). Library went through one round of normalization to a fort - 20. Library constructed by Bento Soares
                                                                                                                                                                                                                                                                                                                                         ypadaio.rl Home sapiens chwa elone 188345 E' similar to gb:x06754 IG Kappa chain preduksok v-III Resiun (HUMAN):.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deuterostonia, chordata; Vertebrata; Gnathostonata; Osteichthyes; Sarcopterygii; Choanata; Terrapoda; Anniota; Mammalla; Theria; Sarcopterygii; Choanata; Terrapoda; Anniota; Mammalla; Theria; Elitera; Archonta; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence *15ps* 299
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.iinl.gov) for further information.
130 gocaqtcagaqtqtgagcaqcaaccagqtaqcctqqtaccaqcaaaaacctqqqccaqgc 189
                                                                                                                                194 GGTPIGGGACAGACTICACTOTOACOATOAGACTGAAGCTGAAGATITGCAGTG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human clone-188345 library-Soares breast 3NbHBst vector*pT7T3D
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                                                                                                     agtotaggacagagttottotocaccatcagcagcctgcagcctgaagattttgcagttt 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Rox 8F01, St. Louis, MO 53108
Fax: 314 286 1810
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Pred No 0 00e+00;
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Advans, W. 1. Cerlavage, A.P., Fleischmann, P.P., Fuldrer, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Ghiu, M.-W., Cline, P. T., Chiton, W. Barle-Hughes, J. Pine, L.D., Flizderald, L.M., Flizhugh, W.M., Fritchman, T. Geodhagen, N.S.M., Kelley, M. Kilmek, K.M., Kelley, T.C., Hadblom, E. Hink'le Jr.P.S., Kelley, M., Kilmek, K.M., Kelley, T.C., Liu, L. Marmarns, S.M., Merrick, J.M., Morror Palaques, R.P., McDonald, L.A., Nguyen, D.T., Pellegrino, S. M., Phillips, C.A., Pyder, S.E., Scrott, J.L., V., Shirley, P., Small, R.V., Spriggs, T.A., Uiterteary, T.K., Welman, T.B., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Collins, E.L., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hatings, G.A., He, W.-W., Hu, J. -S., Greone, J.M., Milley, R.M., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Melssner, P.S., Ollins, E., M., Dillon, P.J., Fannon, M. P., Prosen, C.A., Vu, G.-L., Puben, S. M., Dillon, P.J., Fannon, M. P., Possen, C.A., Vu, G.-L., Puben, S. M., Dillon, P.J., Fannon, M. P., Possen, C.A.
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Other_ESIS: THC22876
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light chain, V region (GB:M29469) (HT:3066).
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Deuterostomia: Chordata: Vertebrata: Grathostomata: Ostolohthyos:
Saroopterygii: Choanata: Tetrapoda; Amniota: Mammaila: Thoria:
Eutheria: Archonta: Primates: Catarrhini: Hominidae; Homo.
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67 GCCAGTCAGASIGIIAGCASCAAIIACIIAGGCCGGIACCASCAGAGAGAGCCGGGGGCGCCCC
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259 ggcagtgggtctnggacagactttcactcttnaccatcagcagcctagagcctgaagatt 318
                                                                                    199 cccaggetecteatetgatgeatgeatecaacagggecaetggeateccagecaggtteagt 258
                                                                                                                                                                                                           187 GGCAGTGGGTCTGGGACAGACTT-CACTCT-CACCATCAGCAGACTGGAGCCTGAAGATT 244
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1 (bases 1 to 359)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lenon,G., Marra,M., Parsons,J., Pifkin,L., Pohlfing,T., Scares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/clone="162780"
113 c R0 q 78
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Source: IMAGE Consortium, LLNL
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Matches 236; Conservative
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Eucaryotae, Metazoa, Chordata, Vertebrata, Gnathostomata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                           147 agaatattgacaacaccacttagcctggtaccagcagaaacctggccagcctcccaggc 206
                                                                                207 tecteatetateataeateeaceagggteactggeateceagaeaggtteagingeagin 266
                                                                                                                                                                   134 TCCTCATCTATGGTGCATCCAGCAGGGCGACTGGCAICCCAGACAGGIICAGIGGCAGTG
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Hillier,L., Clark,N., Fubuque,T., Elliston.K., Hawkins,M.,
Holman,M., Hultman,M., Kncaba,T., Le,M., Lennon G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,P., Williamson,A., Wohldmann,P. and Wilson.P.
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                         5' similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501, St Louis, MO 63108
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91 4%; Pred. No R 99e-289;
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High quality sequence stops: 296
Source: IMAGE Consortium, LLNL
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ses 222; Conservative
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Fax: 314 286 1810
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(Pharmacia) with a modified polylinker host-PHIOB (ampicilin resistant) primer-MISPI Reitel-Not I Reitel-Eco RI Adult human. Ist strand CDNA was primed with a Not I - oligo(d4) primer [5' didtacAAICHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATCHSAATC
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Deuterostomia: Chordata: Vertebrata: Gnathostomata; Osteichthyes;
Sarcopteraydi: Chornata: Tetrapoda: Amniota: Mammalia; Theria;
Sarcopteraydi: Chonnata: Tetrapoda: Amniota: Mammalia; Theria;
I (bases 1 to 171)
Hillier.L., Clark, N., Pubuque, T., Elliston, K., Hawkins, M.,
Hollman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, I., Pohlfing, T., Sares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson A., Wohldmann, P., and
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y147h06 rl Homo sapiens cDNA clone 161435 5' similar to gb:211894
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.
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High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl gov) for further information Trace considered overall poor quality.
                                                                                                                            human clone=161435 library=Scares breast 3NbHBst vector=pT7T3D
202 - cocadactoctoatotalgatgoatcoacoagggcoactggtatocoagcoaggattoog - 261
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Pred, No 6 40e-254:
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Best Local Similarity 94.2%;
Matches 161; Conservative
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EST 10-00L-1220
16 5' similar to qb:M63438
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Hillier,L., Clark,N., Dukuque,T., Elliston,K., Hawkins,M., Hollman,M., Multman,M., Kudaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Sares,M., Tan,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                          76 AGIGITAGCAGCAATTACTTAGCCTGGTAGGAGGAGGAGGTGGGGGAGGGGGAGGTG 137
61 agigiaaqcaqcaactactiaqcciqqtaccaqcaqaaaccigqccaqqrinncaqqcin 12
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Washington University School of Medicine
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Pred. No. 1.44e-235;
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y151gCS.rl Homo sapiens abna alone 161916 5' sir
IG KAPPA CHAIN PRECURSOR V-111 REGION (HUMAN);...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and M Fatima Ponaldo.
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Best Local Similarity 84.7%:
Matches 216: Conservative
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                   F64693 26-MAY-1995
yi22f09 rl Home sapiens cDNA clone 140009 5' similar to gb-M63438
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);.
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Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes,
Sarcopterygii, Choanata: Tetrapoda, Amniota, Mammalia, Theria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 human clone=140009 library=Soares placenta Nb2HP vector=pT7T3D
127 CCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT-CAG 185
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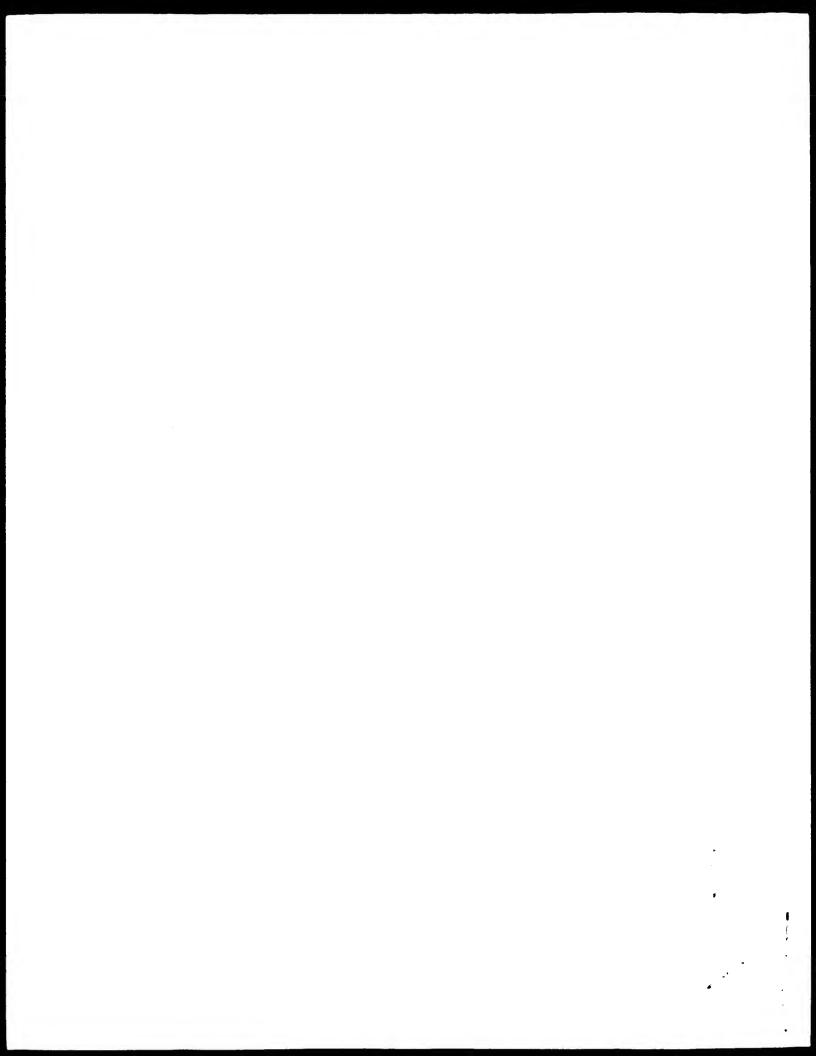
(bases 1 to 438)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hullman,M., Robor,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Prikhin,L., Prohlfing,T., Soares.M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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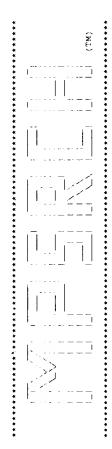
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(Pharmacia) with a modified polylinker host-belin (ampicillin resistant) primer-W13PP1 Psitel-Not I Rsi-c2=Eco RI Adult female. Its strand CDNA was primed with a Not I - oligodil) primer [5] toTTACCAAPTGAAGGGGGGGGGGGGGTTITITITITITITITITI 3], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), double-stranded with Not I and cloned into the Not I and Eco RI sites of a modified pi713 vector (Pharmacia). Library went through one round of normalization to a cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                  yj66e01.rl Homo sapiens cDNA clone 153720 5' similar to qb-X06764
IG KAPPA CHAIN PRECUPSOP V-TIT PEGION (HUMAN)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Best Local Similarity 91.7%;
Matches 176; Conservative
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Eukaryotae: Metazoa; Eumetazoa: Bilateria; Coelomata;
Deuterostomia: Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopteryqii: Choanata: Terrapoda; Amniota: Mammalia: Theria;
Eutheria: Archonta: Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 361)
Hillier.L., Clark.N., Dubuque.T., Elliston.K., Hawkins.M.,
Holman.M., Hultman.M., Kucaba.T., Le.M., Lennon.G., Marra.M.,
Parsons.T. Pifkin.L. Pohlfing T. Scares.M., Tan.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 41.8%; Score 133; DB 28; Length 361; Local Similarity 96 3%; Prod No 3 320-209; Conservative 0; Mismatches 24; Indels 11: Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image llnl gov) for further information
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Tel: 314 285 1800
Fax: 314 286 1810
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WashU-Merck ESI Project
Washington University School of Medicine
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High quality sequence stops: 308
Source: IMAGE Consortium, LLNL
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Search completed: Tue Feb 24 07:16:25 1998 Job time : 292 secs.





Release 2 1D John F Gollins, Biocomputing Pessarch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U K Distribution rights by Intelligenetics, Inc.

n.a. • n.a. database search, using Smith-Waterman algorithm MPsrch_nn Tue Feb 24 13.44.51 1998, MasPar time 19.76 Seconds 740.131 Million cell updates/sec Run on

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>US-08-844-215-15 (1-318) from US08844215.seq

1 GAGGICACGCAGICTCCAGG CTCGAGTGCGTCAGAGGTCC 318 Description: Perfect Score: Seguence Z.A

GGACCAAGGTGGAGATCAAA 318

.CCTGGTTCCACCTCTAGTTT

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD : Nmatch 87521 segs. 22994921 hases x 2

Searched:

Listing first 45 summaries Minimum Match 08 Post-processing:

n-issued Database:

libacki 2:51 3:52 4:53 5:54 6:55 7:56 8:pc190 9:pc191 l0:pc192 ii:pc193 i2:pc194 i3:pc194 i4:pc194

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. Mean 7 613 - Variance 4 275; scale 1 781 Statistics

SUMMARIES

and is derived by analysis of the total score distribution

Result No.	Score	Query	Length	Çi Gi	ä	Description	Pred. No.
7	(1 (1	L' G	5 C Z		PCT-11892-1	Sequence 1. Application	940-18
CI	263	 (1)	546	63	PCT - US95 - 1	()	1.16e-17
3	253	(1) (1)	646	C4	PCT-US94-0	c i	1.156-174
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Sequence 1. Application PL/TUS9312501.
Sequence 1. Application PC/TUS9312503
GENERAL INFORMATION:
APPLICANT: Chang, TSE WEN
TITLE OF INVENTION: ALLERSEN-SPECIFIC 19A MONOCLONAL ANTIEVDIES AND
TITLE OF INVENTION: BELATED PROPORTS FOR ALLERSEY TEFATMENT
NUMBER OF SEQUENCES: 10
CORPESSIONER ACCESS:
ADDRESSEE: Tanox Blosystems, Inc.
STREET: 10301 Stella Link Pd.
                                                                                                                                                                                                 COUNTY, 2 TACS S 2 PORM: COMPUTER PEADABLE FORM: MEDIUM TYPE: 3 5" H) Tensity Diskette TANNITEP: 1BM PS/2 TANNITEP: 1BM PS/2
JT 1
PCT-US93-12501-1 STANDARD; DNA; TNC; 325 RP
                                                                                                                                                                                                                                               COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS, Version 3.30
SOFTWARE: Wordperfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mirabel, Eric P.
PEDISTPATION NUMBER: 31,211
PEDESPENDE/DOCKET NUMBER: TNX92:3
TELECOMMONICATION INTERMATION:
TELEFHONE: 712:664-2288
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APPLICATION NUMBER FO
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PRIOP APPLICATION DATA:
APPLICATION NUMBER.
                                                                                                                                                                        Houston
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                                      01-JAN-1900
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APPLICANT:
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TITLE OF INVENTION: METHODS FOR PRODUCING ANTIRODY LIRRARIES
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNGLOBULIN LIGHT
                                                                                                                       133 CCCASSCICCICAICIIAISCIACAICCAIAAGGICAICIISGCAICCCAGACAGGIICACI 192
                                                                                                                                                                                                   193 GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTT 252
                                                                                                                                                                                                                      187 GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTT 246
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                                                                                                                                                                                                                                                         73 GCCAGTCAGACTGTTAGCAGCAACTACTTAGCCTGGTACAGCACAAACCTGGCCAGGCT 132
                                                                 13 ACGCAGICICCAGGCACCCIGICITIGICICOCAGGGGAAAGAGCCACCCICTCCIGCAGG 72
                                                                                      7 ACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGCAAAGAGAGCACCCTCTGCTGCAGG
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                     Score 272; DB 11; Length 325; Pred No. 1 94e-181; O; Mismatches 20; Indels O;
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ADDRESSEE: The Scripps Research Institute
STREET: 10666 North Torrey Pines Road, TPC8
Sequence 325 BP; 79 A; 93 C; 79 G; 74 T; 0 other;
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PCT-US95-11235-2 STANDARD; DNA; UNC; 646 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
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FILING DATE: 02-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9511235. Sequence 2, Application PC/TUS9511235 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEKATING SYSTEM: PC-DUS/MS-DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02-SEP-1994 PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-1992
                      Ouery Match 85.5%;
Rest Local Similarity 93.6%;
Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PPIOP APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         313 GTTGAAATCAAA 324
                                                                                                                                                                                                                                                                                                             307 GIGGAGATCAAA 318
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TITLE OF INVENTION: METHODS FOR PRODUCING ANTIRODY LIBRARIES
TITLE OF INVENTION: USING UNIVERSAL OF RANGAMIZED IMMUNGSLORULIN LIGHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 263; DB 13; Length 646
Pred. No. 1.16e-174;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 646 BP; 162 A; 187 C, 170 G, 127 T, 0 other;
                                                                                                                                             34,163
P- TSPI 409 1 (PC)
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PCT-US94-01258-2 STANDARD; DNA; UNC; 646 BP.
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APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
PRIOP APPLICATION DATA:
APPLICATION NUMBER: US 08/174,674
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
FILING DATE: 02-FEB-1993 ATTORNEY/AGENT INFORMATION:
                                                                                     NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · 646 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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93.78;
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COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy (
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MOLECULE TYPE:
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METHODS FOR PRODUCING ANTIBODY LIBRARIES
USING UNIVERSAL OF PANDOMIZED IMMUNOCIORULIN LIGHT
                                                                                                                                                                                                                                                                       181 TCCASTGGCASTGGGTGTGGGACAGACTTCACTGTGACGATCAGCAGAGCAGGAGCCTGAA 240
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                                                                                                                                                                                                                    1 GASCICACSCACICICCASCCACCCIGICILISICICASSGSAAAGAGCACCCICICC 60
                                                                                                                                                                                                                                               1 GABOTEARSEARTETECARSEARECTETETETETECARGEGAAAGAGCACCCTCTCC 50
                                                                                                                                                              Score 263; DB 12; Length 646;
Pred. No. 1.16e-174;
0; Mismatches 17; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSER: The Scripps Research Institute
STREET: 10666 No. 5667988th Torrey Pines Road, TPC8
                                                                                                                                      Sequence 645 BP: 162 A. 187 J. 170 G. 127 I. 9 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-300-386A-2 STANDARD; DNA; UNC; 646 BP.
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CLASSIFICATION: 435
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Sequence 2, Application US/08300385A
Patent No. 5657988
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Burton, Dennis R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IRM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                 LENGTH: 545 Dass pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
       28-DEC-1993
                INFORMATION FOR SEQ. ID NO:
SECUENCE CHARACIERISTICS:
LENGTH: 645 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                                                                                                                 Query Match
Best Local Similarity 93.7%;
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APPLICANT: Lerner, R
TILLE OF INVENTION:
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                                                                                 MCLECULE TYPE: CDNA
HYPOTUPETY
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APPLICANT: Barbas,
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       FILING DATE:
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ZIP: 92037
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61 IGCAGGGCCAGICACAGIGIIAGGAGGGCCIACIIAGCCIGGIAGCAGCAGAAAACTRGC 120
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APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 263; DB 7; Length 646; Pred. No. 1.16e-174; O; Mismatches 17: Indels
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                                                                                                                                      APPLICATION NUMBER: US 08/012,566
FILING DATE: 91-FEB-1993
ATTORNEY/AGENT INFORMATION:
 US 08/174,674
                                             US 07/826,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 182, Application US/08053131 Sequence 182 Application US/08053131 Patent No. 561016 Patent No. 561016.
                                                                                                                                                                                                         34,163
                                                                                                                                                                                                                   PEFERENCE/POCKFT NUMBER TS
TELECOMMONICATION INFORMATION:
TELEPHONE 619-554-2937
               FILING DATE: 28-PEC-1993
PRIOR APPLICATION DATA:
APPLICATION NIMBER: US 0773
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
FILING DATE: 30-SEP-1992
                                                                                                                                                                                                                                                                       TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                       646 base pairs
                                                                                                                                                                                                                                                                                                   SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                          NAME: Fitting, Thomas
PEGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                     619-554-6312
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Best Local Similarity 93.7%;
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                       PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
APPLICATION NUMBER:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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375 ACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 262; DB 7; Length 900;
Pred. No. 6.58e-174;
 One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION join(116, 163, 351, 650)
Sequence 900 BP; 220 A; 241 C; 201 G; 238 T; 0 other;
                                                                                                                          Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                    PREDICATION NUMBER: US (17440, 860)
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
PEGISTPATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 6
US-08-053-131-178 STANDARD: DNA: UNC; 812
                                                                                                                                                                                                                                                                                                                                                          14643-9-3
                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FLIGG DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA.
                                                                                 MEDIUM TYPE Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 178, Application US/08053131. Sequence 178, Application US/08053131
                                                                                                                                                                                                                                                                                                                                                      PEFFRENCE/POCKET NUMBER 14
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-326-2400
TELEFAX 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          900 base pairs
CITY: San Francisco
STATE: California
COUNTRY: HEA
                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match R2 4%;
Local Similarity 97.8%;
Les 268; Conservative
                                                                    COMPUTER READARLE FORM-
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STPANDEDNESS
                                                      94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY.
                                                                                                                           SOFTWARE:
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502 GOCAGTCAGAGTGTTAGGAGE---1ACTTAGGCTGGIACCAACAGAAACCTGGCCAGGCT 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Londerg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STPEET: One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: join(199..246, 418..714)
Sequence 812 BP; 201 A; 225 C; 187 G; 199 T; 0 other;
                                                                                                                                                                                 COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0. Version #1.25
CURRENT APPLICATION DATA:
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Local Similarity 95.9%; Pred. No. 7.11e-141;
es 246; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA
APPLICATION NUMBER:
FILING DATE: 16.DEC-1927
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,408
APPLICATION NUMBER: US 07/853,408
APPLICATION NUMBER: US 07/853,408
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14643-9-3
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Smith, William M. PEGISTPATION NUMBER 30,223 PEFERENENCE, DOCKET NUMBER: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEU ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 812 base pairs nucleic acid
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                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                CITY: San Francisco
STATE: California
Patent No. 5661016
GENERAL INFORMATION:
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                                                                                                                                                            USA
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                                                                                                                                                                    94105
                                                                                                                   STPEET:
CITY: S?
                                                                                                                                                            COUNTRY:
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HUMAN NEUFRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMINIODEFICIENCY VIBUS
170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ö
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Fred No. 1.25e-138;
0; Mismatches 50;
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US-08-276-852-152 STANDAED: ENA: UNC: 729 BP.
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FRIGH APPLICATION DATA:
APPLICATION NUMBER: US 07/954 140
FILING NATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 152, Application US/08276852.
Sequence 152, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-F0S/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burton, Dennis R
Barbas, Carlos F
Lerner, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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ATTOPNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               729 base pairs
                                                                                                                                                                            658 GCAGITIAITACIGICAGC 676
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INFORMATION FOR SEG ID NOT
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A4 :8:
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STRANDEDNESS: double
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East Local Similarity A4 18:
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lerner,
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 11; Indels 3; Gaps 1;
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APPLICANT: Kay Pobert M.
TITLE OF INVENTION. Transgenic No. 5661016. Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CUMBER OF SEQUENCES. 197
CURRESPONCENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 215; DB 7; Length 900; Pred. No. 2.23e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                               5: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOZAIION: 30in(180, 227, 347 643)
Sequence 900 BF, 225 A, 244 G, 204 G, 227 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEPATING SYSTEM: PC-DoS/MS-DOS
SUFFMARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
                                                                                                 US-08-053-131-180 STANDARD; DNA; UNC: 900 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION OF PRIOR PRIOR APPLICATION NUMBER: US 07/990,860 FILING LANG: 16-02c-1942 PRIOR APPLICATION NUMBER: US 07/990,860 FILING LANG: 17-02c-1941 PRIOR APPLICATION NUMBER: US 07/863,4608 FILING DATE: 18-02c-1941 PRIOR DATE: 18-02c-1941 PRIOR PAPELICATION NUMBER: US 07/863,4608 FILING DATE: 18-02c-1941 PRIOR PRIOR DATE: US 07/863,4608 FILING DATE: US 07/863,4608 FILING DATE: US 07/863,4608 FILING DATE: US 07/863,4608 FILING DATE: UNIMBER: 30.23 PREEFRURE/POORET UNIMBER: 14643-9-3 FILING DATE: UNIMBER: 14643-9-3
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FILING DATE: 26-APP-1993
CLASSIFICATION: 800
                                                                                                                                                                       Sequence 180. Application US/08053131
Sequence 180. Application US/08053131
Patent No. 5561016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEG ID NO: 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACIERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  247 GCAGIGIAITACTSICAGE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match
Local Similarity 94.5%;
nes 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
: JSA
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                                                                                                                                                    01-JAN-1900
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                                                                                                                                     78 CICAGGCAGITCICCAGGCAGCTGICICICICICAGGGGAAAGAGCACCIICICIGI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 AGGGCCAGTCAGAGTGTTAGCAGCAATTACTTAGCCTGGTACCAGCAGAGCTGGCCAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 GCTCCAAGGCIGGICAIACATGSTGTTTCCAAIAGGGCTCTGGCATCTCAGACAGGTC 257
.38 AGGICCAGICACAGCAIICGCAGCCGCGGGIANGCCIGGIACCAGCAGCAGCONGGGG 197
                                                                                                                     198 GCTCCAAGGCTGGTCATACATGGTGTTTCCAATAGGGCCTCTGGGCATCTCAGACAGGTTC 357
                                                                                                                                                                               138 AGGICTA*ICACAGICÁTICSCASCICSCIASCOTIGGIACCAGCACAAACCIGGCCAG 197
                              4 CTCANOGNATIOTOGAGGGACOSTSTOTTGTOTTGGAGGGAAAASAGOGAOOTTGTOOTGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CTCACGCAGTCTCCAGGCACCCTGTCTTGTCTCCAGGGGAAAGAGCACCACCTCTCCTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN NEUTPALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Pelease #1.0, Version #1 25 (EPO)
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PCT-US95-08743-152 STANDAPD; DNA: UNC; 729 RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHPRENT APPLICATION DATA.
APPLICATION NUMBER: PCT/USG5/OR743
FILING DATE: 11-JUL-1995
FRIOP APPLICATION DATA.
APPLICATION NUMBER: US 08/276,852
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 152, Application PC/TUS9508743. Sequence 152, Application PC/TUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPEPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-JUL-1994
INPOPMATION FOR SEQ ID NO: 152-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           729 base pairs
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EDNESS: double
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124 GCTOCCARGOTTOTTOTTATORITETATOCAGGAGGAGGAGGAGGALAGGALOGAGAGAGAGTTO 183
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                                                                                                               338 ITTCCTCTCCGAGTTTGGTCCCTGACCAAAAGTGTACGAGGAGGCACCATAAAACTGACA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 TITGATCICCACCITEGICCELIGGCEGAACGICAACGIGAGITACCATAAAGCIGACA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 GTAGTACAGTGCAAAGTCTTCAGGCTCCACTGTGGTGATGGTGAGAGTGAAGTCTGTCCC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 GIAALAGAGIGGAAAATGITTAAGTIGGAGIGTGAIGGIGGIGAGAGIGAAGIGIGGC 199
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TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBEFICIENCY VIFUS
NUMBER OF SEQUENCES: 170
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SOFTWARE: PatentIn Pelease #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA-
APPLICATION NUMBER: PCT/MS95/08743
FILING DATE: 11-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
Sequence 729 RP: 156 A: 192 G: 208 G: 173 T: 0 other:
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Local Similarity 84.1%; Pred. No. 1.25e-138;
Hes 265; Conservative 0; Mismatches 50;
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PCT-US95-08743-158 STANDARD; DNA; UNC; 729 BP.
                                                                                                                                                                                                                                                                                                      Sequence 168, Application PC/TUS9508743. Sequence 168, Application PC/TUS9508743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-701-1994
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM-
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           729 base pairs
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EDNESS: double
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                                                                                                                                                             378 AAACTGGAGGAAA 392
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338 ITTCCTCTCCAGITIGGICCCTGGCCAAAGINIANGAGGGAGGCACCALAGACTGACA 397
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                                                                                                                                     APPLICANT: Lerner, Richard A LILLE OF INVENTION: HUMAN NEUTRALIZING MUNCCOONAL ANTIBUDIES TITLE OF INVENTION: TO HUMAN IMMUNOBETICIENCY VIPUS COPPESSONDENTE ADDRESS: 170
                                                                                                                                                                                               ADDRESSEE: The Softings Pescarch Institute, Office of ADDRESSEE: The School Coursel SIPPET: 10666 No. 665118th Torrey Pines Poad, Suite 126, STREET: Mail Drop IPC8 CITY: La Jolla STATE: CA
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Pred. No 1 25e-138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE DNA (genomic)
Sequence 729 BF, 155 A, 192 G. 208 G, 173 T, 0 other.
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Faterish Release #1.0, Version #1.25 CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/276.852 FILING DATE: 18.JUL-1994
CLASSIFICATION: 514
APPLICATION: 514
APPLICATION: AND ATA APPLICATION DATA.
APPLICATION: 30.SEP-1993
US-08-275-852-158 STANDARD: DNA; UNC; 729 8P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
FORMATION FOR CO.
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                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                               Sequence 168, Application US/08276852,
Sequence 168, Application TS/09276952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fitting, Thomas
PEGISTRATION NUMBER: 34,163
PEFERENCE/DOCKET NUMBER: SCH
                                                                                                        APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEG ID NO: SEQUENCE CHARACTERISTICS:
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Local Similarity 84.1%;
les 265; Conservative
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APPLICATION NUMBER:
                                                                                            INFORMATION:
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                                                                            Patent No. 5652138
                                                                                                                                                                                                                                                                                                                     92037
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                               01-JAN-1900
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                                                                                            GENERAL
                    XXXXXX
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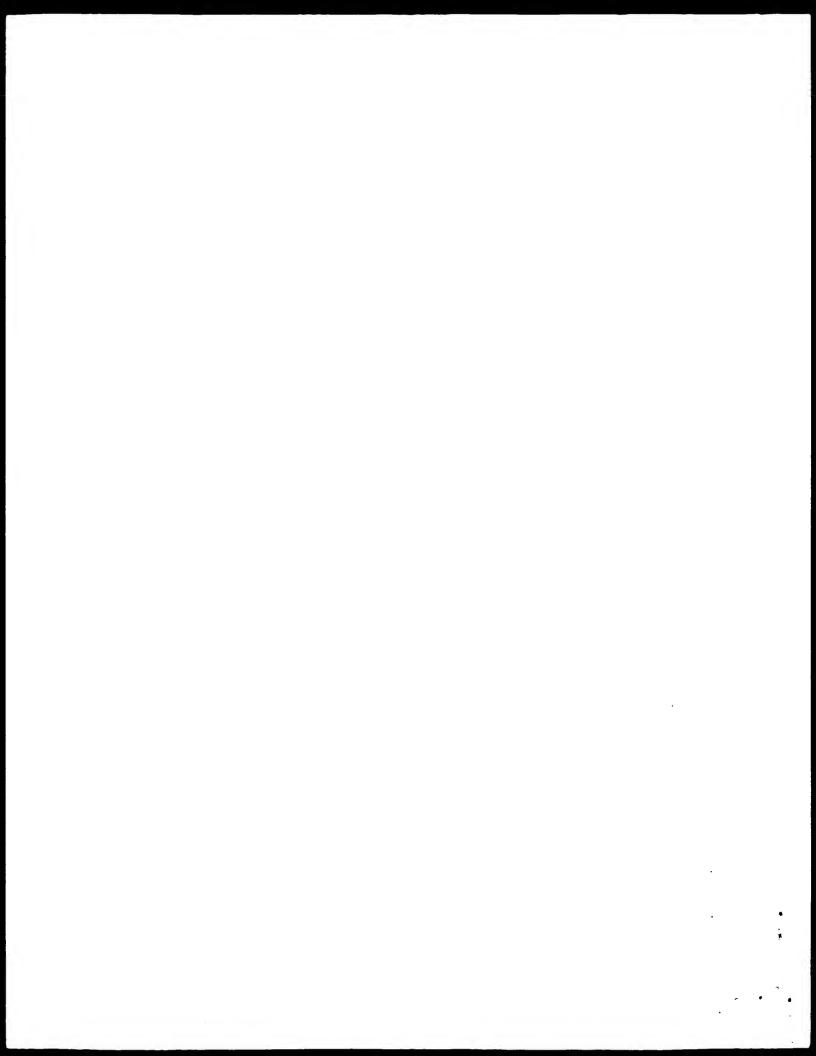
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578 GCTGTGACTSGACCTACABGAGAAGGCCCTTTCCCCTGGAGACAGAGACAGGGCC 637 [1 illili] [1 illili] [1 illili] [1 illili] [1 illi] [1 
                                                 138 GAGGAGCCTGGGAGCCTGGCGAGGTCTCTGCTGGTACCAGGCTAAGTAATTGCTGACTAAC 79
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Pred. No. 1.25e-138;
0; Mismatches 50: Indels '': Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652139th Terroy Pines Poad, Suite 225 STREET: Mail Drop IPC8 CITY: La Jolla
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Sequence 13254 BP: 3205 A: 3559 C: 3251 G: 3238 T: 0 other:
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COMPUTER: Eloppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Pelease #1.0, Version #1.25
CUPRENT APPLICATION DATA:
JT - 12
US-08-276-852-156 STANDARD; DNA; UNC; 13254 BP.
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FILING DATE: 18-JUL-1994
CLASSIPFTATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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Sequence 156, Application US/08276852.
Sequence 156, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Button, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
TELEFAX: 619-554-6312
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nucleic acid
EDNESS: double
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INFOFMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 84.1%;
Matches 265; Conservative
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MEDIUM TYPE: Floppy
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12846 TITGCACTGTACTACTGTCAGGTCTATGGTGCCTCCTACAACACTTTTGGCCAGGGGACC 12905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12786 AGCGGCAGTGGGTCTGGGACAGACTTGACTGTGACGATGACGAGGAGGGGGAGCGTGAAGAC 12845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 12606 CTCACGCAGTCTCCAGGCACCCTGTCTCTGTCTCCAGGGGAAAGAGCCACCTTCTCTGT 12665
12666. Addicentichenschiligerasposposestadetacerachaearaholigae 12725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12666 AGGTGGAGTGAGAGTATGGCAGGGGGGGGGTAGGTGGTAGGAGAGAAGGTGGGCAG 12725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12726 GCTCCAAGGCTGGTCAIACAIGGTGTTTCCAATAGGGCCTCTGGCATCTCAGACAGGTTC 12785
                                                                                                                                                            184 AGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGAT 243
                                                                                                                                                                                                             64 AGGGCCAGTCAGAGTGTTAGCAGCAATTACTTAGCCTGGTAGCGAGCAGCAGAGACCTGGCCAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CICAGGCAGICITCCAGGCACCCIGITITGICITGAGGGGAAAGAGCCACCCICICCIGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNOBELICIENCY VIPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 215; DB 13; Length 13254; Pred No 1.25e-138; 0; Mismatches 50; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECHILE TYPE: DNA (genomic)
Sequence 13254 BP; 3206 A; 3559 C; 3251 G, 3238 T, 0 cther,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) cuprent Application NATA-APA-APALICATION NUMBER: PCT/US95/08743 FILING DATE: 11-JUL-1995
                                                                                                                                                                                                                                                                                                                                        JT 13
PCT-US95-08743-156 STANDAPD; DNA; UNC; 13254 RP
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 156, Application PC/TUS9508743. Sequence 156, Application PC/TUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-UL-1994
INFERRATION FOR SEU ID NO: 156.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.6%; Score 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER IRM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13254 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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nes 265; Conservative
                                                                                                                                                                                                                                                           12906 AAACTGGAGGGAAA 12920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular MOLECHLE TYPE: DNA (9
                                                                                                                                                                                                                                                                                        304 AAGGIGGAGAICAAA 318
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12846 TTTGGACTGTAGTACTAGTGAGGTGTAIGGTGFGTGTGTAGAGTTTTGAGGTTTTAGAGAGGAG
                               244 TITISCASTSTATTACTSTCAGGITTATSGTAACTCACGTTGGAGGTTGGGCCAAGGAAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 TITTOCTCTOJASTITGGTOCCTGSCCAAAAGTGTACGAGGASGAGGACCALAGACTGACA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 TITGAICTC/ACCITGATICCCIIGAACCAACATC/AACATIACCIIACCAIAAASCIICACA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455 AGACCCACTGCCGCTGAACCTGTCTGAGATGCCAGAGGCCCTATTGGAAACACCATGTAT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          515 GACCAGCCTTGCAGCCTGGCGTGAG1 PTGTGGCGGATACCAGGCTACGCGGGGGGGGGGATGCGAAT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sdeb
                  APPLICANT:
TITLE OF INVENTION: HTMAN NEHTPALIZING MONOCLONAL ANTIRODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIEUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM IYPE:: Floppy disk
MEDIUM IYPE:: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 13254;
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Sequence 13254 RF, 3238 A, 3251 C, 3559 G; 3266 T, 9 5thor)
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Felesce #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275.852
FILING DATE: 11-1994
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 13254 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 67.6%; Score 215; DB 13; L Best Local Similarity 84.1%; Prod. No. 1 25e-138; Matches 265; Conservative 0; Mismatches 50;
                                                                                                                                               T 14
PCT-US95-08743-170 STANDARD; DNA; UNC; 13254 BP
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US-08-276-852-170 STANDARD; DNA; UNC; 13254 BP.
                                                                                                                                                                                                         Sequence 170, Application PC/TUS9508743. Sequence 170, Application PC/TUS9508743
                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
                                                               12906 AAACTGGAGAGAAA 12920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 GTAGTACAGTGTAAAGTCTTCAGGGTCCACTCTGGTGATGGTGAGGTGAAGTCTGTCCC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 AGACCCACTGCCGCTGAACCTGTCTGAGATGCCAGAGGCCCTAITGGAAACACCCATGTAT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515 GACCAGCCITGGAGCCFGGCCAGGIIFGIGCFGGTACCAGGCIACGCGGCGGCGGCGAT 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 GAGGAGCCISSSASCCIGGCCAGGICTCIGCTSGIACCAGGCIAAGIAAITGCIGCTAAC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                       APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Lerrar Pichard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBFLICIENCY VIPUS
CORRESPONDENCE: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                           ADDRESSEE: The Scripps Pescarch Institute, Office of ADDRESSEE: Patent Counsel STREET: 1946 No. 5452139th Torrey Pines Poad, Suite 220, STREET: Mail Drop IP63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 13254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
Sequence 12254 9P: 2238 A: 3251 C: 3559 G: 3206 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 215: DB 7: Length 1325-
Pred. No. 1.25e-138:
0: Mismatches 50: Indels
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/276,852
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION WINNEL
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCR1452P
Sequence 170. Application US/08276852.
Sequence 170. Application US/08276852
Patent No. 5552138
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR
IELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 170:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 13254 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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Local Similarity 84.1%;
es 265; Conservative
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24 mtqspptlslspgervtlscrasqsvsssyltwyqqkpqqaprlliygastratsiparf 83
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                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENT).
EUKARYOTA METAZOA: CHOFDATA; VERTEBRATA; TETRAFODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                       IG KAPPA CHAIN V-III REGION (VH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING 1.
                                                                                                                                                                                                                                                  COMPLEMENTARITY - DETERMINING 2.
                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING 3. BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                           Score 548; DB 5; Length 116; Pred. No. 3.01e-98; 7; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                       12757 MW; 27FA1BCE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JUL-1986 (REL. 06, LAST ANNOTATION UPDATE)
11 G RAPPA CHAIN V-I REGION (LAY).
  116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 108 AA
                                                                                                                                                                                                                                                               FRAMEWORK 3
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                                                                                                      SEQUENCE FROM N.A.
MEDLINES, 80087932,
PECH M., ZACHAU H.G.;
NUCLEIC ACIDS RES. 12:9229-9236(1984).
EMBL: X02725; .i NOT_ANNOTATED_CDS.
PIR: A01901; NAHUVH.
HSSP: P01607; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                              84 sgsgsgtdftltisslqpedfavyycqq 111
                                                                                                                                                                                                                                                                                                                                                                                                                        62 SGSGSGTDFTLTISNLEPEDFAVYYCQQ 89
   PRT;
                                                                                                                                                                       HSSP; P01607; 1MCP.
IMMUNOGLOBULIN V REGION; SIGNAL.
                    13-AUG-1987 (REL. 05, CREATED)
                                                                                                                                                                                                                                                                                                                             74.38;
                                                                                                                                                                                                                                                                                                                                      Local Similarity 86.4%;
les 76; Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01871; KIHULY.
HSSP; P01607; 2FGW.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                43
116
115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
50
57
                             13-AUG-1987
 KV3J_HUMAN
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P01605;
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SEQUENCE
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Job time : 15 secs.

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Pred. No. 4.32e-97;
21; Mismatches 12; Indels 1; Gaps
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                                                                                                                                                                        2 ELITQSPATLSLSPGERATLSCRASQSVNKYLAWYQUKPGQAPRLLIYDASNRATGIPARF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 qmtqspstlsasvgdrvaitcrasqnisswlawyqqkpgkapkvliykssslesqvpsrf 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ELTOSPATLSLSPGERATLSCRASQSVNKYLAWYQQRPGQAPRLLIYDASNRATGIPARF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRAIA: TETRAPODA; MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
    COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
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MILSTEIN C.P., DEVERSON E.V.;
EUP. J. BIOCHEW. 49:377-391(1974).

-1- THE C. REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

-1- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

HISSP: PO1607; IDFB.
                                                                                                                                                                                                       63 sgsgsgtdftfisslqpediatyycqqynnwpptfgqgtkvevk 107
                                                                                                                                                                                                                                   62 SGSGSGTDFTLTISNLEPEDFAVYYCQQRSDWV-TFGGGTKVEIK 105
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 97 COMPLEMENTARITY-DET
107 FRANEWORK 4.
88 BY SIMILARITY.
108 ... 11834 MW. 20228BOC CRG32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 107
107 AA; 11703 MW; 04RF9EFD CRC32;
                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-I PEGION (CAR).
                                                                                                                                                                                                                                                                                                 107 AA
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Local Similarity 67.6%;
es 71: Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07-19-37 1998; MasPar time 9.55 Seconds 334.962 Million cell updates/sec Pun on.

>US-08-844-215-9 (1-105) from US08844215 pep 738 Title:

Tabular output not generated.

1 AELICSPATISISPGERATI Description: Perfect Score: Sequence:

..YCQQRSDWVTFGGGTKVEIK 105

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

lianni 2:anni 3:anni 4:ann4 5:unanni 6:unanni 7:unanni 8:unann4 9:unanni 10:unanni 12:unanni 8:unanne 14:unannii 15:unannii 16:unannii 17:unanni

Mean 40.220; Variance 128.295; scale 0.313 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Query Match Length	DB	10	Description	Pred. No
-	695		108	Ļ	644151	Id kappa chain V red	1. ASA 1.
7	683	4 50	144	1	PL0106	garra chain pr	1.106-70
m	678	91.9	111	7	823628	dappa chain	870.6
4	675	91.5	128	7	A56701	cappa chain V r	6.996-69
'n	671		114	7	C54905	cappa chain V	2 290-68
Ψ	657		128	7	S40379	cappa light ch	1 440-66
7	られる		128	7	540345	cappa	1.94e-55
αc	555		125	7	240344	Id kappa light chain	2 616-66
σ	649	87 9	129	7	529627	rappa	1 54e-65
10	641		101	7	557444	chain V	1 640-64
11	631	'n.	108	۲-	H44151	cappa chain 1	i d:
12	626	4	115	7	K3HUVG	cappa chain pr	1.37e-62
13	626	84 9	117	٢	240362	cappa chain	1 370-62
14	620	84.0	115	r-	S11697	Iq kappa chain precu	8.05e-62
15	617	83 6	a, ⊂ L	7	E30609	rappa chain	1 950-61
16	615	83.3	109	r-	A30508	Iq kappa chain V-III	3.52e-61
17	614	۲,	101	7	PHÓGES	Id kappa chain V req	4 720-61
18	612	82.0	129	۲-	S40363	- diedo eddeo	19-05: d
19	611	82 8	10B	7	หรูกลกผ	Ig kappa chain V-III	1 140-60
00	511	82.9	0 01	۲.	35,000	0	1 140.60

PLOID6 #type fragment 1g kappa chain produksor V-J-C region (ISI) - human (Kragment) #formal_name Homo sapiens #common_name man #formal_name homo sapiens #common_name man

ACCESSIONS

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PHONG 4 Ig kappa chain V req 1.54e-60 (1940) Ig kappa chain V req 1.54e-60 (1950) Ig kappa chain V ril 2.77e-60 (1950) Ig kappa chain V-III 4.99e-60 (1950) Ig kappa chain V-III 4.99e-60 (1950) Ig kappa chain V-III 4.99e-60 (1950) Ig kappa chain V-III 6.64e-60 (1950) Ig kappa chain V-III 7.52e-59 (1960) Ig	GNMENTS ragment eqion (JM-10) - human (fragment) sapiens #common_name man nce_revision 27-74n-1994 #*ext_change	<pre>III, C.F : Hom, Y.I : Caot</pre>	tibody libra compared wit ation not gi bulin V regil	core 695: DB 7: Length 108: red, No. 1.85e-71; 4; Mismatches 2: Indels 1; Gaps 1: sqsvssylawyqqkpgqaprlliydasnratqipar 60	OSVNKYLAWYOJKPIQAPKLLIYTASNHATGIPA YPGGTSOWPESÍGGGLKVEİK 106
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\verb|*superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin \\
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L. Exp. Med. (1989) 169:1631-1643
Relationship of variable region genes expressed by a human B
cell lymphoma secreting pathologic anti-Pr-2 erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olee, T., Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M. Kozin, P.; Carson, D. A.; Chen, P. P. Gramman, D. A.; Sh. M. (1992) 175:831-842
Genetic analysis of self-associating immunoglobulin G
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#domain V region #label VRE\
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13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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Pred. No. 1.10e-70;
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*region complementarity-determining 2\
*region complementarity-determining 3\
*domain J region *label JRC\
#domain C region (fragment) *label CPE
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Ig kappa chain V region - human (fragment)
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#length 111 #checksum 3907
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#accession PL0106
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nes 97; Conservative
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RESULT

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Human and mouse monoclonal antibodies to blood group A substance, which are nearly identical immunochemically, use radically different primary sequences.
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CLASSIFICATION #superfamily immunoglobulin V region, immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                 *superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                               Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat,
456701 #type fragment
Ig kappa chain V region precursor (HuA) - human (fragment)
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08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
16-Aug-1996
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                                             #formal_name Homo sapiens #common_name man
19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
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Ig kappa chain V region - human (fragment)
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4; Mismatches 3
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CLASSIFICATION #superfamily immur
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Matches 96; Conservative
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les 96; Conservative
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FICATION **superfamily immunoglobulin V region; immunoglobulin homology
IS heterotetramer; immunoglobulin
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CLASSIFICATION *superfamily immunoglobulin V region; immunoglobulin homology
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Ig kappa light chain (VJ) - human
#formal_name Homo sapiens #common_name man
19-May-1994 #sequence_revision 25-May-1995 #text_change
16-Aug-1996
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if stape light chain (VIC) - human
formal_name Homo sapiens *common_name man
19-May-1994 *sequence_revision 26-May-1995 *text_change
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  #formal_name Homo sapiens #common_name man
19-Way-1994 #sequence_revision 26-Way-1995 #toxt_change
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                                                                                                          Klein, R.; Japhichen, R.; Zachau, H.G.
Eur. J. Immunol. (1993) 23:3248-3271
Expressed human immunoglobulin chi genes and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. (1993) 22:3248-3271
Expressed human immunoglobulin chi genes and their
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 128;
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Pred. No. 1.44e-66;
4; Mismatches 5;
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Best Local Similarity 90.4%;
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                                          16-Aug-1996
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540312

REFERENCE

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##residues 1-125 ##label KLE
##cross-references EMBL:X72454
FICATION #superfamily immunoglobulin V region: immunoglobulin homelogy
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##note the nucleotide sequence was submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walls, M.A.: Hsiao, K.: Harris, L.J.
Nicloic Acids Res. (1993) 21:2201 2929
Vectors for the expression of PCR-amplified immunoglobulin variable domains with human constant regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ltyspatisispgeratisciasysvgsylawyydykpyyapipijydasmatyiparfs 83
                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LIGSPAILSESPGERAILSCRASGSVNKYLAWYQQKPGGAPPLLIYUASNRAIGIPARFS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region - human
#formal_name Homo sapiens #common_name man
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
25-Oct-1995
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#formal_name Hom- sapiens #common_name man
10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change
                                                                                                                                                                                                                                                           5604 missionion
Klein, R : Jaenichen, R : Zachau, H G.
Eur. J. Immunol. (1993) 23:3248-3271
Expressed human immunoglobulin chi genes and their
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##molecule_type mRNA
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                                                                                                                                                                                                                                                        #length 125 #molecular-weight 13668
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88.8%; Score 555; DB 7; I
Best Local Similarity 92.2%; Pred. No. 2.61e-66;
Matches 94; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                     heterotetramer; immunoglobulin
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                                                                         ypermutation.
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Best Local Similarity 89.6%;
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Graff, R.; DeGraw, J.; Fyati, J.; LaPolla, R.; Burton, D. R.; Lerner, R.A.; Thornton, G.B.
P.OC. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
Human combinatorial antibody libraries to hepatitis B surface
                                                                                                                                                                                                                                           *superfamily immunoglobulin V region; immunoglobulin homology *length 107 *checksum 7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide translation not given *superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
Paterson, G : Wilson, G : Kennedy, P G E ; Willison, H.J. Submitted to the EMBL Data Library, June 1995
Analysis of anti-GMI ganglioside IgM antibodies cloned from motor neuropathy patients demonstrates diverse variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                   4 ltgspatlslspgeratlscrasgsvstylawyggkpggspslliydasnraagiaarfs 63
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 aeltqspgtlslspgeratlscrasqsvsssylawyqqkpgqapr1liygassratgipd 60
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
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#formal_name Homo sapiens #common_name man
17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change
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27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
                                                                                                  region gene usage with extensive somatic mutation.
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Immunoglobulin genes of different subgroups are
                                                                                                                                                                                                                                                                                                                   Length 107;
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                                                                                                                                                                                                                                                                                                                   Query Match 86.9%; Score 641; DB 7; Length 107
Best Local Similarity 87.5%; Pred. No. 1.64e-64;
Matches 91; Conservative 7; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 RFSGSGSGTDFTLTISNLEPEDFAVYYCQQRSDWVTFGGGTKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GSGSGTDFTLISNLEPEDFAVYYCQQRSDWV-TFGGGTKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 gsgsgtdftltisslepedfavyycqqrsnwpptfgqgtnvesk 107
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Nucleic Acids Res. (19
                                                                                                                                                                                                                         ##cross-references EMBL:X87898
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Best Local Similarity 86.8%;
Matches 92; Conservative
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#title

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#superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                        An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label SIG\
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#formal_name Homo sapiens #common_name man
06-Mar-1994 #sequence_revision 26-May-1995 #text_change
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                                                                                                         the sequence was determined from the germline gene
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predicted #label MAT\
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#disulfide_bonds #status predicted
#length 115 #molecular-weight 12575 #checksum 8230
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Eur. J. Immunol. (1993) 23:3248-3271
Expressed human immunoglobulin chi genes and their
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No 1 37e-62;
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Pred. No. 1.37e-62;
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Local Similarity 84 68:
es 88; Conservative
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Matches 87; Conser
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*superfamily immunoglobulin V region; immunoglobulin homology
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Structural and idiotypic characterization of the Lehains of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human IgM autoantibodies with different specificities. #cross-references MUID:89215279
                                                                                                                          Ig kappa chain precursor V-III region · human
#formal_name Homo sapiens #common_name man
25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
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#formal_name Homo sapiens #common_name man
29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
15-Aug-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.; Zachau, H.G.
J. Mol. Blol. (1985) 183:291-299
A large section of the gene locus encoding human
immunoglobulin variable regions of the kappa type
                                                                                                                                                                                                                                                                                                                                                                                preliminary, nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 115;
                 63 GSGSTDFTLTISNLEPEDFAVYVQQQRSDW-VIFGGGTKVEIK 105
74 ysgsgteftltisslqsedfavyycqqynnwpltfqqgtkvelk 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 520; DB 7;
Pred. No. 8.05e-52;
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Best Local Similarity 93.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
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REFERENCE
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REFERENCE
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Db 4 ltgspgtlslspgeratlscrasgsvsgnylawygdxpgaprilltydastratgipdrf 63 [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111]
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Search completed: Tue Feb 24 07:19:49 1998 Job time : 12 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time % 01 Seconds 177.704 Million cell updates/sec Tue Feb 24 07-45-01 1998: Run on:

Tabular output not generated.

(1-105) from USO8844215.pep 738 >US-08-844-215-9

1 AELIQSPAILSLSPGERAIL......YCQQRSDWVTFGGGTKVEIK 105 Description: Perfect Score:

PAM 150 Scoring table:

Sequence:

55402 seqs, 5095871 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued libackl 2:51 3:52 4:53 5:54 6:55 7:56 8:PCT90 9:PCT91 l0-PCT92 l1-pCT93 12-PCT94 13-PCT95 14-PCT95

Mean 27.520,

Statistics:

Variance 149 406, scale 0 184

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	di	Description	Pred. No.
	526	4		7	118-08-053-	Sequence 179. Applicat	4 4 RP-39
7	620	84.0	115	7	US-08-053-	181, Applica	1.30e-38
~	616	ω.		13	DCT-US95-0	147,	2 650-38
4	515			7	US-08-276-	147, Applica	2.556-38
S	608	R2.4	-	7	115-08-276-	149, Applica	1.100-37
9	608	82 4	111	~	0-3680-LDd	149	1 100-37
7	909	82.1	107		PCT-US95-0	O	1.560-37
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6	605	82 U		٢	1.5-08-576-	ά	1.870-27
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11	600	R1.3		œ	TIS-08-477-	ν.	4 540-37
12	600	81 3	108	œ.	115-07-634-	ά	4 540-37
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15	594	c	_	٣.	0-3680-1Dd	α.	1 320-36
16	594	Ċ	107	~	US-08-276-	87,	1.32e-36
17	594	c	108	13	Ú-368Ñ-LJd	00	1 320-36
18	594	80.5	108	7	US-08-276-	Sequence 99, Applicati	1.32e-36
19	593	c	_	~	0-565H-TOG	100	1 570-36
20	593	Ö	104	٢	115-08-516-	100, Appli	1.570-36
21	591	(c)		÷ ;	v-i68i-iid	23, App.	2 240-26
22	585	79.3	108	7	US-08-276-	Sequence 110 Applicat	6.490-36

23 585 79.3 108 13 PCT-US95-0 Sequence 110, Applicat 25 581 79.9 10.9 11 PCT-US93-0 Sequence 24, Application 581 78.7 10.7 6 US-07-634- Sequence 87, Application 7 US-07-634- Sequence 87, Application 7 US-08-474- Sequence 87, Application 7 US-08-477- Sequence 87, Application 181 78.7 10.7 6 US-08-477- Sequence 87, Application 181 78.7 10.7 6 US-08-477- Sequence 87, Application 181 78.7 10.7 7 US-08-487- Sequence 87, Application 181 78.7 10.7 7 US-08-487- Sequence 87, Application 181 78.7 10.7 7 US-08-487- Sequence 87, Application 182 581 76.7 10.4 13 PCT-US95-0 Sequence 94, Application 182 584 76.4 10.8 12 13 PCT-US95-0 Sequence 96, Application 182 583 76.3 112 13 PCT-US95-0 Sequence 97, Application 182 583 76.3 112 13 PCT-US95-0 Sequence 183, Application 183 583 75.6 10.8 12 US-08-276- Sequence 183, Application 183 75.6 10.8 12 US-08-276- Sequence 183, Application 184 74.0 10.7 11 PCT-US93-0 Sequence 184, Application 185 73.6 10.7 11 PCT-US93-0 Sequence 184, Application 185 73.6 10.7 11 PCT-US93-0 Sequence 184, Application 185 73.6 10.7 11 PCT-US93-0 Sequence 34, Application 185 73.6 10.7 11 PCT-US93-0 Sequence 34, Application 185 73.6 10.7 11 PCT-US93-0 Sequence 34, Application 185 73.6 10.7 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5	ALIGNMENTS RESULT 10
Application Applic	n Animal bodies Crew e 200

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                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5661016-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
TILLE OF INVENTION: Transgenic No. 5661016-Human Anima
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza. Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
                                                                                                                                                            Score 626; DB 7; Length 115; Pred. No. 4.48e-39; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1 0, Version #1.25 CURRENT APPLICATION DATA:
ELICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                   115 AA.
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REFERPENCE/FOOKET UNMER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                        63 GSGSGTDFTLTISNLEPEDFAVYYCQQRSDW 93
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DOS
                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 115 AA; 12575 MW; 71214 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 181, Application US/08053131
Patent No. 5661016
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 181, Application US/08053131.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07
FILING DATE: 18 MAR-1992
ATTONEY/AGENT INFORMATION:
NAME: SMITCH, WILLIAM M.
REGISTRATION NUMBER: 30,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 17-DEC-1991 PRIOR APPLICATION DATA
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Best Local Similarity 95.6%;
Matches 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                            Length 115;
                                                                                                                                        Indels
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TITLE OF INVENTION: TO HUMAN INDITRALIZI
TITLE OF INVENTION: TO HUMAN IMMUNON
NUMBER OF SEQUENCES: 170
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 147, Application PC/TUS9508743.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 147, Application PC/TUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                                      63 GSGSGTDFTLTISNLEPEDFAVYYCQQRSDW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 109 AA; 11779 MW; 65550 CN;
                                                                   MOLECULE TYPE: protein
JENCE 115 AA; 12599 MW; 70085 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/27
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 147:
 181:
                                                                                                                                                                                                                                                                                                         STANDARD;
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                           LENGIH: 115 amino acids
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amino acid
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          SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEG ID NO:
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                                            amino acid
                                                       linear
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PCT-US95-08743-147
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IP US-08-275-852-147
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Query Match
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    2 AELTOSPGTLSLSPGBRVIVSCRASGSVSNYLAWYQQKPGQAPRLLIYGASNRATGIPD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches 10; Indels 1; Gaps
                                                                APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner. Bichard A
TITLE OF INVENTION: HYMAN NEUTPALIZING MONOTIONAL ANTIPODIFS
INTER OF ENVENTION: TO HUMAN IMMUNOPEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
                                                                                                                        CORPESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 40666 No. 5652138th Torrey Pincs Road, Suite 220,
STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 515; DB 7; Length 109;
Pred No 2 65e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE Patentin Release #1 0, Version #1 25 CURPENT APPLICATION DATA APPLICATION NUMBER US/08/276 RE2 FITTER ATTENDED
                                                                                                                                                                                                                                                               ELLING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
APPLICATION DATA:
PILING TATE: TO SEP-1993
APPLICATION DATA:
FILING NAMER PER US 07/954 140
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM PC-DGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 109 AA; 11779 MW; 65550 CN;
                                      Sequence 147, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
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                     Sequence 147, Application US/08276852
                                                                                                                                                                                                                                                                                                                                                                                34,163
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPAX: 519-554-6312
INFORMATION FOR SEQ ID NO: 147:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                109 amino acids
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                                                                                                                                                                                                                                                                                                                                                                       NAME: Fitting, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 83.5%;
Best Local Similarity 84.9%;
Matches 90; Conservative
                                                                                                                                                                                                                COMPUTER PEADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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01-JAN-1900
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2 AELIGSPGILSLSPGEPATLSGPASGSVSNSYLAWYGYRPGGAPFLLIYGASTFATG1PE 61
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                                                                                                                                            TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIPUS
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                              COPPESPONDENCE ADDRESS:
ADDRESSE: The Scripps Pesparch Institute, Office of
ADDRESSE: Patent Counsel
STPEET: 10666 No. 5652139th forroy Pines Road, Suite 220,
STPEET: Mail Drop IPCB
CITY: La Jolla
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPEPATING SYSTEM: PC-PGS/MS-PGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUPRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
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FILING DATE: 30-SEP-1992
ATTOPNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATE: US 07/954.148
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Sequence 149, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
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JENCE 111 AA; 11956 MW; 63169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FILLING, Thomas
PEJISTPATION NIMBEP: 34,163
PEJEPENCE/POCKET NIMBEP: SCH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2237
                                                                    APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Pichard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 111 amino acids
amino acid
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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PRIOR APPLICATION DATA:
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PCT-US95-08743-149
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2 AELTQSPGTLSLSPGFRATLSCRASQSVSNGYLAWYQQKPGQAPFLLIYGASTRATDIPD 61
                                                                                                                                                                                                                                                                                                                                                                                                   1 AELTQSPATLSLSPGERATLSCPASQSVNK-YLAWYQQKPGQAPRLLIYDASNRATGIPA 59
                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
170
           HUMAN NEUTPALIZING MONOCLONAL ANTIRODIES
TO HUMAN IMMUNODEFICIENCY VIPUS
170
                                                                                                                                                                                                                                                                                                                 Score 608; DB 13; Length 111;
Pred. No. 1.10e-37;
7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 606; DB 13; Length 107; Pred. No. 1.56e-37; 10; Mismatches 7; Indels 2
                                                                                                         PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PFSGSGSGAPFILAISPLEPEDFAVYYCQQYAGSHTFGQGTKLEIK 107
                                                                                            SOFTWARE: Patentin metal.
SOFTWARE: Patentin metal.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PROR APPLICATION DATA: APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 90:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                              Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 90, Application PC/TUS9508743.
                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 111 AA; 11956 MW; 63169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE 107 AA; 11705 MW; 62938 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 107 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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Best Local Similarity 82.1%;
Matches 87; Conservative
                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity 83.0%;
                                                                                                                                                                                                                                                                                                                                                88; Conservative
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                           OPERATING SYSTEM:
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 APPLICANT:
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                                                                                                                                                                                                                                                                                         SEQUENCE
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1 ELTQSPGTUSUSPGEPATLSCPASQSUSNNYLAWYQQKPGQAPPLLIYGSSTFGTGIPDR 60
            1 BLTQSPGTLSLSPGERATLSCPASQSLSNNYLAWYQQKPGQAPPLLIYGSSTFGTGIPDP 60
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                                                                                                                                                                                                                                                                                                 APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALLZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIPUS
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Patent Counsel STREET: 10656 No. 5552138th Torrey Pines Road, Suite 220, STREET. Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: The Scripps Pesearch Institute, Office of ADDRESSEE: Patent Counsel
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                                                 61 FSGGGSGTDFTLTISRLEPEDFAVYYCQHYGNSVYTFGQGTKLEIK 106
                                                                           61 FSGSGSGTDFTLTISNLEPEDFAVYYCQQRSDWV-TFGGGTKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                 107 AA.
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FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 107 AA; 11705 MW; 62938 CN;
                                                                                                                                                                                                                                      Sequence 90, Application US/08276852 Patent No. 5652138 GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 90, Application US/08276852.
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                                                                                                                                                                                                                                                                                Burton, Dennis R
Barbas, Carlos F
                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 amino acids
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INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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les 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ELTQSPATLSLSPGERATLSCRASGSV-NKYLAWYQQKPGQAPFLLIYDASNRATGIPAP 60
 2 ELTQSPATLSLSPGEPATLSCPASQSV-NKYLAWYQQKPGQAPPLLIYDASNPATGIPAP 60
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APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Bichard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCIONAL ANTIRODIES
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                               Patent Counsel
565 No. 5652138th Torrey Pines Poad, Suite 220)
                                                                                                                                                                                                                                                                                                                                                     The Scripps Pesearch Institute, Office of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FSGSGSGTDFILIISRLEPEDFAVYSCQQYGTSPW-TFGQGTKVEIK 106
                           51 FSGGGSGTDFTLTISRLEPEDFAVYYCQHYGNSVYTFGQGTKLEIK 106
                                         61 FSGSGSGTDFTLTISNLEPEDFAVYCQQPSDWV-TFGGSTKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARD PAIGHTE PERONANDUS
CURRENT APPLICATION DATA
APPLICATION MANBER 08,08,275,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 605; DB 7; I
Pred. No. 1.87e-37;
                                                                                                          108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOF APPLICATION DATA.
APPLICATION NUMBER. US OR/178.302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/954,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/954,148 FILING DATE: 30-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCP1452P
                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
JENCE 108 AA; 11769 MW; 65957 CN;
                                                                                                                                                                                                               Sequence 86, Application US/08275852
Patent No 5652138
GENERAL INFORMATION·
                                                                                                                                                                                       Sequence 86, Application MS/08276852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 619-554-2937
                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 amino acids
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STREET: Mail Drop TPC8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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Best Local Similarity 86.0%;
Matches 92; Conservative
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1 ELTOSPGTLSLSPGERATLSCRASQSVISNYLAWYQQKPGQAFFIIIYGVSNRATGIFUR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 4, Gaps
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER PROJECTION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERALINS SYSIEM: PC-LOSS/MS-EUS
SOFTWARE: Patentin Pelease #1.0, Version #1.25 (EPC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FSGSGSGDFILISNLEPEDFAVYYCQQ--RSDWVTFGGGTKVEIK 105
61 FSGSGSGIDFILIISNLEPEDFAVYYCQQ--RSDWVIFGGGIKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FSGSGSGTDFTLTISRLEPEDFAVYSCQQYGTSPW-7FGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                               Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 605, DB 13, 7
Pred, No. 1.87e-37;
3, Mismatches 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE CONTROL OF THE CURRENT APPLICATION NUMBER: PCT/USOS/08743 ETTING DATE: 11-JUL-1995
                                                                                             7.
E.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 08/276,852
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                                                                                                                                                                                                                                                                          Sequence 86, Application PC/TUS9508743 GENEPAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                 Sequence 85, Application PC/TUS9508743
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JENCE 108 AA; 11769 MW; 65957 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86, Application US/08477728
Patent No. 5585089
GENEPAL INFORMATION
FORMATION CATY L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 85, Application US/08477728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 80
                                                                                             SIANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
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LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.0%:
Matches 92, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
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                                                                     JT 10
PCT-US95-08743-86
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Townsend and Townsend Khourie and Crew
       : 379 Lytton Avenue
Palo Alto
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LENGTH: 108 amino acids
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                                                                                                                                                                                                                                                NAME: Smith, William M
PEGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.8%;
Matches 89; Conservative
                              California
                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                           linear
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                                               94301
ADDRESSEE:
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                                      COUNTRY:
                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.3%; Score 600; DB 6; Length 108; Best Local Similarity 84.8%; Pred. No. 4.54e-37; Matches 89; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 SGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 SGSGSGTDFTLTISNLEPEDFAVYCQQRSDWV-TFGGGTKVEIK 105
                                                        SOFTWARE: Patentin Pelease #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 AA
                                                                                                                                                                                                                                                           11823-002600
                                                                                                                                                                           APPLICATION NUMBER: US 07/310,252
PILOR DATE: 13-FEB-1989
PROF APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTOPNEV AGENT INFORMATION
NAME: Smith, William M
RGGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-90260
TELECOMMUNICATION INFORMATION:
                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/540,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
                                                                            APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
JENCE 108 AA; 11590 MW; 64079 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLET, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/07634278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 86, Application US/07634278
                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELERAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5530101
GENERAL INFORMATION:
                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
          94111
                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-634-278-86
 COUNTRY:
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4 LTQSP3TLSLSP3ERATLSCFASQSVSSGYL3WYQQKPGQAPR1UTYGASSPATG1PDRF 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 600; DB 6; Length 108; Pred. No. 4.54e-37; 5; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 SGSGSGTUFTLIISPLEPEDFAVYYCHOYGSLGRIFGGGIRVEIK 108
COMPUTER PREADBLE FORM.

COMPUTER: FROMP disk

COMPUTER: IBM PC compatible

OPBRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SGSGSGTDFTLTISNLEPEDFAVYYCQQRSDWV-TFGGGTKVEIK 105
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                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBEP: IIS 07/540,274
FILING DATE: 28-5EP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILINS DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/290,975 FILING DATE: 28-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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APPLICANT: CO, MAN SUNG
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLEI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, HATOLE E.
TITLE OF INVENTION: IMPROVED HUMAN
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
JENCE 108 AA; 11590 MW; 64079 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 86, Application US/08474040 Patent No. 5693761 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 86, Application US/08474040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,223
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOP SEQ ID NO: 86:
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US-08-844-215-9.rai

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4 LTQSPGTLSLSPGEPATLSCPASQSVSSGYLGWYQQKPGQAPPLLTYGASSRATGIPDRF 63
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Best Local Similarity 84.8%; Pred. No. 4.54e-37;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 87, Application PC/TUS9508743
GENEPAL INFOPMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTHALIZING MONOCLONAL ANTIBRODIES
  APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS
HUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-PC-1990
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP 1990
PRIOR APPLICATION NAMBER: US 07/310,252
FILING DATE: 18-PEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 18-PEB-1989
APPLICATION NUMBER: US 07/310,252
FILING DATE: 18-PEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-PEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-PEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-PEB-1989
APPLICATION NUMBER: US 07/290,975
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 SGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108
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                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTEP: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 87, Application PC/TUS9508743.
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JENCE 108 AA; 11590 MW; 54079 CN;
                                                                         STANDARD:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                             Palo Alto
California
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94301
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PCT-US95-08743-87
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                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LTQSPATLSLSPGERATLSCPASQSVNK-YLAWYQQKPGQAPPILIYDASNRATGIPARF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z. Gapis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.3%; Score 500; DB 7; Length 108;
larity 84.8%; Pred. No. 4.54e-37;
Conservative 5, Mismatches 9; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 SGSGSGIDFILIISRLEPEDFAVYYCQQYGSLGRIFGQGIKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SGSGSGTDFTLLISNLEPEDFAVYSCQQRSDWV-TFGGGTKVEIK 105
                                                                                                                                                                                                      SOFTWARE: Patentin Palease #1.0, Version #1.25
CUPPENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION WOMBER: US/08/474,040
FILING DATE: 07-5UN-1995
CLASSIFCATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą
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                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOW APPLICATION DATA:
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NATA:
APPLICATION NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                         COMPUTER PEADABLE FORM : MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POS/MS-POS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
JENCE 108 AA; 11590 MW; 64079 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CO, Man Sung
SCHNEIDER, William P
LANDOLFI, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 86, Application US/08487200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,223
REFERENCE/COCKET NUMBER: 119
TELECOMMUNICATION INFORMATION: (415) 326-2400
TELEPRAS: (415) 326-242
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUEEN, Cary L.
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les 89; Conserv
                                                                                                                        94301
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US-08-487-200-86
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APPLICANT:
                                                                                                     COUNTRY
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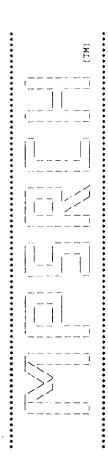
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Query Match

80.5%; Score 594; DB 13; Length 107;

Best Local Similarity 83.0%; Pred. No. 1.32e-36;

Matches 88; Conservative 8; Mismatches 8; Indels 2; Gaps
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
COMPUTER READABLE FORM:
COMPUTER: 100 FORM:
COMPUTER: 
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Search completed: Tue Feb 24 07:46:22 1998 Job time : 21 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intellicemetics, Inc

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

216.418 Million cell updates/sec Tue Feb 24 07:20:07 1998; MasPar time 6:74 Seconds

Tabular output not generated.

(1-105) from #S98844215.pep 738 >US-08-844-215-9 Description: Perfect Score:

1 AELIQSPATLSLSPGERATL.....rcggrsdwytfgggtkveik 105 Sednence:

PAM 150 Scoring table: 111726 seqs, 13889129 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq30 Database:

l:partl 2.part2 3.part3 4.part4 5.part5 6.part5 7:part7
8.part8 9.part9 10.part10 11.part11 12.part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part10 20:part20 21:part10 19:part10 20:part20 21:part20
Mean 30.157; Variance 177.084; scale 0.170 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	E C	dI	Description	Pred. No
-	549	87.9	349	5	R12128	181 IqG aberrant ligh	1.11e-36
2	649		401	(1	C	F 1 of 193 light	۲,
٣	649		414	7	5	1 Ing aberrant 11	1 116-36
4	649	87 9	414	7	P13111	aberrant li	1.116-36
S	626	84.8	115	۲-	R38648	-kappa fradm	4.826-35
9	526		115	11	R62928	n V-kappa	4.82e-35
7	626	8. ¥ è	120	ე;	W03946	DNA fragment wk65.3,	4.820.35
6 0	620		115	7	**	ದ	1 296-34
6	620		115	11	~	n V-kann	1 296-34
10	620	84.0	115	20	W03947		
11	616		109	10	R54275	Anti-HIV gp41 immunog	
12	616		109	19	W01320	\rightarrow	4
13	611		109	10	\sim	chain of Amb	. 61
14	608	82 4	111	5	W01322	VL of Fab, GL 41 1, b	γ-4
15	608	82.4	111	10	R54277	HIV qp41 immun	۲.
15	909		107	22	W08949	light ch	27
17	909	82.1	107	10	P54311	i mi	-
18	909		107	19	W01269	of H	1.27e-33
10	505	A2 0	1 ∞ 0	<u>.</u>	P54307	20.1	1.500-33
20	503	82.0	108	o	W01265	H JO	1 500-33

349 AA;

Sequence

76e- 44e- 44c- 99e-	.04e-3 .04e-3 .04e-3 .04e-3	.480- .930- .930- .930- .930-	00000000000000000000000000000000000000
n lambda liqh Vk-F105 W. rearranged W. 5-JK2. a liqht chain	gion of HIV neur HIV gpl20 immuno gion of HIV neur HIV gpl20 immuno HIV gpl20 immuno	HSV glycoprotein F bi Kappa light chain var VL region of HIV neut Anti-pseudomonas aeru Anti-P. aeruginosa st Human anti-IP ARV HVV	alled V. region 1. HIV gpl20 immun 1. lung tumour ant. 2R Ab L chain V rr At chain variable nt chain variable nt chain variable
R388593 R38673 R36648 C09946	2327337		MARKANA WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLISS WILLIS WILLIS WILLIS WILLISS WILLIS WILLIS WILLIS WILLISS WILLISS WILLISS WILI
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ALIGNMENTS

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Example 5, Fig 16, 104pp; English.

This sequence is deduced from the cDNA clone 489-Vk15 and includes the amino acid sequence beyond the first scop codon. The clone is incomplete, starting from the G of the Arg initiator colon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated antibodies were found to produce hadner antibodies. These heavier antibodies were found to have higher antibodies. These heavier fust a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are see also Q11879 and Q11880.
                                                                                                                                                                                                                                                                                                                                                                                                                       Oligomeric immunoglobulin(s) with high avidity for antiqen(s) formed by duplicating esp. variable region of light chain of lqG
                                          01-AUG-1991 (first entry)
181 19G aberrath light chain with duplicated variable region.
immunoglobulin G: light chain; variable region; duplication;
passive immunity; group B streptococci.
                                                                                                                        Location/Qualifiers
             R12128 standard; Protein; 349 AA.
                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIB.
Shuford WW, Harris LJ, Raff HV;
                                                                                                                                                                                                                  131..243
                                                                                                                                                                 Region 131..243
/label= variable region
                                                                                                                                                                                                                                                                               constant region
                                                                                                                                                    /label= leader peptide
Pegion 18 130
                                                                                                                                                                                                                                                                                                                           07-NOV-1989; US-432700.
                                                                                                                                                                                                                                                                                                                                                                                         WFI; 91-163947/22.
N-PSDB; Q11878.
                                                                                                                                                                                                                                                /note= "L'V 2"
                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                            W09106305-A.
                                                                                                                                                                                                                                                                                                              16-MAY-1991.
                                                                                                                                                                                                                                                                               /label=
                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                  Region
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RESULT
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1;
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Pred. No. 1.11e-36;
3; Mismatches 5; Indels 3; Gaps 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 ltgspatlslspgeratlscrasgsvgsylawyggkpggaprpliydasnratgiparfs 289
                                                                       24 ltqspatlslspgeratlscrasqsvgsylawyqqkpgqaprpliydasnratgiparfs 83
                                                                                                       3 LTQSPATLSLSPGERATLSCRASQSVNKYLAWYQQKPGQAPRLLIYDASNRATGIPARFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LTQSPATLSLSPGERATLSCRASQSVNKYLAWYQQKPGQAPRLLIYDASNRATGIPARFS 52
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is derived from the nucleotide sequence encoding the light chain variable region. The "x" residues represent nonsense codons. The coding sequence has been translated in all 3 reading frames (see also R12130 and R12131). The L'V region is duplicated in so-called "aberrant" light chains (see Q11878), conferring increased avidity on antibodies comprising such aberrant chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligomeric immunoglobulin(s) with high avidity for antigen(s) - formed by duplicating esp. variable region of light chain of IgG
                                   3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 19G aberrant light chain with duplicated variable region. immunoglobulin G; light chain; variable region; duplication; passive immunity; group B streptococci.
                                                                                                                                                                                                                                                                                 01-A00-1991 (first entry)
ORF 1 of 1gG light chain variable region clone.
immunoglobulin G; light chain; variable region; duplication;
passive immunity; group B streptococci.
Score 649; DB 2; Length 349; Pred. No. 1.11e-36; 3; Mismatches 5; Indels
                                                                                                                                           84 gsgsgtdftltisslepedfavyycghrdnwppgatfgggtkveik 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 gsgsgtdftltisslepedfavyycqhrdnwppgatfgggtkveik 335
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                                                                                                                                                                             63 GSGSGIDFILIISNLEPEDFAVYYCOORSDW---VTFGGGIKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "last 3 amino acids of leader and variable
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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R13018 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                   R12129 standard; Protein; 401 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match
Local Similarity 89.6%;
nes 95; Conservative
Query Match
Best Local Similarity 89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (first entry)
                                   95; Conservative
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/label- variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-1990; U06426.
                                                                                                                                                                                                                                                                                                                                                                                                                /label- L'V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 91-163947/22.
N-PSDB; 011879.
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9106305-A.
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                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  region"
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                                                                                                                                                                                                                                                                    R12129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R13018;
                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                    RESULT
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This sequence is deduced from the cDNA clone 4B9-Vk15 and includes the amino acid sequence beyond the first stop codon ("x" in the sequence repersents a nonsense codon). The clone is incomplete, starting from the G of the ATG initiator codon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated variable region, to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 ltqspatlslspgeratlscrasqsvgsylawyqqkpgqaprpliydasnratgiparfs 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LIQSPATLSLSPGERATLS??RASQSVNKYLAWYQQKPSQAPRILITYDASNPATGIPARFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                 Oligomeric immunoglobulin(s) with high avidity for antigen(s) - formed by duplicating esp. variable region of light chain of \lg G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (first entry)
1B1 IgG aberrant light chain with duplicated variable region.
nmwunoglobulin G: light chain; variable region; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 649; DB 2; Length 414; Pred. No. 1.11e-36; 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 gsgsgtdftltisslepedfavyycghrdnwppgatfgggtkveik 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunity; group B streptococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                            Example 5; Fig 16; lu4pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R13111 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIB.
Shuford WW, Harris LJ, Raff HV;
WPI; 91-163947/22.
N-PSDB; Q11878.
                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIB.
Shuford WW, Harris LJ, Raff HV,
WPI: 91-163947/22.
N-PSDB; Q11878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 89.68; es 95; Consermed
                                                                                                                                                                                                                                                                                                                                                                                                                                   the placenta.
See also Q11879 and Q11880.
                                                           244..345
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                131..243
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                           /label= variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= variable region
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                                                                          constant region
                                                                                                                                    US-432700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1989; US-432700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                         06-NOV-1990; U06426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1990; U06426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "L'V 2"
/note= "L'V 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "L'V 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                      07-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR-1993
                                                                                                         .6-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                             label-
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                                               /note=
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US-08-844-215-9.rag

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3 LTQSPATLSLSPGEPATLSGPASGSVNKYLAWYQQKPGQAPPLLTYDASNPATGIPARFS 62
                                                                                                                                                                                                                                                                                                 10-NOV-1994.
25-APR-1994; UO4580.
26-APR-1993; US-053131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94-358263/44.
                                                                                                                                                                                                                                                   chimeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q78852
                                                                                                                                                                                                                                                                  Homo sapiens.
WO9425585-A.
                                                                                                                                                                         07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kay RM,
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                                                                                                                           RESULT
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                                                              This sequence is deduced from the CDNA clone 4M9-Vkl% and includes the amino acid sequence beyond the first stop codon ("x" in the sequence represents a nonsense codon). The clone is incomplete, starting from the G of the ATG initiator codon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated variable region, to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 ltgspatlslspgeratlscrasgsvssylawygdypgaprlllydasnratgiparfs 83
                                                                                                                                                                                                                                                                                                                                                                                        24 ltqspatlslspgeratlscrasqsvgsylawyqqkpqqaprpliydasnratgiparfs 83
                                                                                                                                                                                                                                                                                                                                                                                                                       3 LTQSPATLSLSPGERATLSCPASQSVNKYLAWYQQKPGQAPRLLIYDASNPATGIPARFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 21: Fig 41: 196pp; English.

The V-kappa specific oligonucleotide 050327 was used to probe a human placental queuolic DNA library offound into lambdaEMBL3/sp6/77 bund fraqments containing V-kappa segments from positive phage clones were subcloned into plasmid vectors. Variable gene segments from the resulting clones were sequenced and functional clones were sequenced on the basis of open reading frames, intact donor and acceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were sequences obtained from four different plasmid clones were sequences obtained from four different plasmid clones were sequences obtained the amino acid sequences of the V-kappa regions
                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
'Oligomeric immunoglobulin's) with high avidity for antiqun(s) formed by duplicating esp. variable region of light chain of IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic non-human animals contq. immunoglobulin heavy chain trans gene - used to produce useful antibodies by isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.NOV-1993 (first entry)
Human V-Rappa fragment encoded by clone vk65.3.
Immunoglobulin: light chain variable region; minilocus; isotype switching; unrearranged functional Vk gene segment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 84.8%; Score 525; DB 7; Length 115; Local Similarity 95 5%; Pred No. 4.82e-35; es 87; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                      Length 414;
                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 gsgsgtdftltisslepedfavyycqhrdnwppgatfgggtkveik 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 GSGSGTDFTLTISNLEPEDFAVYYCQQRSDW---VTFGGGTKVEIK 105
                                                                                                                                                                                                                                                                                                                  Score 649; DB 2; I
Pred. No. 1.11e-36;
3; Mismatches 5;
                                                   Example 5; Fig 16; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R38648 standard; Protein; 115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         light chain transgene.
                                                                                                                                                                                                                                               the placenta.
See also Q11879 and Q11880.
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.6%;
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENP-) GENPHARM INT INC.
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Sequence 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-1992; U10983,
17-DEC-1991; US-810279,
18-MAR-1992; US-853408,
23-JUN-1992; US-904068
                                                                                                                                                                                                                                                                                   414 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93-214169/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sabiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 - JUN - 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     switching
                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LIQSPAILSLSPGERAILSCRASGSVNKYLAWYQQKPGGAPKLLIYDASNKAIG1PARFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 626; DB 11; Length 115;
Pred. No. 4.82e-35;
3; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-1997 (first entry)
DNA fragment vk65.3, variable kappa chain protein product.
Variable: kappa chain; gene segment; human; DNA fragment; vk65.3; unrearranged; light chain; minilocus; transgene; transgenic; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heterologous antibody production. The deduced amino acid
aggeneroes of the V-Kappa coding regions are given in E62429 E62931.
Sequence 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increased affinity
Disclosure: Fig. 41: 295pp; English.
Disclosure: Fig. 41: 295pp; English.
Disclosure: Fig. 41: 295pp; English.
Disclosure: Fig. 41: 295pc; English.
OTRES-278pc; respectively) cach centain a V-kappa gene segment organized to form a complete human light chain minilocus that can be used to form a complete human light chain minilocus transgene for expression in a nonhuman transsenic animal for transgene for expression in a nonhuman transcenic animal for transgene for expression in a nonhuman transcenic animal for transgene for expression in a nonhuman transcenic animal for transgene for expression in a nonhuman transcenic animal for transgene for expression in a nonhuman transfer animal for transfer and the form of the first 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for binding a pre-determined human antigen with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human V-kappa vk65.3 región.
Transgenic mouse, transgenic animal; antibody engineering;
variable region; light chain; minilocus transgene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production; heterologous; antibody, gamma; immunoglobulin.
84 gsgsgtdftltisslepedfavyycggrsnw 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 gsgsgtdftltisslepedfavyycqqrsnw 114
                                                                                                                                      63 GSGSGIDFILIISNLEPEDFAVYYCQQPSDW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GSGSGIDFILIISNLEPEDFAVYYCQQRSDW 93
                                                                                                                                                                                                                                                                                                                                                                                    л 6
R62928 standard; Protein; 115 AA.
R62928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W03946 standard; Protein; 120 AA.
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Best Local Similarity 95.6%;
Matches 87; Conservative
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US545806-A.
US545806-A.
29-AuG-1990, 574748.
29-AuG-1990, US-574748.
31-AuG-1990, US-574748.
17-DEC-1991, US-810.
17-DEC-1991, US-810.
18-MAR-1992, US-810.
16-DEC-1992, US-810.
16-DEC-1992, US-9904068.
16-DEC-1992, US-9904068.
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18-NOV-1993; US-155301.
03-DEC-1993; US-161739.
10-DEC-1993; US-165599.
09-MAR-1994; US-209741.
(GENP-) GENPHARM INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 ltgspatlslspgeratlscrasgsvssylawyggkpggaprlliydasnratgiparfs 88
                                                                                                                                                                                                                                                                                                                                                                                                                                3 LTQSPATLSLSPGERATLSGRASGSVNKYLAWYQQKPGQAPPLLIYDASNRATGIPARFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The V-kappa specific oligonucleotide Q50327 was used to probe a human placental genomic DNA library cloned into lambdaEmBla18/F6/T7.

DNA fragments containing V-kappa segments from positive phage clones were subcloned into plasmid vectors. Variable gene segments from the resulting clones were sequenced and functional clones were selected on the basis of open reading frames, intact donor and acceptor splice sites and intact recombination sequences. The agenences obtained from four different plasmid clones were designated p65.3, p65.8 and p65.15 (see Q4422-Q4422).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                       Saps
                                                                                       Example 21: Fig 41: 94pp; English.

The present sequence is the protein product of the variable kappa chain gene segment containing human DNA fragment, vk65.3, which was co-injected along with the human DNA fragments vk65 5, vk65 8 and vk65.15 into half day mouse embryo pronuclei, to generate an unrearranged light chain minilocus transgene. The resulting transgenic mice can be used for the production of heterologous (i.e. human) antibodies against specific antigens, this comprises immunishing a mouse with a preselected antigen and collecting antigen binding heterologous human gamma immunoglobulins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic non-human animals contg. immunoglobulin heavy chain trans gene - used to produce useful antibodies by isotype
                                                    Prodn. of heterologous human immunoglobulin(s) - by immunising
                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin; líght chain variable region; minilocus;
isotype switching; unrearranged functional Vk gene segment;
human light chain transgene.
                                                                                                                                                                                                                                                                                                                            Ouery Match 84.8%; Score 626; DB 20; Length 120; Best Local Similarity 95 6%; Pred. No. 4 82e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 520; DB 7; Length 115; Pred. No. 1.29e-34;
                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4 826-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human V-kappa fragment encoded by clone vk65.5.

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 gsgsgtdftltisslepedfavyycqqrsnw 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GSGSGTDFTLTISNLEPEDFAVYYCQQRSDW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 21; Fig 42; 196pp; English.
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838649 standard; Protein; 115 AA
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Best Local Similarity 93.4%;
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Conservative
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17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
23-JUN-1992; US-904068.
Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93-214169/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 AA;
                    96-383736/38.
                                                                                                                                                                                                                                                                                          120 AA;
                                                                           transgenic mice
                                    N-PSDB; T37180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 93-214109
N-PSDB; Q44223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                   87;
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                                                                                                                                                                                                                                                                                            Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R38649;
                                                                                                                                                                                                                                                                                                                                                                   Matches
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24 ltqspatls1spqerat1scrasqqvssylawyqqkpqqapr1l1ydasnratgiparfs 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LTQSPATLSLSPGERATLSGRASQSVNKYLAWYQQKPGQAPPLLTYPASNRATG1PAPFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 620: DB 11; Length 115;
Pred. No. 1.29e-34;
5, Mismatches 1, Indels 0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA fragment vk65.5, variāble kappa chain protein product. Variāble; kappa chāin; gene segment; human; DNA fragment; vk65.5; unrearranged; light chain; minilocus; transgene; transgenic; mouse; production; heterologous; antibody; gamma; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig. 42, 296Fg. English Muman DNA fragments vk65 3, vk65.8 and vk65.15 (given in Q78822-QN885), respectively) each contain a V-kappa gene segment that can be used to form a complete human light chain minilocus transgene for expression in a nonhuman transgene animal for heterologous antibody production. The deduced amino acid sequences of the V-kappa coding regions are given in P62:28*-P62931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fransgenic non-human animals producing heterologous or chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - for binding a pre-determined human antigen with
                                                                                                                                                                                                                                                                                                         Transgenic mouse; transgenic animal; antibody engineering; variable region; light chain; minilocus transgene; chimeric antibody.
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                                T
R62929 standard; Protein; 115 AA.
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                                                                                                                                                                                                                                           07-JUN-1995 (first entry)
Human V-kappa vk65.5 region.
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Local Similarity 93.48;
nes 85, Conservative
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29-AUG-1990; US-574748.
31-AUG-1990; US-575962.
17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1993; US-161739.
10-DEC-1993; US-165699.
09-MAP-1994; US-209741.
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16-DEC-1992; US-990860
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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109 AA;

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60 RFSGSGSGTDFILIISNLEPEDFAVYYCQQRSDWVTFGGGTKVEIK 105
Seguence
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Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification using primers specific for heavy and light chain amplification products were inserted into a dicistronic vector to produce a library of fragments. E. coli XLI Blue cells were transformed with the library Filamentous phage were produced which expressed the MAb regions on their surface. Panning with gp120 and gp41 resulted in the recovery of immunoractive clones. The light chain VL region sequence R54275 neutralises HIVI
                                                                                                                                                                                                                                                          24 ltqspatlslspgeratlscrasqgvssylawyqqkpqqaprlliydasnratgiparfs 83
                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1994 (first entry)
Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.
Human immunodeficiency virus: HIVI; glycoprotein gp41; epitope:
neutralisation; monoclonal antibody; light chain; variable region;
framework region; complementarity determining region.
                                              Example 21: Fig 42; 94pp; English.

The present sequence is the protein product of the variable kappa chain gene segment containing human DNA fragment, vk65.5, which was co-injected along with the human DNA fragments vk65.3, vk65.8 and vk65.15 into half day mouse embryo pronuclei, to generate an unrearranged light chain minilocus transgene. The resulting transgenic mice can be used for the production of heterologous (i.e. human) antibodies against specific antigens, this comprises immunising a mouse with a preselected antigen and collecting antigen binding heterologous human gamma jamunoglobulins.
                        Prodn. of heterologous human immunoglobulin(s) - by immunising transgenic mice
                                                                                                                                                                                                     84.0%; Score 620, DB 20, Length 115, 93.4%; Pred. No. 1.29e-34; vative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           84 gsgpgtdftltisslepedfavyycqqrsnw 114
                                                                                                                                                                                                                                                                                                                                   63 GSGSGTDFTLTISNLEPEDFAVYYCQQRSDW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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R54275 standard; protein; 109 AA
                                                                                                                                                                                                                                Conservative
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(SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                                                                  Best Local Similarity
Matches 85; Conserv
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                                                                                                                                                                                115 AA;
WPI: 96-383736/38
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             N-PSDB; T37181.
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Monoclonal antibody binding to VI/V2 loop of HIV gpl20 - used in passive immuno: therapy and detection of HIV infection.

Example 3: Fig 19: 366pp. English.

The sequences given in W01320-24 represent the light chain variable regions (VH) of a series of antibody fragments (FAb's) which are immunoreactive with HIV glycoprotein gp41. This sequence represents the sequence of the clone, DL 4119. These sequences represent light chains which bind to the heavy light chain clones given in W01315-19. A monoclonal antibody containing one of these Fab sequences may have the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/ml.

The MAD may be used for determining immunocompetence of a human anti-HIV sequence. 109 AA:
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                                                                                                                                 2 aeltgspgtlslspgervivscrasgsvssnylawyggkpgaprlliygasnratgipd 61
                                                                                                                                                                   1 AELIQSPATLSLSPGERATLSCRASQSVN-KYLAWYQQKPGQAPRLLIYDASNRATGIPA 59
Score 616; DB 10; Length 109;
Pred. No. 2.48e-34;
5; Mismatches 10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-1997 (first entry)
VL of Fab, DL 41 19, binds to HIV gp41.
Heavy chain, light chain; variable region; VH; monoclonal antibody;
HAB; HIV, human immunodeficency virus, glycoprotein, gp120; clore;
virus infectivity assay; precursor gp16; immunocompetence; human;
anti-HIV antibody; detection; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches 10; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.5%; Score 616; DB 19; Length 109; Best Local Similarity 84 9%; Prod No 2 48e-34; Matches 90; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                              60 RFSGSGGTDFTLTISNLEPEDFAVYYCQQRSDWVFGGGIKVEIK 105
                                                                                                                                                                                                                                                                  62 rísgsgsgtdftltisrlepedfavyycggygssgtfgggtkveik 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 rfsgsgsgtdftltisrlepedfavyycqqygssgtfgqgtkveik 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burton DR, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         W01320 standard, Protein, 109 AA.
Query Match
Best Local Similarity 84.98;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCRI ) SCRIPPS RES INST
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18-JUL-1994; US-275852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24..35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W01320;
29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= FR2
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Example: Page 27.28; 36pp; English.

Blood samples were collected from patients immunised with allergens including ragweed (Ambrosia elator) extracts. The dominant allergen in short ragweed (Ambrosia elator) extracts. The dominant allergen in short ragweed is Amb al. Purified PBLs were immortalised and the resultant clones were screened using Amb a l protein. A single cell sublone AL 16-5.2, secreting Amb al-specific 1964, kappa antibody was selected. Total c RNA was prepd. from the AL 16-5.2 cells and first strand cDNA was pred. using oligo dT primers. When the first strand cDNA was used as the template, and the 5' and 3' kappa light chain primers (06654) c 066541) were used in PCR and amplified band of the expected size was noted. The DNA sequence of several subclones confg. this amplified C sequence are shown in 066538 and R56286. Comparison of the deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ltqspqtlslspgeratlscrasqtvssnylawyqhkpgqaprlliyatsirssgipdrf 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LTQSPATLSLSPGEPATLSCPASQSVN-KYLAWYQQKPGQAPPILIYDASNPATGIPARF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 4, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VI of Fab, GL 41 1, binds to HIV gp41.

Wheavy chain, light chain, variable region, VH, monoclonal antibody mash HIV; human immunodeficiency virus; glycoprotein; gp120; clone; virus infectivity assay; precursor gp160; immunocompetence; human; anti-HIV antibody; detection; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL 16-5.2 L-chain sequence with human V region sequences indicates that it is a member of the human VK III subgp.
                                                                                                                                                                                                                                                                                                 Compsn. contg. allergen specific IgA for treating mucosal tissue and conjugates of allergen specific Ig with polymer, for treating IgE mediated allergies and for isolation of specific
                                                                     Light chain of Amb al-spécific 1964 antibody.
Allergen-specific immuoglobulin A; 19A; AL 15-5.2; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 SGSGSGTDFTLITISNLEPEDFAVYYCQQ-R-SDWVTFGGGTKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 tgsgsgtdftltisrlepedfavyycqqfrnsqw-tfgqgtkveik 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 611, DB 10, I
Pred No. 5 61e-34;
10, Mismatches 5,
                                                                                                             allergen Amb a 1; ragweed; Ambrosia elator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W01322 standard; Protein; 111 AA.
               R56286 standard; Protein; 109 AA
                                                                                                                                                                                                                           TANO-) TANOX BIOSYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 82 1%;
Matches 87; Conservative
                                                     04-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                 20.DEC-1993; U12501.
21-DEC-1992; US-994126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA;
                                                                                                                                                                                                                                                                                   N-PSDB; Q66538.
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/label- CDR2
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                                                                                                                                                 WO9414475-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- FR1
                                                                                                                                                                     07-JUL-1994
                                                                                                                                                                                                                                                                                                                                                             allergens
                                                                                                                                                                                                                                             Chang TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                 R56286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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RESULT
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Monoclonal antibody binding to VI/V2 loop of HIV gpl20 - used in passive immuno:therapy and detection of HIV infection.

PT Ranoclonal antibody binding to VI/V2 loop of HIV gpl20 - used in passive immuno:therapy and detection of HIV infection.

PT Ranoclonal antibody and detection of HIV infection.

The sequences given in W01320-24 represent the light chain variable communoreactive with HIV giveoprotein gp41. This sequence represents the sequence of the clone, GL 41. These sequences represent light chains which bind to the heavy light chain clones given in W01315-19. A monoclonal antibody containing one of these Fab sequences may have the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/ml.

The MAD may be used for determining immunocompetence of a human anti-HIV antibody and in the detection of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 aeltgspgtlslspgeratlscrasgsvsngylawyggkpggapriliygastratdipd 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ABLTOSPATLSLSPGERATLSCRASOSVNK-YLAWYOOKPGOAPRLLIYDASNRAIGIPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
82.4%; Score 608; DB 19; Length 111;
Best Local Similarity 83.0%; Pred. No. 9.16e-34;
Matches 88; Conservative 7; Mismatches 10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-HIV gp41 immunoglobúíin light chain V region clone GL 41 1.
Human immunodeficiency virus; H1V1; glycuprotein gp41, epitupe.
neutralisation; monoclonal antibody; light chain; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbas CF, Burton DR, Lerner RA; WPI; 94-135516/16. Webs. 94-135516/16. Web human monoclonal antibodies neutralising HIV - react with gp120 or gp41 and nucleic acid encoding them, useful for in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 rfsgssgadftlaisrlepedfavyycqqyagshtfgqgtkleik 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 RFSGSGSGTDFTLTISNLEPEDFAVYCQQRSDWVFGGGTKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       framework region; complementarity determining region.
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                                                                                                                                                    (SCRI ) SCRIPPS RES INST.
Barbas CF, Burton DR, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burton DR, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 15
P54277 standard; protein; 111 AA
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30-SEP-1992; US-954148.
(SCRI ) SCRIPPS RES INST.
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                                               98 111
                                                                                                                                     18-JUL-1994; US-276852
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                90..97
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                                                                                                                     -JUL-1995; U08743
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                               /label= CDR3
                                                                                      W09602273-A1.
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14-APR-1994.
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/label= FR3
                                                                 /label = FR4
                                                                                                    -FEB-1996
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PT *Or in vitro diagnosis and for passive immuno-therapy
PS Claim 11: Page 217: 248pp: Enalish.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XLI
CC Rlue cells were transformed with the library. Flamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC vith gpl20 and gp41 resulted in the recovery of immunoreactive
CC vith gpl20 and gp41 resulted in the recovery of immunoreactive
CC op41.
SQ Sequence 111 AA:
CC GP41.
SQ Sequence 111 AA:
CC GP41.
SQ Sequence 111 AA:
CC GP41.
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protein - protein database search, using Smith-Waterman algorithm Tue Feb 24 07:17:10 1998; MasPar time 4.91 Seconds 462.245 Million cell updates/sec MPsrch_pp Run on:

>US-08-844-215-8 (1-107) from US08844215.pep 752 1 AELTQSPGTLSLSPGERATI. Tabular output not generated Description: Perfect Score:

PAM 150 Gap 11 Scoring table: Sequence:

....CQLYGNSRWTFGQGTKVEIK 107

59021 seqs, 21210388 residues Searched.

Listing first 45 summaries Post-processing: Minimum Match OA

lipart1 2:part2 3:part3 4:part4 5:part5 5:part5 7:part7 8:part8 9:part9 10:part10 11:part11 swiss-prot34 Database:

Mean 40.565, Variance 71 085; scale 0 571 Statistics. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď								
Result No.	Score	Query Match	Length	DB	ID	Des	Description	uo		Pred. No.
	712	93.4	129		KV3M_HUMAN	121	KAPPA	CHAIN	PRECUR	7.406-136
2	701	92.0	129	ı,	KV3L_HUMAN	13	KAPPA	CHAIN	PRECUR	796-13
3	585	σ	100	ur.	KV3R HUMAN	5	KAPPA	CHAIN	V-JII	556-12
4	~	6	100	v.	KV3E_HUMAN	16	KAPPA	CHAIN	V-III	ις.
S	674	S S S	100	ĸ.	KV 3 D_HITMAN	ŗ.	KAPPA	CHAIN	III-A	-12
9	671	æ	108	L C)	KV3A_HUMAN	SI	KAPPA	CHAIN	V-III	2.89e-126
7		9	109	'n	KV3G_HUMAN	IG	KAPPA	CHAIN	V-III	3.13e-123
8	637	83 5	129	2	KV3H_HTMAN	ŗ	KAPPA	CHAIN	dijidd	4
6	\sim	Ξ.	100	Ŋ	KV3C_HUMAN	IG	KAPPA	CHAIN	PRECUR	.55e-
10		٠.	129	u.	KV3K_HUMAN	5	KAPPA	THAIN	diijadd	0
11	-	σ	100	ur.	KV3F_HUMAN	IG	KAPPA	CHAIN	V-III	ď.
12	10	۳.	115	S	KV3I_HUMAN	15	KAPPA	CHAIN	PRECUR	.726-
13	558	73.2	116	Ω.	KV3J_HUMAN	51	KAPPA	CHAIN	PRECUR	4.990-100
14	~		108	S	KV1M_HUMAN	DI	KAPPA	CHAIN	V-I RE	3.42e-95
15	\sim	6	108	S	KV1R_HUMAN	υI	KAPPA	CHAIN	V-I RE	4 010-93
16	\sim	58.8	134	S	KV4C_HUMAN	51	KAPPA	CHAIN	PRECUR	3.32e-92
17	\sim	80	108	v.	KV1P_HTMAN	ÐΙ	KAPPA	CHAIN	V-I PE	· 40-
18	_	•	107	2	KV1D_HUMAN	91	KAPPA	CHAIN	V-I RE	á
19		æ	108	Ç,	KV1K_HUMAN	ŮΙ	KAPPA	CHAIN	V-I PE	7 910-91
20	_	8	108	S	KV1H_HUMAN	16	KAPPA	CHAIN	V-I RE	
21		67.7	108	Ľ,	KV1F_HUMAN	15	KAPPA	CHAIN	V-I PE	2.278.90
C1	- 4	67.2	108	S	KVI N_HUMAN	IG	KAPPA	CHAIN	V-I RE	1.88e-89

.3%e-8 .13e-8	8-950. 8-900. 8-900. 8-900.	. 77e-8 . 65e-8 . 98e-8	.35e-8 .35c.8 .85e-8	535e	. 146-8 . 306-8 . 316-8	236-7 236-7 236-7
V-I RE V-I RE	V-I RE PRECUR V-I RE		((2,)	V-I PE V-III	V-1 RE PRECUR V-III V-I RE	V·V RE V-III PRECUR
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n. n. n. n. i	KAPPA KAPPA KAPPA KAPPA	KAPPA KAPPA KAPPA	KAPPA KAPPA KAPPA	KAPPA KAPPA KAPPA KAPPA	KAPPA KAPPA KAPPA KAPPA	APP
100	51 51	16 15	51 51	919	22 21 21	1001
Y_HUMA V_HUMA A_HUMA	KVIL_HUMAN KVIW_HUMAN KVIO_HUMAN	KV1E_HUMAN KV1G_HUMAN KV1X_HUMAN	KV1P_HUMAN KV2F_HUMAN KV10_HUMAN	KV1T_HUMAN KV3O_MOUSE KV1A_HUMAN	KV15_HUMAN KV1J_HUMAN KV3G_MOUSE KV1C_HUMAN	KV37_MOUSE KV30_MOUSE KV31_MOUSE
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SULT SULP SULP SULP SULP SULP SULP SULP SULP	ALIGNMENTS	1 3M.HUMAN STANDARD; PKT; 129 AA. 8136:	01-002) 01-002-1990 (REL 16, CREATED) 01-002-1806 (REL 16, 1821 CELIFENCE TRONATE)		KAPPA CHAIN PPECUPSOP V-III PEGION (HIC).	HOMO SAPIENS (HUMAN).	EUKARYUTA: METAZUA; UHURDATA: VERTEBRATA: TETRARUDA; MAMMALIA; EUTHERTA: DRIMATES		71307.	KIPPS T.J. TOMBAVE F. CHEN P.P., CARSON B.A.;	EAF. MEU.	AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCY		PIR; PL0021; K3HUHI.		GLORULIN V PE	L I 20	770	44 44	56 70 FRAMEWORK 2.	71 77 COMPLEMENT	50T 82	110 118	119 129 JK1	43	NLTER 129 AA: 14070 MW; DD00C369 CRC32,	Query Match 93.4%; Score 712; DB 5; Length 129;	94.3%; Pred. No. 7.40e-136	ative	24 ltgspgtlslspgeratlscrasgsvsssylawyggkpggaprlliygassratgipdif 83	3 LTGSPGTLSLSPGEPATLSCPASGSVSSNYLAWYQGPFSQAPFLLIYGASSRATGIFDRF 62	84 sgsgsgidfiliisrlepxdfavyyoggygsspwtfgggikveik 128	
μ ψ ±.		V3M_	01-NOV-199	01-NOV-19	IG KAPPA	HOMO SAPIN	EUNARY (TA)	[1]	MEDLINE;	KIPPS T. H	J. EAF. MI		LEUKE	PIR; PLOO?	HSSP; POI	IMMUNOGLO	SIGNAL	CHALN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DISULFID	SEQUENCE	ery Match	it Local S.	iches 9(24 1tqs			

63 SGSGSGTDFTLTISPLEPEDFAVYYCQLYGNSPWTFSQGTKVEIK 107 ä

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                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 88171307.
KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.:
J. EXP. MED. 167.840-852(1989).
--- DISEASE, THE PROTEIN IS ONE OF THE SUPPRACE IMMUNOSLORULIN MAUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHPONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANDREWS D.W., CAPRA J.D.;
BIOCHEMISTRY 20:5816-5822(1981).
-!- THIS CHAIN WAS ISOLATED FPOM AN IGM WITH ANTI-GAMMA GLOBFILIN
                                                                                                                                                                                                                                                IG KAPPA CHAIN V-III REGION (HAH). FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHOPDATA; VERTERRATA; TETRAPODA: MAMMALIA;
EUTHERIA: PRIMATES.
                                                                            EUKARYOTA; METAZOA; CHOPDATA; VEPTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING 1
                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING 2
                                                                                                                                                                                                                                                                                                                                                                                            Score 701; DB 5; Length 129;
Pred. No. 2.79e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 sgsgsgtdftltisrlepedfavyycqqygtsprtfgggtkveik 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14073 MW; 2C44B85E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA: 11775 MW: 00R5DD5D CPC32;
                     01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG AAPPA CHAIN PRECURSOR V-III REGION (HAH).
HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                      FPAMEWORK 2
                                                                                                                                                                                                                                                                                                                                      SEGMENT
                                                                                                                                                                                                                                                                                                              FRAMEWORK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 685;
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 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-1987 (REL 04, LAST ANNOTA IG KAPPA CHAIN V-III REGION (SIE)
                                                                                                                                                                                                                           IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                            Match 92.0%;
Local Similarity 94.3%;
es 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.68
 STANDARD;
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IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                   PIR; PL0022; K3HUHA.
HSSP; P01507; 1AAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A01892; K3HUSI.
HSSP; P01607; 1DFB.
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129 1
129 AA;
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                                                                                                                                                                                          LEUKEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVITY.
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KV3L_HUMAN
P18135;
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SEQUENCE
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                                     4 ltqspgtlslspgeratlscrasqsvssgylgwyqqkpgqaprlliygassratgipdrf 63
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               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                         ANDREWS D.W., CAPPA J.D.;
BIOCHEMISTRY 20:5816-5822(1981).
-!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
              0;
                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHORDATA: VERTERRATA: TETRAPODA: MAMMALIA:
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EURAPYOTA: METAZOA: CHOBDATA: VERTEBRATA: TETRAFODA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 685; DB 5; Length 109;
Pred. No. 1.55e-129;
              Indeis
                                                                                             64 sgsgsgtdftltisrlepddfavyycggygsspqtfgggskveik 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 SGSGSGTDFTLTISRLEPEDFAVYYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 sgsgsgtdftltisrlepedfavyycqqygslgrtfgqgtkveik 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUTER L., BARNIKOL H U., WATANABE S., HILSCHMANN N.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972).
-'- THE G REGION OF THIS CHAIN HAS THE INV (3) MARKER.
Best Local Similarity 91.4%; Fred. No. 1.55e-129; Matches 96; Conservative 6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 109 109 109 11746 MW; 7D8F5D75 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11789 MW; D03795B1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SECUENCE UPDATE)
22-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-III REGION (TI)
                                                                                                                                                                                                     21-JUL-1986 (REL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
220-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-III REGION (WOL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
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                                                                                                                                                                             109 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Query Match
Best Local Similarity 92.4.
Best Local Similarity 92.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.98;
                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              PIR; A01896; K3HUWL.
HSSP; P01607; 1DFB.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                           68
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HSSP; P01607; ZIMM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AA;
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                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE; 82046598.
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KV3D_HUMAN
P01622;
                                                                                                                                                                 LT 4
KV3E_HUMAN
P01623;
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SEQUENCE
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BENTLEY D.L.;
NATURE 307777-80(1984).
NATURE 307777-80(1984).
PIP: A01894; K3HUNG.
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Local Similarity 83.0%;
nes 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M12740; G553486; -.
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1199
129
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129 AA:
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HSSP; P01607; 1AAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 84093600.
                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 9
KV3C_HUMAN
P01621;
                                                                                                                                                                                                               KV3H_HUMAN
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NON_TER
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                                                                           4 ltgspgtlslspgeratlscrasgsvsnsflawyggkpggaprlliyvassratgipdrf 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQQRPGQAPRLLIYGASSPATGIPLRF 62
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                                      0; Gaps
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EUKARYOTA: META20A: CHOPDATA: VEPTEBRATA: TETPAPODA: MAMMALIA:
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1987 (REL. 04, CREATED)
20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-III PEGION (GOL) (PHEUMATOID FACTOR).
HOWO SAPIENS (HUMAN).
EUKAPYOTA:
EUKAPYOTA:
MAMMALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ċ
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Score 674: DB 5: Length 109;
Fred. No. 5.75c-127;
6: Mismatches 4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 88.1%; Score 671; DB 5; Length 108; Best Local Similarity 84.8%; Pred No 2.89e-126; Matches 89; Conservative 12; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEWKIRK M., CHEN P.P., CARSON D.A., POSNETI D., CAPPA J D
MOL IMMUNOL 23-239-244(1995)
                                                                                                                                                      64 sgsgadftltisrlzpedfavyycqqygsspftfgqgskleik 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 SGSGSGTDFTLTISPLEPEDFAVYYCOLYGNSRWTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11830 MW; 893DCC4A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11635 MW: 46D6B68E CPC32;
                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-III REGION (B6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMUNOGLOBULIN V REGION; RENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                        PRT: 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPT: 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RY SIMILAPITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- THIS IS A BENCE-JONES PROTEIN
PIR, A01891; K3HUB6,
HSSP; P01607; IMCP.
                                                                                                                                                                                                                                                                                                              21-JUL-1986 (REL. 01, CREATED)
Query Match
Best Local Similarity 90.5%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MILSTEIN C.;
FEBS LETT. 2:301-304(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                        STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOGLOBULIN V REGION.
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HSSP: P01607, 10FB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10FB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 85230578.
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108
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                                                                                                                                                                                                                                                                    KV3A_HUMAN
P01619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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NON_TER
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SEQUENCE FROM N.A.
MEDLINE: 86177570.
JIRIK F.P. SORGE J. FONG S., HEITZMANN J.G., CURD J.G., CHEN P.P.,
GOLDFIEN R., CARSON D.A.;
PROC. NATL. ACAP. SCJ. U.S.A. R3.2195-2199(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 mtgspatlsvspqeratlscrasgsvsnn-lawyggkpgqpprlllygastratgiparf 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LIQSPGILSLSPGEBAILSCPASQSVSSNYLAWYQQPPGQAPPLLIYGASSMAICIPCRF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 Gaps
                                                                                                                                                                                                                                                                                                                20-MAP-1987 (PEL 04, CPEATED)
01-NOV-1990 (PEL 16, LAST SEQUENCE UPDATE)
01-NOV-1990 (PEL 18, LAST SEQUENCE UPDATE)
101-NOV-1990 (PEL 18, LAST ANNOTATION UPDATE)
105 KAPPA CHAIN PRECURSOR V-III PEGION (CLL) (PHEUMATOID FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS KAPPA CHAIN V-III PEGION (CLL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKAPYOTA; METAZOA; CHOPDATA; VERTEBPATA; TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARDATA, VERTEBRATA, TETRAPODA, MAMMALIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (PEL 16, LAST ANNOTATION UPDATE)
IS KAPPA CHAIN PRECUPSOR V-III PESION (NS9) (FPASMENT).
                                                                                                      64 sąsąsątdfiltisrlepedfavyycggygssprsfągatkveik 108
                                                                                                                                                        63 SGSGSGTDFTLTISRLEPEDFAVYYCQLYGNSRWIFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 637; DB 5; Le
Pred. No. 2.45e-118;
12; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2F344868 CRC32;
                                                                                                                                                                                                                                                                    129 AA.
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BY SIMILARITY.
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                                                                                                                       IG KAPPA CHAIN V-III PEGION (IARC/BL41).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 ltqspgtls1spgesatlscrasqsvssn-lawyqqkrgqsprllirdassrangipdrf 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 611; DB 5; Length 128;
Prod No 2 716-112:
4; Mismatches 10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQPPGQAPPLIJYGASSRATGIPDPF 62
                                                                                                      1; Indels 0; Gaps
                                     IG KAPPA CHAIN V-III REGION (NG9).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                  KLOBECK H.G., MEINDL A., COMPRIATO G., SOLOMON A., ZACHAU H.G. NUCLEIC ACIDS RES. 13:6499-6513(1985).
EMBL, 200021, G33179, -.
PIR, A01899, K3HU41.
HSSP, PO1607, 3HFM.
IMMUNGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING 3. JK1 SEGMENT,
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTAPITY - DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY - DETERMINING 2.
                                                                                   Score 622; DB 5; Length 100; Pred. No. 7.55e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 sgsgsgtdftliisrlepedfavyycggystspytfgggtkleik 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 SGSGSTDFTLTISRLEPEDFAVYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                      01-07N-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN PRECURSOR V-III PEGION (IARC/BL41).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14070 MW; 318E08AF CRC32;
                                                                 100 AA; 10729 MW; 99A75223 CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV3F_HUMAN STANDARD; PRT: 109 AA. 101624; 21-701-1986 (REL. 01, CREATED) 21-301-1986 (REL. 01, LAST SEQUENCE UPDATE) 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                              68 sgsasgtdftltisrlepedfavyycqqyqnsq 100
           IMMUNOGLOBULIN V REGION; SIGNAL; HYBRIDOMA
                                                                                                                                                                        63 SGSGSGTDFTLITISRLEPEDFAVYYCQLYGNSR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAMEWORK 3
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                                                                                                                                                                                                                        PPT:
                                                                                    81.6%;
93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85 7%:
                                                                          Query Match
Best Local Similarity 93.000
Nove 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90; Conservative
                                                                                                                                                                                                                       STANDAPD:
                                     100
                                                       100
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128
128 AA;
HSSP; P01607; 1AAG
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 86041852.
                                                                                                                                                                                                                     KV3K_HUMAN
P06311;
                                             DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                   NON_TER
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 mtqspvtlsvspgeratlscrasqsisnsylawyqqkpsqsprlliygastratgiparf 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.173SPGTLStSPSERATLSCPASLSVSSNYLAWYQQPPAGAPPLLIYGASSPATGIPDPF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LTQSPGTLSLSPGERATLSGRASQSVSSNYLAWYQQPPGQAPRLLIYGASSRATGIPDRF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 560: DB 5; Length 115;
Pred. No. 1.72e-100;
3; Mismatches 3; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                       KLÄPPER D.G., CAPRA J.D.;
ANN. INST. FASTEUP IMMUNCL. 127C:251-271(1976)
-!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
                                              EUKAPYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG KAPPA CHAIN V-III REGION (VG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY - DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 605; DB 5; Length 109;
Pred. No. 6.69e-111;
13; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 sgsgsgteftltisslgsedfavyycggynnwpptfgggtrveik 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 SGSGSGIDFILIISRLEPEDFAVYYCQLYGNSRWIFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AGG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-NOV-1990 (PEL. 16, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN PRECURSOR V-III PEGION (VG) (FPAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 FRAMEWORK 1.
54 COMPLEMENTARITY-DET
69 FRAMEWORK 2.
76 COMPLEMENTARITY-DET
108 FPAMEWOPK 3.
115 COMPLEMENTARITY-DET
109 BY SIMILARITY-DET
115
115
1155 MW; 37E182FC CRC32;
                                                                                                                                                                                                                                                                                                         23 89 BY SIMILARITY.
109 109
109 AA; 11922 MW; A0C42C88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDILME, 85087932.
PECH M., SACHAU H.G.;
NUCLEIC ACIDS RES. 12:9229-9236(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 sgsgsgtdftltisslepedfavyycq 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMEL; XO1668; ; NOT_ANNOTATED_CDS.
PIR: A01900; K3HUVG.
HSSP; PO1607; LAAG.
IMMONGCLOBULIN V RECION; SIGNAL.
IG KAPPA CHAIN V-III REGION (POM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (REL. 05, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 79.0%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 58;
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les 80; Conservative
                                                                                                                                                                                                              ACTIVITY.
PIR, A01897; K3HUPM.
HSSP; P01607; 1DFB.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
>115
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                   HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43
115
115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV3I_HUMAN
P04433:
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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NON_TER
                                                                                                                     SEQUENCE.
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24 mtqspptlslspqervtlscrasqsvsssyltwyqqkpgqaprlliygastratsiparf 83
                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LTOSPGTLSLSPGERATLSCPASOSVSSNYLAWYOOPPGGAPPLLIYGASSPATGIPDPF 62
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAPRA J.D., KLAPPER D.G.:
SCAND. J. IMMONCL. S:57*684(1976).
--- THE SECOND AND THIRD PYDEPVAPIABLE PEGIONS OF THIS CHAIN APE-
IDENTICAL WITH THOSE OF THE HYMAN POW V-III WAPPA CHAIN, WITH
WHICH II SHARES CERTAIN IDIOTYPIC DETERMINANTS.
--- THIS CHAIN WAS ISOLATED FROM AN ISM WITH ANTI-SAMMA GLORULIN
ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                           c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-I REGION (LAY).
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHOPDATA; VERTERRATA: TETPAPPEN MAMMALIA:
                                                                                            EUKAPYOTA; METAZOA; CHOPDATA; VEPTEBPATA; TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                     IG KAPPA CHAIN V-III PEGION (VH)
PPAMEWOPK 1
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                                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING 2.
                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING 3 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                   Score 558; DB 5; Length 116; Pred No. 4 99e-100;
                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                    IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENI)
                                                                                                                                                                                                                                                                                                                                              12757 MW: 27FA1BGE CRC32:
                               13.405-1947 (REL. 95. CPFATEN)
13.40G-1987 (REL. 05. LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16. LAST ANNUTAILON UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                   PECH M., ZACHAPI H. G.;
NUCLBIC ACIDS RES. 12-9229-9236(1984)
EMPL: X02725; -; NOI_ANNOIAIED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 sgsgsgtdftltisslqpedfavyycq 110
            PRT;
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                                                                                                                                                                                                               IMMUNOGLOBULIN V REGION; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87 4%:
Matches 76; Conservative
            STANDARD;
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HSSP; P01607; 2FGW.
IMMUNGELOBULIN V REGION.
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HSSP; P01607; IMCP.
                                                                                                                                                                                                                                                                                                                                             116 AA:
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                                                                                                                              SEQUENCE FROM N.A.
MEDLINE: 85087932.
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         KV3J_HUMAN
P04434;
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P01605;
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                                                                                                                                 2 ELTGSPGTLSLSPGEFATLSGFASGSVSSNYLAWYGGRFGGAPRULIYGASSFATGIPDR 61
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                                                                                        Saps
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EURAPYOTA; METAZOA; CHOPDATA: VEPTERPATA; TETPAPUDA; MAMMALIA;
    COMPLEMENTAPITY - DETERMINING 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 3%; Score 528; DR 5; Length 108; 63.2%; Pred. No. 4.01e-93;
                                                                  Score 537; DB 5; Length 108;
                                                                             Pred. No. 3.42e+95;
21; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 fagasasqteftltinslapedfatyyolqyssfp+tfqqqtkvevk 107
                                                                                                                                                       62 fsgsgsgtdfffisslapediatyycqqynnwpp+fgqqtkvevk 107
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                                             TEDED DUNGTET
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21-JTL-1996 (PEL. 01, LAST SEQUENCE HPDATE)
21-JAN-1988 (PEL. 06, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-I REGION (WEA).
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                         BY SIMILARITY.
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                                                                             Best Local Similarity 67.0%;
Matches 71; Conservative
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MEDLINE; 83273707.
GONI F., FRANGIONE B.;
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108 AA;
   899
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Best Local Similarity
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KV1R_HUMAN
P01610;
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Search completed: Tue Feb 24 07:17:24 1998

Job time : 14 secs.

	(TM)
1	>

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:17:42 1998: MasPar time 7.33 Seconds 444.542 Million cell updates/sec Run on:

Tabular output not generated

>US-08-844-215-8 (1-107) from USO8944215 pep 762 Description: Perfect Score:

1 AELTQSPGTUSLSPGERATE Sedneuce.

COLYGNSRWIFGOGIKVEIK 107

Scoring table:

PAM 150 Gap 11

95051 seqs, 30459580 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir53 Database:

Trannl 2.unr2 3.anr3 4.ann4 5.unann1 6.unann2 7.unann3 8.unann4 9.unann5 10.unann6 11.unann7 12.unann8 13.unann9 14.unann10 15.unann11 16:unann12 17.unenc

Mean 40.550; Variance 149.293; scale 0.272 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		ď			SUMMARIES					
Result No.	Score	Query Match	Length	DB	ID	Desc	Description	uo		Pred. No.
1	712	93.4	108	۲.	C30508	5	Kappa	chair		2 170.63
2	712		621	C1	K3HUHI	i H	kappa	chair	precu	2.170-63
m	710	93.2	107	^	PH0965	Ĭď	kappa		V req	
4	702	55	901	۲-	130601	i t⊤	Kappa	253:0	V-111	2,850-62
2	701	95.0	671	Cł	КЗИПИА	+ •	kappa		i Jose	3 6.80-62
9	700	σ. 5	100	7	じょうだい	13	kappa	chain	V-111	4 760-62
7	697	م 7	128	7	919025	b	kappa	chain	V req	1.03e-51
80	969	91.2	109	7	R30601	6	kappa	chain	V-111	1 726-61
6	694	91.1	109	7	H30601	Ig	kappa		>	2.23e-61
10	692	8 06 8	109	7	F44151	Id	kappa	chain	>	
11	692	8.06		٢	F30607	Гd	kappa		V-III	3.73e-61
12	691	90.7		7	G30501	Пq	kappa	chain	V-III	.82
13	689	⊅ ∪ 5		٢	550635	Ħ	kappa	chain	V req	0
14	688	90.3		7	PH0963	19	kappa	chain	V red	
15	687	90.2		^	A3060R	Гđ	kappa	rhain	V-111	1 350-60
16	686	0.06		^	846369	10	light	chain	varia	1.74e-60
17	686		134	7	538643	19	kappa	chain	Leg V	1 746-60
18	685	69.9	104	C 1	TM:HE A	E.	kappa	0.1840	V-117	5 560-60
19	585		100	C.	I STILLS I	14	kappa	21840	V-III	5 260-60
50	684	(T)	E01	4	H44151	F	карра	chain	ροż Λ	2.920-60

MAHUHI #type complete

Ig kappa chain precursor V-111 region (Hic) - human
#formal_name Homo sapiens #common_name man
30 **vn-1940 #sequence_revision 30.7un-1940 #text_change
FLC021
PLC021

ACCESSIONS REFERENCE

ORGANISM DATE

RESULT ENTRY TITLE

kappa chain V-III 3.	kanna chair V-111 o	kappa chain V-III 1	tissm antibody VI 2	kappa chain V-III 3.	kappa chain V.III 9.	kappa chain V-111 1.	kappa chain V req 2.	Kappa chain . num 4.	kappa chain ' hum 8.	kappa chain - hum 1	kappa chain precu 1.	kappa chain V-III 2.	Kappa Chain - num 3.	kappa chain V req 5.	kappa light chain 3	Mappa chain - hom 2	kappa chais · hum 3.	kappa chain V red 3	9	ENTS		**) demind - (0:0) de	re) - mumam (ilagmeno) mon_name man	sion 29-Jun-198		., McGinnis, D., Arjonilla, M.L.; on D., Solomon, A., Mondoz, F.,	רשירה משירה משירה	ه ځار	בועמ אונה קווועוטהני טרעניי ינוניט				immunoglobulin r; immunoglobulin ≉checksum 1607	712; PR 7: Length 108; No. 2.17e-63; Mismatches 2: indels 0: Gaps 0:	lawyqqkpqqaprlilyqassratqıpdr	[[]]]]]]] GASSKA1G1	ygsspwtfgggtkleik 108	SNSEWIFGQGTKVEI
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21 77	1 6	24	un Ci	26	- 20 1 - 1	58	30	3. L	3.60	34	35	۲۰ <u>۱</u> ۳۰ ۱	, o	0 6 6 M	4	4,1	4.		4 4 0		RESULT	ENTRY	ORGANISM	DATE	ഗജ	ro ana	-1	# # Tit	#Cro	Ŭ # U ™	**	## E	KEYWORDS SUMMARY	Query Mat Pest Ling Matches	g	23	qq	Ωÿ

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*superfamily immunoglobulin V region; immunoglobulin homology
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Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. (1988) 167:840-852
Autoantibody-associated Kappa light chain variable region
gene expressed in chronic lymphocytic leakemia with little
or no somatic mutation. Implications for etiology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                   An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                                                                                                  The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoantibody, chronic lymphocytic leukemia; heterotetramer;
immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PH0965 #type fragment
Ig Kappa chain V region (64 CLL-BRA) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 ltqspqtlslspqeratlscrasqsvsssylawyqqkpqqaprlliyqassratgipdrf 83
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predicted #label MAT\
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#region complementarity-determining 2\
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#region complementarity-determining 2\
#region framework 3\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *region J segment (JRI)\
*disulfide_bonds *status predicted
*length 129 *molecular-weight 14070 #c
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3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                    ##cross-references GDB:136266
                                                                                                                                                     *cross-references MUID:88171307
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*superfamily immunoglobulin V region; immunoglobulin homology
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J. Exp. Med. (1988) 167:840-852
Automatibody-associated kappa light chain variable region
gene expressed in chronic lymphocytic leukemia with little
or no somatic mutation. Implications for etiology and
                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #fitle Structural and idiotypic characterization of the L chains of
human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
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#formal_name Homo sapiens #common_name man
29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
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Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
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                                                                                                                    2; Indels
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  #region complementarity-determining
#length 107 #checksum 7830
                                                                                            Pred. No. 3.63e-63;
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Fred. No. 2.85e-62;
                                                                     Score 710; DB 7;
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*cross-references MUID:88171307
*accession PL0022
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                                                                                         Best Local Similarity 95.2%;
Matches 100; Conservative
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           **Cross-references GDB:136266

An immuncqiobulin hererotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha delta, epsilon, agmma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                                                                    autoantibody; chronic lymphocytic leukemia; heterotetramer;
                                                                                                                                                                                                                         *domain signal sequence *status predicted *label SIG\
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Structural and idiotypic characterization of the L chains
human IgM autoantibodies with different specificities.
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#formal_name Homo sapiens #common_name man
29-Jun-1999 sequence_revision 29-Jun-1999 #text_change
IG-Aug-1996
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                                                                                                                                                                                                                                                                                              *region complementarity-determining 1\
*region complementarity-determining 2\
*region complementarity-determining 3\
*region separate (JK1)\
*fagisalfide_bonds *status predicted
*length 129 *molecular-weight 14073 *checksum 7361
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*length 109 *checksum 5191
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##residues 1-109 ##label GON
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Best Local Similarity 95.2%;
Matches 100; Conservative
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RESULT

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##CTOSS-references EMBL:Z11894
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
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S20636 #type complete
Ig Kappa chain V region - human
#formal_name Horn sapiens #common_name man
20-Feb-1995 #sequence_revision 20-Feb-1945 #text_change
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Pred. No. 1.72e-61;
3; Mismatches 3: Indels
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Matches 99; Conservative
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Human combinatorial antibody libraries to hepatitis B surface
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                                                                                                                  Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.
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Ig Kappa chain V region (JM-01) - human (fragment)
Formal name Homo sapiens #common_name man
27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
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Fernandez, J.; Carson, D.; Solomon, A.: Mendez, E.;
Frangione, B.
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Ig kappa chain V-III region (Bor) - human (fragment)
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Pred. No. 2.23e-61;
4; Mismatches 3; Indels
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Pred. No. 3.73e-61;
                                                                                               (1989) 142-3158-3163
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#length 109 #checksum 5518
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#length 109 #checksum 5951
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##residues 1-109 ##label GON1
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91 1%;
Best Local Similarity 93.3%;
Matches 98; Conservative
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H30601; E30601
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  ACCESSIONS
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                   PEFEPENCE
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1-109 ##label GON #superfamily immunoglobulin homology heterotetramer; immunoglobulin
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#formal_name Homo sapiens #common_name man
29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
#formal_name Homo sapiens #common_name man
29-Jun-1989 #sequence_revision 29-Iun-1989 #text_change
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Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
                                                                                                                               Goni, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
                                                                                                                                                           Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
Frangione, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 109;
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Ig kappa chain V region - human
#formal_name Homo sapiens #common_name man
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Pred No 3 73e-61;
                                                                                                                                                                                                               J. Immunol. (1989) 142:3158-3163
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Matches 97; Conservative
                                                 16-Aug-1996
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##cross-references EMBL:Z11893
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
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Ig kappa chain V region (G6+ CLL-SMI) - human (fragment)
*formal_name Homo sapiens *common_name man
17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change
16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Martin, T.: Duffy, S.F.; Carson, D.A.: Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
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                                                                                   Lee, S.K. Bridges, L.S. Koopman, W.T.; Schroeder, H.W. submitted to the EMBL Data Library, April 1992
$20635
                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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1g kappa chain V-III region (Son) - human (fragment)
#formal_name Homo sapiéns *common_name man
29-Jun-1989 *sequence_revision 29-Jun-1989 *text_change
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                              #length 110 #molecular-weight 11965 #checksum 136
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                                                                                                                                                                                                                                                                                                                                                            Score 689; DB 7; Length 110; Pred. No. 8.07e-61;
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*region complementarity-determining 1\
*region framework 2\
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#region framework 3\
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*length 109 *checksum 5292
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                                                                                                                                                                                                                                                                                       heterotetramer; immunoglobulin
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                                                                                                                                                                  preliminary
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Matches 98; Conservative
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                      16-Aug-1996
                                                                                                                                                                                       ##molecule_type mRNA
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##molecule_type protein
##residues
1-109 ##label GON
FICATION #superfamily immunoglobulin V region; immunoglobulin homology;
DS heterotetramer: immunoglobulin
tX #length 109 #checksum 6031
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                                                                                                                                                                                  #title Structural and idiotypic characterization of the L chains human IgM autoantibodies with different specificities. #cross-references MUID:89215279
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                                                                               Chen, P.P.: McGinnis, D.; Arjonilla, M.L.;
L.I.; Garson, D.; Solomon, A.; Mendez, E.;
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90.2%; Score 687; DB 7; Length 109; Best Local Similarity 92.4%; Pred. No. 1.35e-50; Matches 97; Conservative 4; Mismatches 4; Indels
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                                                                                                                                                            (1989) 142:3158-3163
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                                                                                                                                   Francione, B.
16-Aug-1996
A30608
                                                                               Goni, F.R.; (
Fernandez,
                                                                                                                                                              J. Immunol.
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                                                         A30601
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                                                                                    #authors
                                                                                                                                                                 #journal
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:44:44 1998; MasPar time 2.89 Seconds 188.570 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-8 (1-107) from US08844215.pep 762 1 AELTQSPGTLSLSPGERATL Description: Perfect Score:

Sequence:

COLYGNSRWIFGQGTKVEIK 107

PAM 150 Gap 11

Searched:

Scoring table:

56402 seqs, 5095871 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued libackl 2:51 3:52 4:53 5.54 6.55 7.56 8:PCT90 9.PCT91 l0-PCT92 ll-PCT91 12-PCT94 l3-PCT95 14:PCT96 Database:

Mean 27.478; Variance 143.457; scale 0.192 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Ouerv							
°Z	Score	Match	Length	DB	ID	Description	n C		Pred. No
1	269		108	13	PCT-US95-0	Sequence		Applicati	1 950-46
7	697		108	7	US-08-276-				1.95e-4
٣,	685		107	13	PCT-US95-0			Applicati	1 806-4
4	685		107	7	US-08-276-				1.80e-4
S	685		108	9	US-08-477-		86, Ar	d	1.80e-4
9	685		108	7	US-08-474-		86, Ar	Applicati	-
7	685		108	9	US-07-634-		86, A	oplicati	Ä
8	685		108	7	US-08-487-		86, A	oplicati	
6	684		108	13	PCT-US95-0		99. A	pplicati	7
10	584		108	٢	US-08-276-		99, Ar	oplicati	2.1
11	683		109	Π	PCT-US93-0		23, Ar	oplicati	2.5
12	680		δύ.	۲. د م	0-36SD-LJd		147, 7	Applicat	4
13	Ū89		109	۲-	CS-08-276-	Sequence	147, 7	Applicat	5.5
14	670	87.9	104	13	PCT-US95-0	Sequence	100,	0, Applicat	7
15	670		104	۲~	US-08-276-	Sequence	1001	Applicat	
16	670		111	13	PCI-US95-0	Sequence	149, 7	Applicat	2.90e-4
17	670	87.9	111	7	7	Sequence		Applicat	2.90e-4
18	562		108	7	US-08-276-	Sequence	110, 2	Applicat	1.28e-4
19	662		108	ã	PCT-US95-0	Sequence	110, 4	Applicat	1.28e-4
20	959		107	7	US-08-275-		۹.		3.87e-4
21	656	86.1	107	13	PCT-US95-0		87, Ar	Applicati	r~
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Applicati 6.22c.42 Applicati 1.57c.41 Applicati 1.57c.41 Applicati 1.87c.41 Applicat 9.95c.41 Applicat 9.95c.41 Applicati 3.01c.40 Applicati 4.36c.40 Applicati 9.38c.39 Applicati 9.38c.39 Applicati 9.38c.39 Applicati 9.36c.39 Applicati 9.36c.39 Applicati 9.46c.39 Applicati 9.46c.39 Applicati 9.46c.39 Applicati 9.46c.39 Applicati 9.46c.39 Applicati 9.66c.39 Applicati 9.66c.39 Applicati 9.66c.39 Applicati 9.66c.39 Applicati 9.66c.39

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                     APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
                                                                                                                                                               ADDRESSE: The Scripps Research Institute, Office of STREET: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 229, STREET: Mail Drop TPC8 CITY: La Jolla STATE: CA COUNTRY.
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Pred. No. 1 95e-46;
2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NR/276,852
FILING DATE: 18-JUL-1994
CLASSIFFCATION: 514
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                  108 AA.
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                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION INMESS 10 08/178,302
FILING DATE: 30.5EP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                  PRT;
                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 108 AA; 11769 MW; 65957 CN;
                                                                                             Application US/08275852
                                                                           Sequence 86, Application US/08276852
                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,163
PEFERENCE/DOCKET NUMBER SCP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPHONE:
                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 86:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 amino acids
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fitting, Thomas REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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Best Local Similarity 92.5%;
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scrip
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                      Patent No. 5652138
GENERAL INFORMATION:
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ID PCT-US95-08743-90
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                 US-08-276-852-86
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                                                                                              Sequence 86,
                                                         01-JAN-1900
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Sequence 90, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HEREOF ADPRESS:
ADPRESSEE: 174 Scripps Pescarch Institute, Office of
ADRESSEE: Patent Counsel
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                  TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNOPEFICIENCY VIRUS COMPUTER READABLE FORM:
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APPLICATION DATA:
FILLING DATE: 11-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.9%; Score 685; DB 13; Length 107 Best Local Similarity 89.6%; Pred. No. 1.80e-45; Matches 95; Conservative 8; Mismatches 3; Indels
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PRING DATE: 11-002.

PRIOR APPLICATION DATA:

APPLICATION NYMBEP: 115 08/276,852

APPLICATION NYMBEP: 119 4
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                                                                                              Sequence 90, Application PC/TUS9508743.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
JENCE 107 AA; 11705 MW; 62938 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 90, Application US/08276852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFFLING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 90;
SEQUENCE CHARACIERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                           Floppy disk
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                                             01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ELTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPRLLIYGASSRATGIPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 685, DB 7; Length 107;
Pred. No. 1.80e-45;
8; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FSGGGGGTDFTLTISRLEPEDFAVYYCQHYGNSVYTFGQGTKLEIK 105
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Patent No. 5589189
GENERAL HYPERALION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHOOL OF THE CONTROL OF THE COMPANIED INMUNOCIOBLIAM CORPRESONDENCES: 11
APPRENDENCE IDWISSEL IDWISSEL IDWISSEL AND TOWNSEND AND THE COMPANIED INMUNOCIOBLIAM COMPANIES IN TOWNSEND AND THE COMPANIES IN TOWNSE
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                                                    UPERALING SIGHT : C. DOS/MS. DOS
SOFTWARE. PATENTIN PELGASE #1 0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/275,852
FILING DATE: 18 JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
FILING DATE: 30-5EP-1993
FILING DATE: 30-5EP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING YSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/954.148 FILING DATE: 30-SEP-1992 ATTORREY/ADDREST INFORMATION:
                                                                                                                                                                                                                                                                                                                         SCR1452P
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 107 AA; 11705 MW; 62938 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 86, Application US/08477728.
                                                                                                                                                                                                                                                                                                         34,163
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 90:
                                                                                                                                                                                                                                                                                                                                                                                                                                       107 amino acids
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                                                                                                                                                                                                                                                                                NAME: Fitting, Thomas REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 89.9%;
Local Similarity 89.6%;
les 95; Conservative
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STREET: TWO ...
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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APPLICANT: OUTER, CARY L.
APPLICANT: CO. Man Sung
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HYMANIZED IMMINGGOBLINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.9%; Score 685; DB 6; 192.4%; Pred. No. 1.80e-45; ative 4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/POCKET WIMPER 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-2400
           CLASSIFICATION: 424
PROF APPLICATION DATA:
APPLICATION UNMERF: US 07/594,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR DAPLICATION NUMBER: US 07/590,274
APPLICATION NUMBER: US 07/590,274
APPLICATION NUMBER: US 07/590,274
APPLICATION NUMBER: US 07/310,252
                                                                                                                                                                                               APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 108 AA; 11590 MW; 64079 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86, Application US/08474040 Patent No. 5693761
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MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                               30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 326 2422
INFORMATION FOR SEG ID NO: 86:
SEQUENCE CHARACTERISTICS:
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07-JUN-1995
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amino acid
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                                                                                                                                                                                                                                                                                                                                          NAME: Smith, William M
PEGISTPATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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nes 97; Conservative
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California
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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US-08-844-215-8.rai

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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: QUEEN, Cary L.
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDEP, William P
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
CORPESPONDENCES: 113
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 685; DB 7; Length 108; Pred No 1 80e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA
                                                                                                                                                                                                                                                                               11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 057/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-5EP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH WALLIAM M
REGISTRATION NUMBER: 30,233
                                        APPLICATION NUMBER: US/08/474,040 FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPT;
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 108 AA; 11590 MW; 64079 CN;
  FC - DOS/MS - DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 86, Application US/07634278 Patent No. 5530101 GENERAL INFOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 86, Application US/07634278.
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1182
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO. 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 379.Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDAPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92 4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97; Conservative
  OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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4 LIQSPGILSLSPGERATLSCRASQSVSSGYLGWY@@KPGQAPRILITYGASSRAIGIPDRF 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COELINGH, Kathleen L
APPLICANT: SELICK, Harold E
TITLE OF INVENTION: IMPROVED HIMANIZED IMMUNOSLOBLINS
UNMER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

89 94; Score 685; DR 6; Length 108;
Best Local Similarity 92.4%; Pred. No. 1.80e-45;
Matches 97; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 SGSGSGTDFTLLTISRLEPEDFAVYYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 SGSGSGIDFILTISPLEPEDFAVYYCQQYGSLGPTFGQGTKVEIK 108
                                        SOFTWARE: Patentin Pelease #1 0, Version #1 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: Townsend and Townsend and Crew
379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                       11823-002600
                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBEP: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 108 AA; 11590 MW; 64079 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 86, Application US/08487200 Patent No. 5693762
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SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 86, Application US/08487200.
                                                                                                                                                                                                                                                                                                                               PEGISTPATION NUMBER: 30.223
REPERRANGE/DOCKET UNMBER: 1183
TELECHMUNICATION INFORMATION:
TELEPHONE: (415) 326-240
TELEFAX: (415) 326-242
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                  /AGENT INFOLD—
Smith, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Patent No. 5693702 GENERAL INFORMATION:
GENERAL INFORMATION:
OUGEN, Cary L
                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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APPLICANT ·
APPLICANT :
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                                                                                                                                                                                                                                                                                                                    NAME .
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519-554-2937
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                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HOMAN IMMUNODEFICIENCY VIEUS NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (FPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 89.9%; Score 585; DB 7; Length 108; Best Local Similarity 92.4%; Pred. No. 1.80e-45; Matches 97; Conservative 4; Mismatches 4; Indels
             ...patible
...piSTEM: ...patible
...piSTMARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FLING DATE: 7-JUN-1995
RIOR APPLICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 SGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 SGSGSGIDFILIISRLEPEDFAVYYCQLYGNSRWTFGQGIKVEIK 107
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                                                                                                PRICE APPLICATION: 424
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRICE APPLICATION NAPA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRICE APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRICE APPLICATION NUMBER: US 07/290,975
APPLICATION NUMBER: US 07/290,975
APPLICATION NUMBER: US 07/290,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT/US95/08743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                       APPLICATION NUMBER: US 07/290,975 FILING DATE: 28-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Application PC/TUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
JENCE 108 AA; 11590 MW; 64079 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 99, Application PC/TUS9508743.
                                                                                                                                                                                                                                                   30,223
                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INDEMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      NAME: Smith, William M
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                       108 amino acids
                                                                                                                                                                                                                                                                                                                                             single
ZIP: 94301.
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                    TYPE.
STRANDEDNESS: SIF
                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Fred. No. 2.17e-45; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ELIQSPGILSLSPGERAILSCRASQSVSSNYLAWYQCRPGQAPRLLIYGASSPATGIPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN NEUTRALIZING MONOCLONAL ANTIHODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Read, Suite 220,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FSGSGSGIDFILSISRLEPEDFAVYYCQQYGTSPYTFGQGTQLDIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 FSGSGSGIDFILIISPLEPEDFAVYCQLYGNSPWIFGQGIKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
FILING DATE: 11-JUL-1995
PRICR APPLICATION DATA:
APPLICATION NIMBER: US 08/275,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,163
PEFEFENCE/POCKET NUMBER: SCR1452P
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUPRENT APPLICATION DATA:
APPLICATION NYMBEP. "S/09/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1
                                                                                                                                                                                                                    MOLECULE TYPE: protein
JENCE 108 AA; 11738 MW; 63142 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 99, Application US/08276852
Patent No. 5652138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 99, Application US/08276852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Burton, Dennis R
APPLICANT: Burton, Carlos F
APPLICANT: Lerner, Richard A
ITILE OF INVENTION: TO HUMAN NEUTF
ITILE OF INVENTION: TO HUMAN IN
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ratent couns.
Patent 10666 No 565213
STREET: Mail Drop IPC8
CITY: La Jolla
STAIE: CA
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fitting, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity 89.7%;
Matches 94; Conservative
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APPLICANT: Barbas, III, Carlos F.
APPLICANT: Chanck, Robert M.
APPLICANT: Crowe, Jr., James E.
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 29
                                                                                                                Score 684, DB 7, Length 108, Pred, No. 2.17e-45; 7; Mismatches 5, Indels
                                                                                                                                                                                                                     61 FSGSGSGTDFTLSISRLEPEDFAVYYCQQYGTSPYTFGQGTQLDIK 106
                                                                                                                                                                                                                                    62 FSGSGSGTDFTLTISRLEPEDFAVYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1 0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Wetherell, Jr., Ph.D., John R. REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US93/08786
FILING DATE: 16-SEP-1993
                                                                                                                                                                                                                                                                                                  PRT:
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 108 AA; 11738 MW; 63142 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rsv 6L+ 11L+ 21L; anad 22L
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application PC/TUS9308786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application PC/TUS9308786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                  STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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CLONE: raw fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                 Query Match 89.8%;
Best Local Similarity 88.7%;
Matches 94, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: Sin
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                      LT 11
PCT-US93-08786-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90067
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                                                                                                                                                                                                                                                                                                                                                  01-JAN-1900
                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                       6; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNOBELICIENCY VIRUS NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.2%: Score 680: DB 13: Length 109: Best Local Similarity 91 6%; Pred No 4.55e-45; Matches 98; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25 (EPO)
                                                                Length 109;
                                                                                                                                                                   62 RFSGSGSGTDFTLTISRLEPEDFAMYYCQQYDISPYTFGQGTKLEIK 108
                                                                                                                                                                                  61 RFSGSGSGTDFTLTISRLEPEDFAVYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSG-TFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISRLEPEDFAVYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                109 AA
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                                                               Score 683; DB 11;
Pred. No. 2.61e-45;
                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OL TYPENTION.

TITLE OF SEQUENCES: 170
COMPUTER PEARABLE FORM.

MEDIUM TYPE: Floppy disk

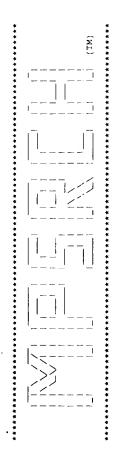
"VENTIER: IBM PC compatible
""" FORM.

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GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                           Sequence 147, Application PC/TUS9508743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 109 AA; 11779 MW; 65550 CN;
                          LOCATION: 1.109
ICE 109 AA; 12099 MW; 62556 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 147, Application Rs/AR2768F2
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                                                                                                                                                                                                                                                 STANDARD;
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                                                  Ouery Match
Best Local Similarity 89...,
Best Local 96; Conservative
             NAME/KEY: Peptide
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PCT-US95-08743-147
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FEATURE:
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                                       SEQUENCE
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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US-08-276-852-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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Pred. No. 4.55e-45;
....marches 4; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AELTQSPGTLSLSPGERVIVSCRASQSVSSNYLAWYQQKPGQAPRLLIYGASNRATGIPD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AELTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPRLLIYGASSRATGIPD 60
                                   APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOPEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
                                                                                                     ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREFT 10666 No. 5552138th Torrey Pines Road, Suite 220, STREET Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSG-TFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RESGSGSGTDFTLTISRLEPEDFAVYYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 AA.
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                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           SCR1452P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 100, Application PC/IUS9508743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 100, Application PC/TUS9508743.
       Sequence 147, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 109 AA; 11779 MW; 65550 CN;
                                                                                                                                                                                                                                                                                                                                      NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                 : 109 amino acids
amino acid
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 91.6%;
les 98; Conservations
                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                USA
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                                                                                                                                                               COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH:
                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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1 QSPGTLSLSPGERATLSCRASQSLSNNYLAWYQQKPGQAPRJLIYGSSTRATGIPDRFSG 60
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Pred. No. 2.90e-44;
7, Mismatches 3; Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 QSPGTLSLSPGERATISCRASQSVSSNYLAWYQQPPGQAPPLLYGASSRATGIPDRFSG 64
  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HIMAN IMMINOPEFICIENCY VIRUS
170
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APPLICANT: Barbas, Carlos F
APPLICANT: Berber, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MANACLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOPERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Aberent Counsel
STREET: 10666 No. 552138th Torrey Fines Fual, Suite 220,
STREET: Mail Drop 1PC8
                                                                                                                                                                         SOFTWARE Patentin Release #1.0, Version #1.25 (EPC) CURRENT APPLICATION DATA:
APPLICATION NABER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ. ID. NO: 100:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGSGTDFTLTISRLEPEDFAVYYCQQYGNSVYTFGQGTKLEIK 103
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18-JUL-1994
                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 104 AA; 11367 MW; 58892 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 100, Application US/08276852 Patent No. 5652138
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                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity 90.3%;
Matches 93; Conservative
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CC FILING DATE: 30-SEP-1993
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION NUMBER: US 07/954,148
CC PRIOR APPLICATION NUMBER: US 07/954,148
CC ATTORNEY/AGENT INFORMATION:
CC ATTORNEY/AGENT INFORMATION:
CC RECISTRATION NUMBER: 34,163
CC TELECOMMUNICATION INFORMATION:
CC TELECOMMUNICATION
CC TELECOM
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Release 2 1D John F. Collins, Riccomputing Pescarch Unit. Copyright (c) 1993, 1994, 1995. University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07 18 21 1948. MasPar time 6 66 Seconds 223.141 Million cell updates/sec Pun on

Tabular output not generated.

>US-08-844-215-8 (1-107) from US08844215.pep 762 1 AELTQSPGTLSLSPGEPATL. Title: Description: Perfect Score:

Sedneuce.

111726 segs, 13889129 residues Searched:

PAM 150 Gap 11

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseg30
l:part1 2.part2 1:part3 4.part4 5.part5 6.part6 7.part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Mean 29.905; Variance 165.350; scale 0.180 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query Match	Sength	DB	ΙD	Description	Pred. No
1		91.5	10.8	· c	P54307	Anti-HIV gp120 immupo	1.576-42
7	697		108	19	W01265	C:	1.57e-42
3	694	ä	129	7	R38672	٠.	2.640.42
4	685	6.68	101	10	R54311	Anti-HIV ap120 1mmuno	1.256-41
Ŋ	685	6	107	13	W01269	VL region of HIV neut	1.26e-41
9	684	6	108	19	W01278	region of HIV	1.50e-41
7	684		108	6	R54316	ap120 im	1.50e-41
æ	584		109	10	R55285	۵	1500-41
6	683		109	σ	R50217	HSV glycoprotein F bi	1.78e-41
10	680		109	13	W01320	VI. of Fab, DL 41 19,	3.00e-41
11	680		109	10	R54275		3.00e-41
12	673		107	7	-	nbda 1	1.01e-40
13	670		104	19	W01279	VL region of HIV neut	1.70e-40
14	670		104	σ	R54317	Anti-HIV gp120 immuno	1.70e-40
15	670	87.9	111	19	W01322	_	1 700-40
16	670		111	10	R54277	p41	1.70e-40
17	662		108	19	W01289		6.78e-40
18	652	85 9	129	۲-	F41286	rearranged v	5.786-40
19	999		214	19	W07615		07-065 6
20	629	85 5	129	^	F38573		1 140-39

1.92e-39	.92e-3	.92e-3	.286-	B 20 - 3	.83e-3	.57e-3	2.57e-38	.57e-3	.10e-3	.43e-3	.43e-3	.44e-3	146-	.44e-	.09e-3	.09e-3	.09e-3		70e 3	.70e-3	.70e-3	.37e-3	.37	e-3
ti-HIV gp120 immun	ior	ng tum	IV gp120 imm	ohulin	cerative colitis a	7 qp120 immun	region of H	V glycoprotein F b	eqion of HI	IV GP	ion o	region o	IV qp41 immin	, SS 41	nan V-kappa vk	vk65.8	Human V-kappa fragmen	м др120 іші	100 001	ti-HIV qp	ion o	region of H	-HIV qp12	V qpl
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ALIGNMENTS

108 AA;

Seguence

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vX325-JK2. Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS; Ch4: receptor; hybridoma; polymerase chain reaction; PGP; heavy; light;

AA.

.r R38672 standard; Protein; 129

01-NOV-1993 (first entry)

R38672;

RESULT

Location/Qualifiers

50

..129

/label= sig_peptide 'label= mat_protein

Peptide

Protein

117..129

44..55 71..77

> CDR1 CDR2 CDR3

'label≖

/labellabel-

Region Segion

1..116

'label= vk325

sed ton Region 'label= Jk2

chain; epitope; immune deficiency.

Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions (VL) of series of monoclonal antibodies (MAb's) which are immunoreactive with HIV glycoprotein gpi20 and are capable of monutalising HIV. This sequence represents the sequence of the JKI gene clone, b24. A MAb containing this VL sequence has the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay binds mature gpi20 preferentially over the precursor gpi60. The MAD may be used for determining immunocompetence of a human anti-HIV mad antibody and in the detection of HIV infection
                                                                              1 eltgspgtlslspgeratlscrasgsvisnylawyggkpggaprlliygvsnratgipdr 60
                                                                                                            2 ELTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPRLLIYGASSPATGIPDR 61
                                              Gaps
                                                                                                                                                                                                                                                                    28-JAN-1997 (first entry)
VL region of HIV neutralising MAb, clone b24.
Heavy chain, light chain; variable region; VH; monocional antibody; MAb; HIV; human immunodeficiency virus; glycoprotein; gpl20; clone; virus infectivity assay; precursor gpl60; immunocompetence; human; anti-HIV antibody; detection; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive immuno:therapy and detection of HIV infection.

Example: Fig 11: 366pp: English: English and Figure in W01261-92 represent the light chain variable
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0
               Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 108;
                                              Indels
                                                                                                                                                         62 FSGSGSGTDFTLTISRLEPEDFAVYYCQLYGNSRWTFGGGTKVEIK 107
                                                                                                                                            61 fsgssgstdftltisrlepedfavyscqqygtspwtfgggtkveik 106
Score 697; DB 10; Le
Pred. No. 1.57e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 91.5%; Score 697; DB 19;
Local Similarity 92.5%; Pred. No. 1.57e-42;
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                         r 2
W01265 standard; Protein; 108 AA.
               Query Match 91.5%;
Best Local Similarity 92.5%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-1994; US-276852.
(SCRI ) SCRIPPS RES INST.
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WPI; 96-179601/18
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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"Met encoded by ATC (sic)" Pro encoded by GCA (sic)" "Leu encoded by GTG (sic)"

erence 1

Misc_dif

110..117

/note= "Gly encoded by GAI (sic)" Misc_difference 114

Misc_difference 113

Misc_difference 99 Misc_difference 35

'note= "Ser encoded by AAC (sic)" 'note= "Pro encoded by GIT (sic)"

Misc_difference 116

WO9312232-A.

24-JUN-1993

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24 ltqspqtlslspqeratlscrasqsvsssylawyqqkpqqptlliyqassratgipdrf 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LTGSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQPPGQAPPLLIYGASSRATGIPPRF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
Disclosure, Page 74-75, 109pp; English.
The nucleotide sequence of F105 Vk (Q42707 - sequence differs from other F105 Vk sequences given elsewhere in the specification) was compared with germline gene Humwk325 (Q42706), showing 97.7% similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the Vk III subgroup gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA segments encoding monoclonal antibody - which binds to \ensuremath{\mathsf{gpl}}\xspace20 and neutralises HIV, for treating AIDS, and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 129;
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Pred. No. 2.54c-42;
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(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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WPI; 93-214174/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 91 1%;
Local Similarity 93.3%;
es 98; Conservative
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10-DEC-1991; US-804652.
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ID R5
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R54311 standard; protein, 107 AA.

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2; Mismatches

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1 eltqspgtlslspgeratlscrasqsvisnylawyqqkpgqaprlliygvsnratgipdr 60

2 ELIQSPGIĮSLSPGERATISCRASQSVSSNYLAWYQQPPGQAPRILIYGASSPATGIPPP 61

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/label= FR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymphocyte mRNA was converted to CDNA and subjected to DCR amplification using primers specific for heavy and light chain variable regions. The amplification products were inserted into a dicistronic vector to produce a library of fragments. E.coli XLI Blue cells were transformed with the library. Filamentous phage were produced which expressed the MAD regions on their surface. Panning with 9p120 and 9p41 resulted in the recovery of immunoreactive clones. The light chain VK region sequence R54311 is from a gp120-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 eltqspqtlslspqeratlscrasqslsnnylawyqqkpgqaprlliygsstrgtgipdr 60
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89.9%, Score 685; DB 10; Length 107;

Best Local Similarity 89 6%; Pred No. 1 26e-41;

Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 BLIQSPGTLSLSPGEPATLSCRASQSVSSNYLAWYQQPPSQAPFLLIYGASSPATGIPDP 61
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VL region of HIV neutralising MAD, clone B20.
Heavy chain: light chain; variable region; VH· monoclonal antibody.
MAD; HIV; human immunodeficiency virus; qlycoprotein; gpi20; clone; virus infectivity assay; precursor gp160; immunocompetence; human; anti-HIV antibody; detection; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human monoclonal antibodies neutralising HIV - react with appl20 or gp41 and nucleic acid encoding them, useful for in vivo or in vitro diagnosis and for passive immuno-therapy Example; Page 180; 248pp; English.
                10-NOV-1994 (first entry)
Anti-HIV gpl20 immunoglobulin light chain variable region B20.
Human immunodeficiency virus: HIV1: glycoprotein gpl20: epitope: neutralisation; monoclonal antibody; kappa light chain; varlable region; framework; complementatity determining region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 FSGSGSGTDFTLTISRLEPEDFAVYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                     Location/Qualifiers
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Barbas CF, Burton DR, 1
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                                                                                                                                Homo sapiens.
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Region
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                                                                                                                                                                                                                                          /label- CDR1
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regions (VL) of a series of monoclonal antibodies (MAP's) which are immunoreactive with HIV glycoprotein gpl20 and are capable of neutralising HIV. This sequence represents the sequence of the JK2 gene clone, B20. A MAB containing this VL sequence has the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50.8 at a concentration of less than 700 ng of antibody/ml, and hinds mature gpl20 preferentially over the precursor gpl60. The MAB antibody and in the detection of HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ELTQSPGTLSLSPGEPATLSGPASGSVSSNYLAWYQQPPGQAPPLLIYGASSPATGIPDR 61
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VL region of HIV neutralising MAb, clone b6.
Heavy chain: light chains variable verses of WH; monoclonal antibody;
MAb; HIV; human immunodeficiency virus; glycoprotein; gpi2C; clone;
virus infectivity assay; precursor gpi60: immunocompetence; human;
anti-HIV antibody; detection; HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                       passive immuno:therapy and detection of HIV infection.
Example: Fig 11: 366pp: English.
The sequences given in W01261-92 represent the light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FSSSSGIDFILISKLEPEDEAVYCCLYGNSRWIFGGSTKVEIK 107
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(SCPI ) SCRIPPS RES INST
Barbas CF, Burton DR, I
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18-JUL-1994; US-2768
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W09602273-Al.
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Region
/label= CDR2
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/label= CDR2
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                                                                                                    The sequences given in W0126192 represent the light chain variable regions (VL) of a series of monoclonal antibodies (MAb's) which are immunoreactive with HIV glycoprotein gp120 and are capable of neutralising HIV. This sequence represents the sequence of the JK2 gene clone, b6. A MAD containing this VI, sequence has the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/ml, and binds mature gp120 preferentially over the precursor gp160. The MAD may be used for determining immunocompetence of a human anti-HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Imphocyte mRNA was converted to cDNA and subjected to PCR amplification using primers specific for heavy and light chain variable regions. The amplification products were inserted into a dicistronic vector to produce a library of fragments. E.coli XLI Blue cells were transformed with the library. Filamentous phage were produced which expressed the MAb regions on their surface. Panning with gpl20 and gp41 resulted in the recovery of immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                            1 eltgspgtlslspgeratlscraggsissnylawyggkpggaprlliygasnratgipdr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ELTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPRLLIYGASSRATGIPDR 61
                                                                                                                                                                                                                                                                                                                                                                        O, Gaps
                                                 Monoclonal artibody binding to VI/V2 loop of HIV gpl20 - used in passive immuno therapy and detection of HIV infection Example; Fig 11: 366pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human monoclonal antibodies neutralising HIV - react with appl20 or gp41 and nucleic acid encoding them, useful for in vivo or in vitro diagnosis and for passive immuno-therapy Example; Page 186; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1994 (first entry)
Anti-HIV gpl20 immunoglobulin light chain variable region b6.
Human immunodeficiency virus; HIV1; glycoprotein gpl20; epitope;
neutralisation; monoclonal antibody; kappa light chain;
variable region; framework; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                 89.8%; Score 684; DB 19; Length 108; 88.7%; Pred. No. 1.50e-41; vative 7, Mismatches 5, Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 fsgssgstdftlsisrlepedfavyycqqygtspytfgqgtqldik 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 FSGSGSGTDFTLTISRLEPEDFAVYYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                          antibody and in the detection of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                 Lerner PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R54316 standard; protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCRI ) SCRIPPS RES INST.
(SCRI ) SCRIPPS RES INST
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                 Burton DP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1993; U09328.
30-SEP-1992; US-954148.
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                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                108 AA;
                               96-179601/18
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                                                                                                                                                                                                                                                                                                                                                                          94
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/label- FR1
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                 Barbas CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barbas CF,
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                     Query Match
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Blood samples were collected from patients immunised with allergens including ragweed (Ambrosia elator) extracts. The dominant allergen in short ragweed (Ambrosia elator) extracts. The dominant allergen in short ragweed (Ambrosia elator) extracts. The dominant allergen in short ragweed (Ambrosia elator) extracts. The dominant allergen then fused with mouse mylome acli line 653 and the resultant clones were screened using Amb a l protein. A single cell sublone AL 16-5.2. Secreting Amb alloaded in 165-5.2 cells and first strand cDNA was used so pred. Using oligo dT primers. When the first strand cDNA was used as the template, and the 5.2 and 3' kappa light chain primers (066540). O66541) were used in PCR and amplified band of the expected size was noted. The DNA sequence of several subclones cong. this amplified sequence and its deduced AA sequence are shown in 066538 and R56286. Comparison of the deduced that it is a member of the human VK III subgp.
                                                                                                                                                                         1 eltqspgtlslspgeratlscragqsissnylawyqqkpgqaprlliygasnratgipdr 60
                                                                                                                                                                                                    2 ELTQSPGTLSLSPGERATI.SCRASQSVSSNYI.AWYQQRPGQAPRI.LIYGASSRATGIPDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ltgspgtlslspgeratlscrasgtvssnylawyghkpggapr1lliyatsirssgipdrf 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 IJQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPRLLIYGASSRAJGIPDRF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0, Gaps
                                                                                                                               0; Gaps
clones. The light chain VK region sequence R54316 neutralises HIV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-1994 (first entry)
HSV glycoprotein F binding MAb clone rsv6/11/21/22L VH/VL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compsn. contg. allergen specific IgA for treating mucosal tissue and conjugates of allergen specific Ig with polymer, for treating IgE mediated allergies and for isolation of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light chain of Amb al-spécific 1gG4 antibody.
Allergen-specific immuoglobulin A; 1gA; AL 15-5.2; light chain;
allergen Amb a 1; ragweed; Ambrosia elator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
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Pred. No. 1.50e-41;
                                                                                    Score 584; DB 9; Length 108;
Pred. No. 1.50e-41;
                                                                                                                               5; Indels
                                                                                                                                                                                                                                                           61 fsgsgsgtdftlsisrlepedfavyycqqygtspytfgqgtqldik 106
                                                                                                                                                                                                                                                                                                      62 FSGSGSGTDFTLTISRLEPEDFAVYYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 tgsgsgtdftltisrlepedfavyycqqfrnsqwtfgqgtkveik 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           R56286 standard; Protein; 109 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TANO-) TANOX BIOSYSTEMS INC.
                                                                         Local Similarity 88.78;
les 94; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 89.8%;
Best Local Similarity 87.6%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1994.
20-DEC-1993; U12501
21-DEC-1992; US-994126.
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                                           108 AA;
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                                           Sequence
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                                                                                    Query Match
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                      gp120
                                                                                                                               Matches
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Human neutralising monoclonal antibodies to respiratory syncytial virus - for treatment prophylaxis and diagnosis of PSV and other diseases of the respiratory tract diseases of the respiratory tract.

The sequences given in R50215-19 represent the heavy and light chain variable domains of various clones of a human monoclonal antibody which binds to an epitope on qlycoprotein F of respiratory syncitial wirds (RSV) These antibodies may be used as a reagent for the diagnosis of RSV disease and other viral mucosal diseases, eq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          influenza virus, rhinovirus and coronavirus. They are particularly useful in ameliorating RSV when delivered directly to the lungs, and may also be used for treating pneumonia and bronchiolitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 aeltqspgtlslspgeratlscratqsissnylawyqqrpqqaprlliygasnratdipd 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AELTQSPGTLSLSPGEPATLSCPASQSVSSNYLAWYQQPPGQAPFLLIYGASSPATGIPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VL of Fab, DL 41 19, binds to HIV gp41.

Wheavy chain: light chain: variable region: VH: monoclonal antibody: MAD: HIV: human immunodeficiency virus: glycoprotein; gp120; clone; virus infectivity assay: precursor gp160; immunocompetence; human; anti-HIV antibody; detection: HIV infection.
Complementarity determination region; CDR3: human; bronchiolitis;
monoclonal antibody; epitope; giyroprofein E: influenza virus;
respiratory syncitial virus; RSV; disease; rhinovirus; coronavirus;
lung; pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       watch 89.5%; Score 683; DB 9; Length 109;
Local Similarity 89.7%; Pred. No. 1.78e-41;
nes 96; Conservative 6. v:--...
                                                                                                                                                                                                                                                                                                                                                                                                       Burton DR, Chanock PM, Crowe JE, Murphy BR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rfsgsgsgtdftltisrlepedfamyycqqydispytfgqqtkleik 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQLYGNSRWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                        (SCRI ) SCRIPPS RES INST.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                             Location/Qualifiers
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W01320 standard: Protein: 109 AA.
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                                                                                                                         24..35
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                                                                                                                                                                                                                                                                                                                                           16-SEP-1993; U08786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     94-118147/14.
                                                                                                                                                                                                                                                                                                                                                         16-SEP-1992;
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                                                                                                                                                                                                     'label- CDR2
                                                                                                                                                                                                                                                                  /label- CDR3
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                                                                                                                                         /label- CDR1
                                                                                                                                                                       FR2
                                                                                                                                                                                                                                   FR3
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                                                                                                                                                                                                                                                                                               FR4
                                                                                                           /label- FR1
                                                                                                                                                                                                                                                                                                                          31-MAR-1994
                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                       Barbas CF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                        label-
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immunoreactive with HIV givoprotein gp41. This sequence represents the sequence of the clone, DL 41 19. These sequences represent light chains which bind to the heavy light chain clones given in W01315-19. A monoclonal antibody containing one of these Fab sequences may have the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/mil. The MAD may be used for determining immunocompetence of a human anti-HIV antibody and in the detection of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 aeltgspgtlslspgervivscrasgsvssnylawyggkpggaprlliygasnratgipd 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AELIJOSPGTLSLSPGEPATLSCPASQSVSSNYLAWYQQPPGQAFPLLLYGASSRAIGIPD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-HIV gp41 immunoglobůlin light chain V region clone DL 41 19. Human immunodeficiency virus; HIVI, glycoprotein gp41: epirope; neutralisation; monoclonal antibody; light chain; variable region: framework region; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                        fragments (FAb's) which are
                                                                                                                                                                                                                                                           Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used spassive immuno:therapy and detection of HIV infection.

Example 3: Fig 10: 36fpp: Enallsh.

The sequences given in W01320-24 represent the light chain var.

regions (VH) of a series of antibody fragments (FAb's) which as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Rest Local Similarity 91.5%; Prod No. 3.00e-41;
Matches 98; Conservative 4; Mismatches 4: Indolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 rfsgsgsgtdftlttsrlepedfavyycggygssg-tfgggtkveik 107
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30-SEP-1992; US-954148.
(SCRI ) SCRIPPS RES INST.
Barbas CF, Burton DR, L
                                                                                                                                                                                     18-JUL-1994; US-275852
(SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                     11-JUL-1995; J08743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA;
                                                                                                                                                                                                                                   Barbas CF, Burtol
WPI; 96-179601/18
                                                       Region
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR2
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/label= CDR2
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Region
                                   /label= FR3
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                                                                                                             /label= FR4
                                                                                                                                                                                                                           Barbas CF
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WPI: 94-135515/15

3 LIQSPGILSLSPGERATLSCKASOSVSSNYLAWYOURFGQAPHLLIYGASSHAIGIPDRF 62

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                                                                                                                                                            Blue cells were transformed with the library. Filamentous phage were produced which expressed the MAb regions on their surface. Panning with gpl20 and gp41 resulted in the recovery of immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replacement of entire antibody framework regions with those of human antibodies, this method involves only the introduction of human residues into those positions not critical for antigen binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AELTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPRLLIYGASSRATGIPD 60
                                                                                                                                                                                                                                                                                                                                                                                                2 aeltqspqtlslspgervivscrasqsvssnylawyqqkpgqaprlliygasnratgipd 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies prepr. used for treatment of auto-immune diseases - by replacement of critical residues to reduce immunogenicity but retain binding affinity, etc.

Claim 2: Page 93-94: l60pp; English.

The consensus amino acid sequences for the subgroups of light chains (hKI - R38590, hK3 - NGK, hK2 - GST, hL1 - R38591, hL2 - R38592, hL3 - R38593, hL3 - R38593, hL4 - R38593, hL4 - R38599, and hL5 - R38690) of human variable domains may be used to prepare, for example, a modified mouse antibody variable domain that retains the affinity of the natural domain for antigen while exhibiting reduced
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                           clones. The light chain VL region sequence R54275 neutralises HIV1
               gp120 or gp41 and nucleic acid encoding them, useful for in vivo or in vitro diagnosis and for passive immuno-therapy claim 11; Page 215-216; 248pp; English.

Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification using primers specific for heavy and light chain variable regions. The amplification products were inserted into a dicistronic vector to produce a library of fragments. E.coli XLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This ensures that the binding properties of the modified antibody
                                                                                                                                                                                                                                                                                                                                                        4; Indels 1;
New human monoclonal antibodies neutralising HIV - react with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1993 (first entry)
Human lambda light chain subgroup 3 (hL3).
Antibody; variable domain; light; L; heavy; H; consensus; affinity; antigen; immunogenicity; humanisation; framework.
                                                                                                                                                                                                                                                                                                                 Length 109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenicity in humans.
Unlike other methods of humanisation, which advocate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 rfsgsgsgtdftltisrlepedfavyycqqygssg-tfgqgtkveik 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved in less than 50% of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (XOMA ) XOMA CORP. Fishwild DM, Kohn FR, Little RG, Studnicka GM;
                                                                                                                                                                                                                                                                                                               Score 680; DB 10;
Pred. No. 3.00e-41;
                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R38593 standard; peptide; 107 AA.
                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 91.6%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-1991; US-808464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "residue conserv
known sequences of hL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-DEC-1992; U10906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are not diminished.
                                                                                                                                                                                                                                                                       109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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regions (VL) of a series of monoclonal antibodies (MAb's) which are immunoreactive with HIV glycoprotein pp120 and are capable of meutralising HIV. This sequence represents the sequence of the JK2 gene clone, s6. A MAb containing this VL sequence has the capacity to reduce HIV infectivity titrs in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/Ml, and binds mature gp120 preferentially over the precursor gp160. The MAb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1\ \mathsf{qspgtlslspgeratlscrasqslsnnylawyqqkpgqaprlliyqsstratgipdrfsg}\ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 QSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQPPGQAPP11.1YGASSPATG1PDPFSG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 11; 366pp; English.
The sequences given in W01261-92 represent the light chain variable
                                                                                                                                                        Heavy chain; light chain; variable region; VH; monoclonal antibody; MAD; HIV; human immunodeficiency virus; qiycoprotein; qpl20; clone; virus infectivity assay; precursor qpl60; immunocompetence; human; anti:HIV antibody, detection, HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            may be used for determining immunocompetence of a human anti-HIV antibody and in the detection of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
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Anti-HIV gpl20 immunoglobulin light chain variable region s6.
Human immunodeficiency virus; HIVI; glycoprotein gpl20, epitope:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 670; DR 19; Length 104;
Pred. No. 1 70e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
63 SGSGSGIDFILIISRLEPEDFAVYYCQLYGNSRWIFGQGIKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     passive immuno:therapy and detection of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ggsgtdftltisrlepedfavyycqqygnsvytfgqgtkleik 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                            VL region of HIV neutralising MAb, clone s6.
                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                          W01279 standard; Protein; 104 AA.
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90.38;
                                                                                                                           (first entry)
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nes 93; Conservative
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(SCRI ) SCRIPPS RES INST
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                                                                                                                          29-JAN-1997
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4 ltgspgtlslspgeratlscrasgsvss-ylawyqkpgaprlllygassratgipdrf 62

Best Local Similarity 92.4%; Pred. No. 1.01e-40; Marches 97; Conservative 2; Mismatches 5; Indels 1; Gaps

Score 673; DB 7; Length 107;

88.3%;

Query Match

Ma.ches

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Example: Page 186-187: 248pp: Epglish.

Example: Page 186-187: As converted to CDNA and subjected to PCF amplification primers specific for heavy and light chain avariable regions. The amplification products were inserted into a dicistronic vector to produce a library of fragments. E. coli XLI Rlue cells were transformed with the library. Filamentous phage were produced which expressed the MAD regions on their surface. Panning with qp120 and gp41 resulted in the recovery of immunoreactive clones. The light chain VK region sequence R54317 neutralises HIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 qspqtls1spqerat1scrasqs1snnylawyqqkpqqapr111iygsstratgipdrfsg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 QSPGTLSLSPGEPATLSCPASQSVSSNYLAWYQQPPGQAPPLLIYGASSRATGIPDRFSG 64
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VL of Fab, GL 41 1, binds to HIV gp41.
VL of Fab, GL 41 1, binds to HIV gp41.
Mab, HIV, human immunodeficiency virus; glycoprotein; gp120; clone; virus infectivity assay; precursor gp160; immunocompetence; human; anti-HIV antibody; detection; HIV infection.
               variable region: framework; complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 670; DB 9; Length 104;
Pred No 1 70e-40;
7; Mismatches 3; Indels
neutralisation; monoclonal antibody; kappa light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ggsgtdftltisrlepedfavyycqqyqnsvytfgqqtkleik 103
                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   Barbas CF, Burton DR, Lerner RA;
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W01322;
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Les 93; Conservative
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(SCRI ) SCRIPPS PES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 AA;
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                             Homo sapiens.
                                                                                                                                                          CDR2
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Monoclonal antibody binding to VI/V2 loop of HIV gpl20 - used in passive immuno:therapy and detection of HIV infection.

PT Rample 3; Fig 19; 36Pp: Baplish.

The sequences given in W01220-24 represent the light chain variable regions (VH) of a series of antibody fragments (FAb's) which are Immunoreactive with HIV giveoprotein gp41. This sequence represent light chains which bind to the heavy light chain clones given in W01315-19. A monoclonal antibody containing one of these Fab sequences may have the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/m1 antibody and in the detection of HIV infection.

Sequence III AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 aeltgspgtlslspgeratlscrasgsvsngylawyggkpggaprlliygastratdipd 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AELTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPKLLIYGASSRAIGIPD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

87.9%; Score 670; DB 19; Length 111;
Best Local Similarity 87.9%; Pred. No. 1.70e-40;
Matches 94; Conservative 8; Mismatches 4; Indels 1
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                                                                                                                                                                                                Burton DR, Lerner RA;
                                                                                                                                                    18-JUL-1994; US-276852.
(SCRI ) SCRIPPS RES INST.
Barbas CF, Burton DR, I
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01-FEB-1996.
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Releas Copyri	Release 2 1D John F Collins, Riocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
MPsrch_pp prot	protein - protein database search, using Smith-Waterman algorithm
Pun on:	Tub Feb 24 07-15-25 1940. Mashar time F 37 Seconds 498.040 Million cell updates/sec
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Title: Description: Perfect Score: Sequence:	>US-08-844-215-7 (1-126) from USO8844215.pep 949 1 EVQLLESGSEVKKPGSSVKVGSCWGWFDPWGQGTLVTVSS 126
Scoring table:	PAM 150 Gap 11
Searched:	59021 soqs, 21210389 residues
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	<pre>swiss-prot34 1:part1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7 8:part8 9:part9 10:part10 11:part11</pre>

### Chacth DR ID Description Pred, No. 62.3 17 5 HV18_HUMAN IG HEAVY CHAIN VI RE 1 1040-110 56.1 17 5 HV18_HUMAN IG HEAVY CHAIN PRECUR 1.60-96 56.3 17 5 HV18_HUMAN IG HEAVY CHAIN PRECUR 1.10-92 50.4 14 5 HV18_HUMAN IG HEAVY CHAIN PRECUR 1.10-92 50.4 14 5 HV18_HUMAN IG HEAVY CHAIN PRECUR 1.10-92 47.8 140 5 HV18_MOUSE IG HEAVY CHAIN V REGI 1.90-92 47.8 140 5 HV50_MOUSE IG HEAVY CHAIN V REGI 1.90-76 46.9 120 5 HV70_MOUSE IG HEAVY CHAIN V REGI 1.90-76 46.9 130 5 HV70_MOUSE IG HEAVY CHAIN V REGI 1.90-76 46.9 130 5 HV70_MOUSE IG HEAVY CHAIN V REGI 1.90-76 46.9 130 5 HV70_MOUSE IG HEAVY CHAIN V REGI 1.90-76 46.9 130 5 HV70_MOUSE IG HEAVY CHAIN V REGI 1.45-74 45.9 117 5 HV70_MOUSE IG HEAVY CHAIN V REGI 1.46-74 45.9 117 5 HV70_MOUSE IG HEAVY CHAIN V REGI 1.46-74 45.9 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.24-74 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26-73 45.0 117 5 HV70_MOUSE IG HEAVY CHAIN PRECUR 1.26		* 01.0			SUMMARIES					
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.449; Variance 70 285; scale 0 590

Statistics:

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40	7	σ,	12	Ŋ	HV23_MOUSE	IG	HEAVY			.37e-
41	4	α.	1.1	Ľ.	HV03_CAPAU	C.	HEAVY	-	12	11e-
C .	5	œ.		ь		S	HEAVY	CHAIN	V PEGI	: Se-
43	v.	α.	F.	ư	HV37_MOUSE	C)	HEAVY	-		.02e-
44	9	ω	11	'n	HUMA	IG	HEAVY	\leftarrow		.736-
45	S	ω	11	r,	SHOW	ij	HEAVY	CHAIN		.73e-
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n 15 e 5 e 5 e 7 e A N Y	
HILA HUMAN STANDARD; PRT: 117 AA. P01742; 21-JUL-1986 (REL. 01. CAST SEQUENCE UPDATE) 21-JUL-1986 (REL. 01. LAST SEQUENCE UPDATE) 22-JUL-1986 (REL. 01. LAST SEQUENCE UPDATE) 23-SEQUENCE 24-MAXDAL M.J., EDELMAN G.M.; 24-MAXDAL M.J., EDELMAN G.M.; 25-MAXDAL M.J., EDELMAN G.M.; 26-MAXDAL M.J., EDELMAN G.M.; 27-MACHAISTRY 9:3189-3196(1970). 28-MAXDAL M.J., EDELMAN G.M.; 29-MAXDAL M.J., EDELMAN G.M.; 20-MAXDAL M.J., EDELMAN G.M.; 21-MACHAISTRY 9:3189-3196(1970). 21-MACHAISTRY 9:3189-3196(1970). 21-MACHAISTRY 9:3189-3196(1970). 21-MACHAISTRY 9:3189-3196(1970). 21-MACHAISTRY 9:3189-3196(1970). 21-MACHAISTRY 9:3189-3189-3189-3189-3189-3189-3189-3189-	
PRI: 117 AA. EQUENCE UPDATE) NOTATION UPDATE) U., GALL W.E., GOTILIEB P.D U). PYPROLIDONE CAPBOXYLIC ACID FC83E175 CRC32: SCORE 591: DB 5: Length 11' Pred. No. 1.04e-110;	Y 100
STANDARD; PRT: 117 AA. (REL. 01. CPEATED) (REL. 01. LAST SEQUENCE UPDATE) (REL. 01. LAST SEQUENCE UPDATE) (REL. 01. LAST SEQUENCE UPDATE) (RUMAN). (RIMATES. 064024. EDELMAN G.M.; EDELMAN G.M.; (Y 9:3161-3170(1970). OND. 064027. EDELMAN G.M.; Y 9:3161-3170(1970). (OND. 01. PVP LIN V REGION. 11. A. 1272 MM; FC89217D CRC32 22 96 11. A. 1272 MM; FC89217D CRC32 11. AA. 12472 MM; FC89217D CRC32 11. Mimatepes 12. Mimatepes 13. Mimatepes 14. Mimatepes 15. Mimatepes 16. Mimatepes 17. Mimatepes 18. Mimatepes 19. Mimatepes	aqkrqqrrtisooschiaymeissisedaajy Joo
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STANDARD; (REL. 01, LAS (REL. 01, LAS (REL. 01, LAS (REL. 01, LAS AIN V-1 REGIO US (HUMAN). PRIMATES. (1064024. E.A. RUTISHA (Y. 9:3161-3170 (1064027. EDELMAN G.M.; EDELMAN G.M.; Y. 9:3161-3170 (1064027. EDELMAN G.M.; Y. 9:3161-3170 (1064027. EDELMAN G.M.; Y. 9:3161-3170 (1064027. EDELMAN G.M.; EDELMAN G.M.; Y. 9:3161-3170 (1064027. EDELMAN G.M.; EDELMAN G.M.; Y. 9:3161-3170 (1064027. EDELMAN G.M.; EDELMAN G.M.; AN 9:3161-3170 (1064027. EDELMAN G.M.; EDELMAN G	TADESTATG
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MEDLINE: 88296408.
MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q., ONNO H., FUKUHARA S., HONJO T.;
EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOY-1991 (REL. 20, CREATED)
01-NOY-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOY-1991 (REL. 20, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN PRECURSOR V-I REGION (V35).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VEPTERRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION (HG3).
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                                                                                                                                                                                                                                                                                                                    Match 56.1%; Score 532; DB 5; Length 117; Local Similarity 75.3%; Pred. No. 1.15e-96; es 73; Conservative 13; Mismatches 11: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 54.3%; Score 515; DB 5; Length 117; Local Similarity 71.1%; Pred. No. 1.21e-92; es 69; Conservative 13; Mismatches 15; Indels
                                                                                                                                            MEDLINE; 83144028.

RECHAVI G., RAM D., GLAZER L., ZAKUT R., GIVOL D.; PPOC NATL ACAD. SCI. U.S.A. 80:855-859(1983).

EMBL; J00240; G553411; -. PIR; A02024; HVHUHG.

HSSP; P01810; IPVB.

IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA; 12946 MW; BCC8B1DB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.aqkfqgrvtstrdtsistaymelsrlrsddtvvyyca 116
P01743;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V-1 REGION (HG3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 117
117 AA: 13009 MW; FAA560D1 CRC32;
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PIR; S00476; HVHU35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 83144028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01810; 1FVB
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P23083;
                                                                                                                                                                                                                                                                                           SEQUENCE
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SEQUENCE
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16 qtqlvqsgaevrkpgasvrvsckasgytfidsyihwirqapghglewvgwinpnsggtny 75
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KENTEN J.H., MOLGAARD H.V., HOUGHTON M., DERBYSHIRE R B., VINEY J., BELL L.O., GOULD H.J.;
PROC. NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                           BENNICH H.H., JOHANSSON S.G O., VON BAHR-LINDSTROM H.; (IN) IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS, BACH M.K., ED., PP.1-36, MARCEL DEKKER, NEW YORK, (1978).
-1- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN. PIR. A02026; ELHUND.
HSSP; PO1607; 1FGV.
                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 486; DB 5; Length 143;
Pred. No. 8.38e-86;
28; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V PEGION (ND).
                                                                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID
                                21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V-1 REGION (ND) (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                             15
143 IG HEAVY CHAIN V PE
16 PYRPOLIDONE CARBOXY
111 T -> V (IN REF. 2).
50 IH -> HI (IN REF. 2)
121 MISSING (IN REF. 2)
143
15 16051 MW, 6D605E13 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
101-BANY CHAIN V-I REGION (MOT).
             143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 86203277.
KOJINA M., KOIDE T., ODANI S., ONO T.;
MOL. IMMUNOL. 23:169-174(1986).
PIR; A02029.
HSSP; P01772; 8FAB.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V SEGMENT
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                      IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 51.2%;
Local Similarity 54.3%;
les 70; Conservative
            STANDARD;
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                                                                                                                EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                143 AA;
                                                                                                                                                                                                    [2]
SEQUENCE OF 16-142
                                                                                                                                      SEQUENCE FROM N.A.
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T 4
HV1C_HUMAN
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NON_TER
SEQUENCE
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SIGNAL
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DISULFID
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                   SHERR PRESENTANT SCHOOL PRESEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 qvqlvqsgaevkkpgssarlsckvsqddfntydihwvrqapqralewmavvhpsddrtty 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 evglggsgaelvkagssvkmsckatgytfssyelywvrgapgggledlgyissssaypny 60
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                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
1G HEAVY CHECKSOR V REGION (93G7).
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VEPTERRATA: IETPAPODA; MAMMALLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKAPYOTA: METAZOA; CHORDATA; VEPTERPATA; TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                Score 478. DB 5. Length 125;
Pred No 5 36e-84.
26; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.5%; Score 470; DB 5: Length 114;
70.4%; Pred No 4 80e-82;
7ativo 17; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; AÖ2022; GIMSAA.
HSSP; P01772; IFGV.
IMMUNGCLOBULIN V REGION; ANTIARSONATE ANTIBODY.
10MU-TER 114 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 aqkfqqrvtitadestntaymelsslrsedtavyfcav 98
         107 D SEGMENT
1125 J SECMENT
96 BY SIMILARITY.
1125
113579 MW: 6745C023 CRC22:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKFOGRVTITADESTATGYMELSSLPSEDTAVYYCAM 98
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 AA.
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 70.4%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      64: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD
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         99 1
108 1
22 1
125 1
125 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
STRAIN-A/J;
STRAIN-A/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA: RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; PODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 llivss 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 7
HV02_MOUSE
P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 6
HV00_MOUSE
P01741;
DOMAIN
DOMAIN
DISULFID
NON_TER
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCWGWFDPWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gvgllqpgtelvkpgasvnisckasgytftsywmhwirgrpggjiewigginpsnggtny 60
                                                                                                                                                                                                                                                                                                                                                                                           20 evglqqsgaelvragssvkmsckasgytftsyginwvkqrpqqglewigyinpgngyiny 79
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLESGSEVKKPGSSVKVSCRASGGSFRSYNFNWVRQAPGGGLEWMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLLESGSEVKKPGSSVKVSCRASGGSFPSYNFNWVPDAPGGGLEWMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                 5: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                             CAFRA J.D., SCIENCE 215.309-311(1992).
EMEL: FORDAS: G19507; --
PIF: A02028: HWSG7.
HSSP: P01789; 6FAB.
IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , SIEKEVITZ M., BEYPETTHEP K., RAJEWSKY K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKAPYOTA: METAZOA; CHORDATA; VEPTEBPATA; TETPAPODA; MAMMALIA:
                              , TUCKER P.W.,
                                                                                                                                                                                                            IG HEAVY CHAIN V PEGION (93G7)
                                                                                                                                                                                                                                                                                               Query Match 47.8%; Score 454; DB 5; Length 140; Best Local Similarity 56.3%; Pred. No. 2.68e-78; Matches 71; Conservative 23; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 47.0%; Score 446; DB 5; Length 120; Best Local Similarity 53.2%; Pred. No. 1.98e-76; Matches 57; Conservative 25; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 V SEGMENT.
105 D SEGMENT.
106 D SEGMENT.
96 BY SIMILARITY.
120
1231 MW. REECOLBA CHC22:
MEDLINE, 82152819.
SIMS J., PARRITIS T H., ESTESS P., SLAUGHTEP C
                                                                                                                                                                                                                                                      15514 MW; 0700D5C8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101-JAN-198R (REL 06, CPEATED)
01-JAN-198R (REL 06, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL 21, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V PEGION (ACRR 15.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 84182519.
DILDROP P _ ROVENS J , S1
EMBO J. 3:517-523(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNOGLOBULIN V REGION
                                                                                                                                                                                                         140
                                                                                                                                                                                                                               140 140
140 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIR, A02037; MHMS15.
HSSP; P01772; 1FGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 1
22
120 1
120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 pltvss 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 8
HV50_MCUSE
P06329;
                                                                                                                                                                                                                                 NON_TER
SEQUENCE
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NON_TER
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DOMAIN
                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                              CHAIN
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61 ekfkgkttltvdkssstaymqlrsltsedsavyfcars-v-yyg-gs-y-yfdywgggtt 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 valqqsgaelvragssvkmsckasgytftsyginwvkqrpggqlewigyinpgngytkyn 60
                                                                                                                                                                                                                                                                                                                                                                                                                       2 VQLLESGSEVKKPGSSVKVSCRASGGSFRSYNFNWVRQAPGQGLEWMGGIIPMFGTANYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 81234548.
BOTHWELL A L.M , PASKIND M., PETH M , IMANISHI-KAPI T., PAJEWSKY K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION (B1-8 / 186-2).
                                                                                                                                                                                                                                                                                                                                                                     5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL 24:625-637(1981).
-:- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).
                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTERRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                       Match 46.9%; Score 445; DB 5; Length 120; Local Similarity 55.2%; Pred No. 3 39e-76; es 69; Conservative 25; Mismatches 26, Indels
                                                                                                                                                                                                                                                                     HSSP, PO1789; 6FAB.
IMMUNOGLORULIN V PEGION; ANTIARSONATE ANTIBODY; HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V PEGION (R1-8 / 186-2)
                                                                                                                                                                                                                                                                                                               120 AA; 13307 MW; BBA8CCA1 CRC32;
                                     21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                              IG HEAVY CHAIN V REGION (36-65).
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV07_MOUSE STANDARD; P P01751; P01752; 21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, J00529; G195115; -. PIR; A02034; MHMS18. HSSP; P01810; 1JHL.
               STANDAPP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                           PIR; A02028; HVMSG7.
                                                                                                                         EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; RODENTIA,
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                                                                                                                                                   SEQUENCE FROM N A MEDLINE; 83131846
                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 ltvss 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 VTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6
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            HV03_MOUSE
P01747;
                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                     Matches
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RESULT
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                                                                                                                                                                                                                                     80 nekfkskatltvdkpsstaymqlssltsedsavyycar-y-dyy--gs--syfdywqqqt 133
                                                                                                                                                                  20 gvglggpgaelvkpgasvklsckasgytftsywmhwvkgrpgrglewigridpnsggtky 79
                                                                                                                                                                                                    1 EVQLLESGSEVKKPGSSVKVSCPASGGSFPSYNFNWVPQAPGQGLEWMGGTIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 evqlqqsqpelvkpgasvkisckasgytftdyymnwvkqshqkslewigdinpnnggtsy 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIEKEVITZ M., BEYPEUTHEP K , PAJEWSKY K
                                                                                                                                     ý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAÎN V REGION (MOPC 104E).
MUS MUSCULUS (MOUSE).
BUKAPYOȚA: METAZOA, CHORDAȚA: VEPTERRATA: TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                   Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Mismatches 24; Indels
                                                                                                                                   27; Mismatiches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 441; DB 5; Length 118;
Pred. No. 2.90e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ngkfkgkatltvdksssatymelrsltsedsavyycargy 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 V SEGMENT.
104 D SEGMENT.
118 J SEGMENT.
9 BY SIMILARITY.
118
: 12934 MW; 2D1DCE77 CRC32;
                                                                                                  Score 445; DB 5; Pred. No. 3.39e-76;
                                                                  15419 MW; PEB2C7DA CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
IGH HEAVE CHAIN V REGION (AC38 205.12).
MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-UUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA
                 TH2 SEGMENT
BY SIMILARITY.
 D SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (PEL. 06, CPEATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.0%;
Matches 57; Conservative
                                                                                                  Query Match
Best Local Similarity 54.0%;
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECULIA
MEDLINE: 84182215.
DILLOPOP R., BOVENS J., ST
PARO J. 3:517-523(1984).
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMUNOGLOBULIN V REGION
124
139
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A02040; MHMS38.
HSSP, P01772, 1FGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
22
118
118 AA;
                             139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                      134 tltvss 139
                                                                                                                                                                                                                                                                                                                                    121 LVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV12_MOUSE
P01756;
                                                                                                                                     ,
68.
                                                                                                                                                                                                                                                                                                                                                                                                   HV51_MOUSE
P06330:
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SEQUENCE
                               DISULFID
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                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VOLLESGSEVKKPGSSVKVSCRASGGSFPSYNFNWVPQAPGGGLEWMGGIIPMFGTANYA 61
                                                                                                                                                                                                                                                                  1 evglggsgpelvkpgasvkmsckasgytftdyymkwvkgshgkslewigdinpnnggtsy 60
                                                                                                                                                                                                                                                                                             1 EVQLLESGSEVKKPGSSVKVSCPASGSFPSYNFNWVPQAPGQGLEWMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                    Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6:
MEDLINE: 81234548.
BOTHWELL A.L.M., PASKIND M., PETH M., IMANISHI-KARI T., PAJEMSKY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY PELATED GENES THAT COULD ENCODE V RESIONS OF NPB ANTIRODIES.
        KEHPY M R., FUHPMAN J.S., SCHILLING J W., POSEPS J., SIRLEY CHOOD L.E.;
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JUL-1986 (REL. 16, LAST ANNOTATION UPDATE)
1G HEAVIN PRECURSOR V REGION (102).
1G HEAVIN PRECURSOR V REGION (102).
EUKARYOTA: METAZOA: CHOPDATA: VERTEBRATA, TETPAFODA, MAMMALIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V PEGION (102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY - DETERMINING 1
                                                                                                                                                                                                        Score 438, DB 5; Length 117;
Pred. No. 1.45e-74;
22; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 436; DR 5; Length 117;
Pred No 4 24e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                         61 nqkfkgkatltvdkssstaymqlnsltsedsavyycardy 100
                                                                                                                                                                                                                                                                                                                                                  61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 qkfkgkatltvdkssstaymqlssltsedsavyycai 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12867 MW; 4BDD1982 CRC32;
                                                                                                                                                               117 117 117 117 117 117 AA: 12983 MW; 1F6CC304 CRC32:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                         PPT; 117 AA
                                                                                                                                       BY SIMILARITY.
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                                                                                                                       IMMUNOGLOBULIN V REGION; GLYCOPRUTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNOGLOBULIN V RFGION: SIGNAL
                                                                                                                                                                                                          Query Match
Best Local Similarity 56.0%;
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.88
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Matches 59; Conservative
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                                                                                                                                       96
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                                                                                           PIR; A02039; MHMS4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 83075344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIP; A02032
                                                                                                                                                                                                                                                                                                                                                                                                       HV06_MCUSE
P01750;
                                                                                                                                                   CARBOHYD
NON_TER
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NON_TER
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLLESGSEVKKPGSSVKVSCPASGGSFPSYNFNWVPQAPGGGLEWMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 435; DB 5; Length 117;
Pred. No. 7.25e-74;
25; Mismatches 15; Indels 0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- THE SEQUENCES OF 10 HYBPIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFEEP PROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUP IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION (VH558 A1/A4).
FRAMEWORK 1.
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                                                                                                                  MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZGA; CHGRDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MCUSE).
EURAPYOTA: METAZOA: CHOPDATA: VEPTERPATA: TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTAPITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.7%. Score 434: DB 5: Length 117; 54.0%. Pred. No. 1.24e-73, ative 23; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHILLING J', CLEVINGER B., DAVIE T M., HOOD L.;
NATURE 283-35-40(1980).
                                                                                                 IG HEAVY CHAIN PRECUPSOR V REGION (VH558 A1/A4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 96 BY SIMILARITY.
117 117
117 AA: 13024 WW: E7548ACS GRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12971 MW; A60F2B13 CPC32;
                                             01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-77L-1986 (REL. 01, CREATED)
21-37L-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V REGION (J558).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA
                 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK
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                                                                                                                                                                                                                                                   EMBL; M13787; G466291; -.
PIR: AC2029; HVMSA1.
PSSP: POLT72; IFOR.
IMMUNOSLOBULIN V REGION: SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE D AND J SEGMENTS.
--- THIS PROFILEN BINDS DEXTHAN.
PIR, A26142; MHMSJ5.
HSSP, P01789; ZFGW.
                                                                                                                                                                                                                    YANCOPOULOS G.D., ALT F.W.;
CELL 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 58.8%;
Matches 57; Conservative
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Matches 68; Conservative
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                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA
                                                                                                                                                    EUTHERIA; RODENTIA
                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 85099340.
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LT 14
HV52_MOUSE
P06327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV13_MOUSE
P01757;
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NON_TER
SEQUENCE
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